ONLINE SUPPLEMENT

Endothelial Caveolar Hub Regulation of ATP-induced eNOS Subcellular Partitioning and Domain-Specific Phosphorylation

Short title: Caveolar Hubs for ATP-induced eNOS Regulation

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EXPANDED METHODS

ATP Treatment: Protocols were approved by the University of Wisconsin-Madison Animal Care Committee [1]. Primary endothelial cell lines from three biological replicates were utilized. For the whole cell experiments, analyses were performed in duplicate. In brief, uterine arteries from pregnant ewes were dissected and the endothelial cells were isolated using collagenase digestion procedures and fluorescence activated cell sorting (FACS) to ensure they were devoid of vascular smooth muscle cell contamination. The procedure for isolation and validation of the cell lines have been described previously and consisted of performing Western analysis for PECAM, eNOS and smooth muscle myosin (negative control) [2, 3]. Further, preparations were examined for the typical endothelial cell phenotypic cobblestone morphology and were maintained in culture to passage 4 as described previously [3]. These cells were cultured on slides or T75 flasks until ~80% confluence was achieved. After a 4-h serum withdrawal, cells were treated with media with or without ATP (5 min, 100µM). The time and dose were selected based on a previously published study [4] and a preliminary time course study at 0 min, 1 min, 2.5 min, 5 min, and 10 min of ATP treatment showing peak dissociation of eNOS from the caveolar scaffolding protein cav-1 at 5 min.

Caveolar isolation, peptide digestion, and proteomic analysis: Passage 3 cells were grown to approximately 80% confluence in a T75 flask and then split (passage 4) into five T75s for each cell line. Following ATP treatment, for each cell line, the protein from the respective five T75s were pooled and then caveolar isolation was performed using discontinuous sucrose density gradient centrifugation as described previously [5, 6]. In brief, cells were collected in a 0.5 ml sodium carbonate buffer (pH 11) containing phosphatase inhibitors and protease inhibitors. A light scattering band confined to the 5-35% sucrose interface was observed when enriched with caveolar membranes. The cell suspension was homogenized and sonicated on ice. The protein concentration was measured and adjusted to same protein loading amounts between samples using the sodium bicarbonate buffer. Following this step, proteins from aliquots of caveolar fractions were extracted by precipitation with equal volume of 15% ice trichloroacetic acid, incubated 1hr on ice, and centrifuged for 10 minutes (4 °C) at 16,000 x g. Pelleted proteins were re-solubilized and denatured in 10µl of 6M Urea and 100mM NH_4HCO_3 for 10 minutes then diluted to 50 µl for digestion with 1µl of 25mM DTT, 7 µl acetonitrile, 22 µl MilliQ water and 10 µl of 20 ng/µl trypsin (Trypsin Gold, PROMEGA Inc.) in 25 mM NH_4HCO_3 [7]. Following digestion for 2 hrs at 42°C, 10 µl trypsin solution was added and incubated at 37 °C. The reaction was terminated by acidification with 2.5% trifluoroacetic acid. As described previously, peptides were analyzed by nanoLC-MS/MS using the Agilent 1100 nanoflow system (Agilent, Palo Alto, CA) connected to a hybrid linear ion trap-orbitrap mass spectrometer (LTQ-Orbitrap, Thermo Fisher Scientific, San Jose, CA) equipped with a nanoelectrospray ion source [8]. Capillary HPLC was performed using an in-house fabricated column with integrated electrospray emitter essentially [9] except for the usage of a 360 µm OD (OD = Outer Diameter) x 75 µm ID (ID = Inner Diameter) fused silica tubing. The column was packed with 5 µm C_{18} particles (Column Engineering, Ontario, CA) to approximately 12 cm. Sample loading (8 µl) and desalting were achieved using a trapping column in line with the autosampler (Zorbax 300SB-C18, 5 µM, 5 x 0.3 mm, Agilent). HPLC solvents were as follows: Loading: 1% (v/v) ACN, 0.1M acetic acid; A: 0.1M acetic acid in water, and B: 95% (v/v) acetonitrile, 0.1M acetic acid in water. Sample loading and desalting were done at 10 µL/minutes with the loading solvent delivered from an isocratic pump. Gradient elution was performed at 200 nL/minutes and increasing %B in A of 0 to 40 in 200 minutes, 40 to 60 in 20 minutes, and 60 to 100 in 5 minutes. The LTQ-Orbitrap was set to acquire MS/MS spectra in data-dependent mode as follows: MS survey scans from m/z 300 to 2000 were collected in profile mode at a resolving power of 100,000. MS/MS spectra were collected on the five most-abundant signals in each survey scan. Dynamic exclusion was employed to increase dynamic range and maximize peptide identifications. This feature excluded precursors up to 0.55 m/z below and 1.05 m/z above previously selected precursors. Precursors remained on the exclusion list for 15 seconds. Singly-charged ions and ions for which the charge state could not be assigned were rejected from consideration for MS/MS. Tandem mass spectra were extracted, charge state deconvoluted and deisotoped by BioWorks version 3.1. Raw MS/MS data were searched against NCBI non-redundant *Bos taurus* amino acid sequence database (Bos_taurus_020209; 64765 entries; for trypsin digestion) using in-house *Sequest* search engine (ThermoFinnigan, San Jose, CA; version 28, rev. 13) with a fragment ion mass tolerance of 0.50 Da, a parent ion tolerance of 2.5 Da and methionine oxidation as variable modification [10-12]. We utilized the *Bos taurus* database as there exists a close morphological-paleontological and immunological phylogentic relationship as well as a mere 2.92 ± 0.08% difference in the gene positions between the sheep and cow [13, 14]. Scaffold (version 2.06.02; Proteome Software Inc., Portland, OR) was used to validate MS/MS based peptide and protein identifications. Peptide identifications were accepted if they could be established at a probability of $P < 0.05$ as specified by the Peptide Prophet algorithm [15]. Protein identifications were accepted if they could be established at probability $P < 0.05$ and contained at least ‘two’ identified peptides. Protein probabilities were assigned by the Protein Prophet algorithm [16]. Proteins that contained similar peptides and could not be differentiated based on MS/MS analysis alone were grouped to satisfy the principles of parsimony. An estimate of protein enrichment was determined by using a normalized spectral count method similar to that described and validated recently by Stevenson and coworkers [17]. As described previously, counted spectra are provided by Scaffold in five different forms: 1) unique peptides, 2) unique spectra, 3) number of identified spectra and 4) percent of total spectra, and 5) unweighted spectral counts [8, 17]. In addition to these, the Scaffold software version 2.06.02 provides a more sophisticated parameter called quantitative value to estimate protein enrichment and is derived from averaging the spectrum counts across biosamples within groups, followed by averaging the spectral counts between groups, and then multiplying the spectrum counts in each group by the average divided by the individual biosample. Commonly observed impurities (keratins) and any protein (hemoglobin and unnamed protein) not found in standard endothelial caveolar analyses were not included for categorization. Manual classification was performed to identify the association of the proteins with nitric oxide based on previously published manuscripts. ATP transporters, ATPases, and ATP synthases were classified as ATP-related proteins. To our knowledge, the proteins that were not associated with NO or ATP were further sub classified into various cellular processes. In cases of very little information on the specific protein isoform and its relationship with NO, proteins were classified based on publications on the protein family.

Immunoisolation: Endothelial cells were lysed with a buffer containing 4 mM sodium pyrophosphate, 50 mM 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid, 100 mM sodium chloride, 10 mM ethylenediaminetetraacetic acid, 10 mM sodium fluoride, 2mM sodium orthovanadate, 2 mM phenylmethanesulfonylfluoride, 1% V/V Triton X-100, 5 ug/ml aprotinin, 5ug/ml leupeptin, and 1ug/ml microcystin, pH 7.4. Lysates were loaded with beads (Carbolink Immobilization kit; Pierce, Rockford, IL) coupled to anti-cav-1 antibody (Cell Signaling Tech. Inc.). The cav-1 bound fraction was subsequently eluted according to manufacturer’s instructions.

Immunoblotting: Solubilized protein was quantified using a modified Lowry assay procedure (Bio-Rad Laboratories, Inc., Hercules, CA), and equal volume or mass of protein were separated by size on 4-20% polyacrylamide gels (150 V, 42 min; Mini Protean II, Bio-Rad Laboratories, Inc.) alongside Rainbow molecular weight markers (Bio-Rad Laboratories, Inc.) before transfer to Immobilon P membranes (100 V, 1 h). The Immobilon P membranes were probed using the enhanced chemiluminescence reagent detection system, as described by Amersham Pharmacia Biotech (Arlington

Heights, IL), and exposed to Hyperfilm (Amersham Pharmacia Biotech). Antibodies to cav-1 and GAPDH were obtained from Cell Signaling Technologies Inc., total eNOS from BD Transduction laboratories, and all phosphorylated eNOS antibodies from Millipore Inc with the exception of Ser1179 (Cell Signaling Tech. Inc.).

Statistics: Effects of ATP on subcellular distribution were analyzed using a two-way mixed ANOVA with treatment group as between factor and subcellular compartment as within factor. When appropriate, an analysis of simple effect was performed using one-way ANOVA. Further pairwise comparisons were performed when appropriate using Bonferroni or Fisher's protected least significant difference. For immunoisolation data, Student's T test was utilized to compare Control and ATP treatment groups. Level of significance was established at $P < 0.05$ *a priori*. $0.05 < P < 0.1$ were considered statistical trends.

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Database Name: the Bos_taurus_020209 database
Version: unknown
Taxonomy: All Entries
Number of Proteins: 64765

Search Engine: Sequest
Version: 27, rev. 13
Samples: All Samples
Fragment Tolerance: 0.50 Da (Monoisotopic)
Parent Tolerance: 2.5 Da (Monoisotopic)
Fixed Modifications:
Variable Modifications: +16 on M (Oxidation)
Database: the Bos_taurus_020209 database (unknown version, 64765 entries)
Digestion Enzyme: Non-specific
Max Missed Cleavages: 2

Peptide Thresholds: 95.0% minimum
Protein Thresholds: 95.0% minimum and 2 peptides minimum

Group	Subject	Protein Name	Protein accession numbers	Protein molecular weight (Da)	Protein identification probability	# unique peptides	# unique spectra	# total spectra	% total spectra	% sequence coverage	Peptide sequence	Best SEQUEST XCorr score	Calculated +1H Peptide Mass (AMU)
Control	6006	TIMM23 protein	gi|134025149,gi|139947578,gi|215274655	21,809.90	99.80%	2	2	2	0.02%	12.90%	NVQILNMVTR	3.24	1,203.65
Control	6006	TIMM23 protein	gi|134025149,gi|139947578,gi|215274655	21,809.90	99.80%	2	2	2	0.02%	12.90%	YLVQDTDEFILPTGANK	3.51	1,923.97
Control	6006	Chain B, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591027,gi|110591030,gi|114686,gi|27807305,gi|599873,gi|74356487	18,544.10	100.00%	2	2	2	0.02%	7.50%	IQEYEKELEK	2.97	1,308.67
Control	6006	Chain B, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591027,gi|110591030,gi|114686,gi|27807305,gi|599873,gi|74356487	18,544.10	100.00%	2	2	2	0.02%	7.50%	IQEYEKELEKMR	2.32	1,611.80
Control	6006	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	10	16	0.17%	9.24%	DLDGNGYPDLIVGSFGVDK	3.83	1,980.96

Control	6006	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	10	16	0.17%	9.24%	DVPGRSPASSGPQILK	3.56	1,608.87
Control	6006	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	10	16	0.17%	9.24%	LAGMEPTPTLTLTGQDEFGR	4.84	2,150.04
Control	6006	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	10	16	0.17%	9.24%	QATLTQTLLIQNGAR	3.93	1,627.91
Control	6006	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	10	16	0.17%	9.24%	TIQFDFQILSK	3.11	1,339.73
Control	6006	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	10	16	0.17%	9.24%	VTAPPEAEYSGLVR	5.3	1,488.77
Control	6006	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	10	16	0.17%	9.24%	VYIYLQR	2.74	954.5407

Control	6006	PREDICTED: similar to EGF-like repeats and discoidin I-like domains 3	gi|119895885	52,071.20	100.00%	2	2	2	0.02%	7.96%	GTNEDMVFHGNVDNNTPYANSFTPPIK	3.51	2,995.35
Control	6006	PREDICTED: similar to EGF-like repeats and discoidin I-like domains 3	gi|119895885	52,071.20	100.00%	2	2	2	0.02%	7.96%	NVIDPPIYAR	2.26	1,157.63
Control	6006	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	4	7	12	0.13%	29.20%	AMAEEMNEKQVYDAHTK	2.68	2,010.89
Control	6006	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	4	7	12	0.13%	29.20%	ASFTTFTVTK	2.4	1,102.58
Control	6006	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	4	7	12	0.13%	29.20%	YVDSEGHLYTVPIR	2.79	1,648.83
Control	6006	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	4	7	12	0.13%	29.20%	YVDSEGHLYTVPIREQGNIYKPNNK	5.87	2,934.47
Control	6006	RTN3 protein	gi|115305093,gi|122132179,gi|146231798,gi|151554368,gi|32880223,gi|38327594	25,478.60	99.80%	2	4	4	0.04%	5.49%	TQIDHYVGIAR	3.66	1,272.67
Control	6006	RTN3 protein	gi|115305093,gi|122132179,gi|146231798,gi|151554368,gi|32880223,gi|38327594	25,478.60	99.80%	2	4	4	0.04%	5.49%	YKTQIDHYVGIAR	3.15	1,563.83
Control	6006	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	5	6	7	0.08%	20.10%	DNFHGLAIFLDTYPNDETTER	2.95	2,468.14
Control	6006	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	5	6	7	0.08%	20.10%	DNVDDPTGNFR	3.17	1,249.54

Control	6006	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	5	6	7	0.08%	20.10%	LPTGYYFGASAGTGDLSDNHDIISMK	5.15	2,746.27
Control	6006	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	5	6	7	0.08%	20.10%	NRDHDTFLAVR	3.09	1,343.68
Control	6006	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	5	6	7	0.08%	20.10%	SPKDNVDDPTGNFR	4.43	1,561.72
Control	6006	LOC789567 protein	gi|148878411,gi|155372329	34,911.10	99.80%	2	2	2	0.02%	4.81%	SQDKLNQVSSEIR	2.93	1,503.78
Control	6006	LOC789567 protein	gi|148878411,gi|155372329	34,911.10	99.80%	2	2	2	0.02%	4.81%	SQDKLNQVSSEIREK	5.03	1,760.91
Control	6006	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	4	4	4	0.04%	8.93%	EIILVDDYSNDPEDGALLGK	3.09	2,176.07
Control	6006	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	4	4	4	0.04%	8.93%	EIILVDDYSNDPEDGALLGKIEK	3.36	2,546.29
Control	6006	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	4	4	4	0.04%	8.93%	NKFNQVESDKLR	3.43	1,477.78
Control	6006	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	4	4	4	0.04%	8.93%	QHPYTFPGGSGTVFAR	3.83	1,721.84
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	ADIGVAMGIAGSDVSK	3.47	1,506.75
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	AVAGDASESALLK	4.46	1,231.65

Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	AVFQANQDNLPILK	3.1	1,570.86
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	AVFQANQDNLPILKR	2.18	1,726.96
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	EQPLDEELKDAFQNAYLELGGLGER	3.89	2,834.38
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	EVSMDDHKLSLDELHR	1.93	1,939.92
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	EVSMDDHKLSLDELHRK	2.87	2,068.01
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	GVGIISEGNETVEDIAAR	4.85	1,829.92
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	IVEIPFNSTNK	2.63	1,261.68
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	KADIGVAMGIAGSDVSK	4.9	1,634.84
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	LNIPVSQVNPR	4.13	1,236.71
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	LSLDELHR	2.38	982.5317

Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	LSLDELHRK	2.04	1,110.63
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	MSINAEEVVVGDLVEVK	4.37	1,846.95
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	NMVPQQALVIR	2.27	1,284.71
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	QAADMILLDDNFASIVTGVEEGR	3.44	2,480.20
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	QAADMILLDDNFASIVTGVEEGRLIFDNLKK	3.49	3,435.78
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	QGAIVAVTGDGVNDSPALK	3.62	1,811.95
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	QGAIVAVTGDGVNDSPALKK	3.89	1,940.05
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	SPDFTNENPLETR	4.11	1,519.70
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	VDNSSLTGESEPQTR	3.66	1,619.75
Control	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	22	35	53	0.58%	24.10%	VIMVTGDHPITAK	4.24	1,397.75

Control	6006	PREDICTED: similar to C4b-binding protein alpha chain precursor (C4bp) (Proline-rich protein) (PRP)	gi|76677514	21,762.00	99.80%	2	3	3	0.03%	15.40%	LSLEIEKLEQEKR	3.11	1,614.91
Control	6006	PREDICTED: similar to C4b-binding protein alpha chain precursor (C4bp) (Proline-rich protein) (PRP)	gi|76677514	21,762.00	99.80%	2	3	3	0.03%	15.40%	LSVEKDQYVSPETVTVR	3.62	1,950.02
Control	6006	COL18A1 protein	gi|133778103,gi|134085613,gi|157742960	135,049.70	99.80%	2	2	2	0.02%	2.33%	LFVAQAGGADPEKFQGLISELR	4.05	2,346.25
Control	6006	COL18A1 protein	gi|133778103,gi|134085613,gi|157742960	135,049.70	99.80%	2	2	2	0.02%	2.33%	LQDLYSIVR	2.88	1,106.62
Control	6006	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	3	3	3	0.03%	28.40%	AFDLLVDRPVTLVR	2.54	1,613.94
Control	6006	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	3	3	3	0.03%	28.40%	AYQDRYHDLGAHYSAR	2.24	1,922.89
Control	6006	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	3	3	3	0.03%	28.40%	RTPAPSPQTSLPNPITYLTK	2.74	2,182.19
Control	6006	ribosomal protein L18	gi|59858459,gi|62752012,gi|75060915,gi|75775560,gi|89573893	21,518.10	100.00%	3	4	4	0.04%	18.10%	ILTFDQLALDSPK	3.13	1,460.80
Control	6006	ribosomal protein L18	gi|59858459,gi|62752012,gi|75060915,gi|75775560,gi|89573893	21,518.10	100.00%	3	4	4	0.04%	18.10%	TNRPPLSLSR	3.01	1,140.65
Control	6006	ribosomal protein L18	gi|59858459,gi|62752012,gi|75060915,gi|75775560,gi|89573893	21,518.10	100.00%	3	4	4	0.04%	18.10%	TNSTFNQVVLK	2.86	1,250.67

Control	6006	RecName: Full=Isocitrate dehydrogenase [NADP], mitochondrial; Short=IDH; AltName: Full=Oxalosuccinate decarboxylase; AltName: Full=NADP(+)-specific ICDH; AltName: Full=IDP; AltName:	gi|109891934,gi|28461205,gi|430,gi|73587323	50,807.00	99.80%	2	2	2	0.02%	5.97%	LIDDMVAQVLK	2.59	1,260.69
Control	6006	RecName: Full=Isocitrate dehydrogenase [NADP], mitochondrial; Short=IDH; AltName: Full=Oxalosuccinate decarboxylase; AltName: Full=NADP(+)-specific ICDH; AltName: Full=IDP; AltName:	gi|109891934,gi|28461205,gi|430,gi|73587323	50,807.00	99.80%	2	2	2	0.02%	5.97%	LNEHFLNTSDFLDTIK	3.51	1,906.95
Control	6006	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	3	6	8	0.09%	5.54%	HTLGENIADNGGLK	3.91	1,438.73

Control	6006	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	3	6	8	0.09%	5.54%	RRDEELIYHK	2.12	1,358.72
Control	6006	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	3	6	8	0.09%	5.54%	TPESSHEGLITDPHSPSR	4.42	1,946.92
Control	6006	RecName: Full=Citrate synthase, mitochondrial; Flags: Precursor	gi|109820508,gi|113461977,gi|88954189	51,755.90	99.80%	2	2	2	0.02%	5.79%	GLVYETSVLDPDEGIR	2.67	1,762.89
Control	6006	RecName: Full=Citrate synthase, mitochondrial; Flags: Precursor	gi|109820508,gi|113461977,gi|88954189	51,755.90	99.80%	2	2	2	0.02%	5.79%	IVPNILLEQGK	2.19	1,223.74
Control	6006	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	5	5	6	0.07%	23.50%	KGHAAPTPTPVKPPR	2.72	1,553.89
Control	6006	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	5	5	6	0.07%	23.50%	LATMLETLR	2.56	1,063.58
Control	6006	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	5	5	6	0.07%	23.50%	LEANHGLLVAR	3.35	1,192.68
Control	6006	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	5	5	6	0.07%	23.50%	RIQSNLGALSR	3.93	1,214.70
Control	6006	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	5	5	6	0.07%	23.50%	SHDTTSNTLAQLLAK	4.48	1,599.83
Control	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	13	23	83	0.90%	62.10%	DNIQGITKPAIR	3.57	1,325.75

Control	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	13	23	83	0.90%	62.10%	DNIQGITKPAIRR	2.67	1,481.85
Control	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	13	23	83	0.90%	62.10%	ISGLIYEETR	4.27	1,180.62
Control	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	13	23	83	0.90%	62.10%	ISGLIYEETRGVLK	3.02	1,577.89
Control	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	13	23	83	0.90%	62.10%	KTVTAMDVVYALK	3.93	1,454.79
Control	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	13	23	83	0.90%	62.10%	KTVTAMDVVYALKR	5.56	1,610.89
Control	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	13	23	83	0.90%	62.10%	RISGLIYEETR	2.56	1,336.72
Control	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	13	23	83	0.90%	62.10%	RKTVTAMDVVYALK	3.67	1,610.89

Control	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	13	23	83	0.90%	62.10%	TVTAMDVVYALK	3.92	1,326.70
Control	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	13	23	83	0.90%	62.10%	TVTAMDVVYALKR	3.35	1,482.80
Control	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	13	23	83	0.90%	62.10%	VFLENVIR	3.28	989.5778
Control	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	13	23	83	0.90%	62.10%	VFLENVIRDAVTYTEHAK	6.18	2,105.10
Control	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	13	23	83	0.90%	62.10%	VLRDNIQGITKPAIR	4.47	1,694.01
Control	6006	RecName: Full=Cleft lip and palate transmembrane protein 1 homolog	gi|110278913,gi|114051439,gi|84708720	75,864.60	100.00%	3	3	4	0.04%	4.63%	ALNTFIDDLFAFVIK	3.57	1,726.94
Control	6006	RecName: Full=Cleft lip and palate transmembrane protein 1 homolog	gi|110278913,gi|114051439,gi|84708720	75,864.60	100.00%	3	3	4	0.04%	4.63%	NLLTGETEADPEMIK	3.43	1,676.81

Control	6006	RecName: Full=Cleft lip and palate transmembrane protein 1 homolog	gi|110278913,gi|114051439,gi|84708720	75,864.60	100.00%	3	3	4	0.04%	4.63%	NLLTGETEADPEMIKR	2.28	1,832.91
Control	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	15	16	0.17%	21.00%	ALEHHRSEIQAEQDR	3.32	1,818.88
Control	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	15	16	0.17%	21.00%	ATEKQHIALALEK	2.46	1,451.82
Control	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	15	16	0.17%	21.00%	AVDEAADALLK	2.79	1,115.59
Control	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	15	16	0.17%	21.00%	KAVDEAADALLK	3.2	1,243.69
Control	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	15	16	0.17%	21.00%	LAEQELQFR	2.44	1,133.60
Control	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	15	16	0.17%	21.00%	LAQQEKQEQVKIESLAK	5.25	1,970.09
Control	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	15	16	0.17%	21.00%	MKTASADLPTVPLGSAVEAIR	2.68	2,143.14
Control	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	15	16	0.17%	21.00%	QHIALALEK	4.55	1,022.60
Control	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	15	16	0.17%	21.00%	SVIENAKKEEVAGAK	4.87	1,572.86
Control	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	15	16	0.17%	21.00%	TASADLPTVPLGSAVEAIR	4.26	1,868.01
Control	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	15	16	0.17%	21.00%	TDHPETGEGKPKPATSEAASSTSVR	3.15	2,598.23
Control	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	15	16	0.17%	21.00%	VQEQELKYEFEQDLSEKLAEQELQFR	3.44	3,256.60

Control	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	15	16	0.17%	21.00%	VVSQYHELVVQAR	4.38	1,527.83
Control	6006	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	3	5	6	0.07%	13.50%	GLFTGLTPR	2.76	961.5467
Control	6006	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	3	5	6	0.07%	13.50%	SAATLITHPFHVITLR	3.3	1,777.01
Control	6006	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	3	5	6	0.07%	13.50%	VLIQVGYEPLAPTVGR	4.43	1,711.97
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	AAALRPEEDGAFRPSEAFETLQK	3.81	2,533.27
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	AEESAAHLPEEIR	2.97	1,451.71
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	AEESAAHLPEEIRR	2.41	1,607.81
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	AEESAAHLPEEIRRLEEELGQLK	3.66	2,647.37
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	ALKEVVKEIQTSVK	3.8	1,571.94

Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	ASVGQVESDLK	3.63	1,132.58
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	ASVGQVESDLKMLR	3.55	1,548.81
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	DFTSLENTVEERLTELTK	2.44	2,125.07
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	DLSDGIHVVK	1.71	1,082.58
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	ELVSLKQEQQR	3.93	1,357.74
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	ERDFTSLENTVEER	4.86	1,724.81
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	ERDFTSLENTVEERLTELTK	3.02	2,410.21
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	EVVKEIQTSVK	3.33	1,259.72

Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	FKEAADSEHHTLQALTEK	4.24	2,055.01
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	GLGEAQLSLAGDVDELKR	3.67	1,870.99
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	GLLEDLRNDLDR	1.96	1,428.74
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	GLLEDLRNDLDRLFVK	2.95	1,916.06
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	IETNENNLESAK	2.28	1,361.65
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	ILRAEESAAHLPEEIR	3.38	1,833.98
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	KPPPAPQQHPPPPAPHPQQQHPPQHPQNQAHGK	2.47	3,630.83
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	LEEELGQLK	2.98	1,058.57

Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	LQNEILKDLSDGIHVVK	4.09	1,921.08
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	LQNEILKDLSDGIHVVKDAR	5.16	2,263.24
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	LQSVEDGVQAAR	4.17	1,272.65
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	QREELGQGLQGVEQK	5.54	1,698.88
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	RLEEELGQLK	3.24	1,214.67
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	SINDNIAIFTDVQK	3.96	1,577.82
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	SINDNIAIFTDVQKR	5.06	1,733.92
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	STIQTMESDVYTEVK	3.31	1,746.81

Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	STIQTMESDVYTEVKELVSLKQEQQR	4.33	3,085.54
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	TAVDSLVAYSVK	3.23	1,252.68
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	VQEQVHTLLGR	4.07	1,279.71
Control	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	33	58	77	0.84%	54.50%	VQSLQATFGTFESLVR	3.85	1,782.94
Control	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	10	12	19	0.21%	46.30%	AATFGLILDDVSLTHLTFGKEFTEAVEAK	3.36	3,123.63
Control	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	10	12	19	0.21%	46.30%	DLQNVNITLR	3.74	1,185.66
Control	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	10	12	19	0.21%	46.30%	FDAGELITQR	3.4	1,149.59
Control	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	10	12	19	0.21%	46.30%	IFTSIGEDYDER	3.75	1,444.66
Control	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	10	12	19	0.21%	46.30%	IFTSIGEDYDERVLPSITTEILK	3.58	2,639.38
Control	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	10	12	19	0.21%	46.30%	ILFRPVASQLPR	2.6	1,396.84
Control	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	10	12	19	0.21%	46.30%	KLEAAEDIAYQLSR	3.21	1,606.84
Control	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	10	12	19	0.21%	46.30%	NITYLPAGQSVLLQLPQ	3.44	1,855.03
Control	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	10	12	19	0.21%	46.30%	NVPVITGSKDLQNVNITLR	3.75	2,081.17

Control	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	10	12	19	0.21%	46.30%	SRNITYLPAGQSVLLQLPQ	4.67	2,098.17
Control	6006	ras-related C3 botulinum toxin substrate 1	gi|27806443,gi|51702785,gi|6007014,gi|73587375	21,432.60	100.00%	3	4	4	0.04%	14.10%	KLTPITYPQGLAMAK	3.06	1,647.91
Control	6006	ras-related C3 botulinum toxin substrate 1	gi|27806443,gi|51702785,gi|6007014,gi|73587375	21,432.60	100.00%	3	4	4	0.04%	14.10%	LDLRDDKDTIEK	2.78	1,460.76
Control	6006	ras-related C3 botulinum toxin substrate 1	gi|27806443,gi|51702785,gi|6007014,gi|73587375	21,432.60	100.00%	3	4	4	0.04%	14.10%	LTPITYPQGLAMAK	3.42	1,519.82
Control	6006	Interferon induced transmembrane protein 1 (9-27)	gi|112362418,gi|118151192,gi|118151350,gi|118151354,gi|119919513,gi|14279576,gi|14279578,gi|148744152,gi|32480628,gi|73586549,gi|73587371	13,631.00	99.80%	2	3	3	0.03%	13.70%	KMVGDITGAQSYASTAK	2.88	1,743.86
Control	6006	Interferon induced transmembrane protein 1 (9-27)	gi|112362418,gi|118151192,gi|118151350,gi|118151354,gi|119919513,gi|14279576,gi|14279578,gi|148744152,gi|32480628,gi|73586549,gi|73587371	13,631.00	99.80%	2	3	3	0.03%	13.70%	MVGDITGAQSYASTAK	4.5	1,615.76
Control	6006	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	4	4	4	0.04%	26.90%	ALAAAGYDVEK	3.13	1,107.57

Control	6006	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	4	4	4	0.04%	26.90%	ALAAAGYDVEKNNSR	3.5	1,578.79
Control	6006	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	4	4	4	0.04%	26.90%	ASGPPVSELITK	2.21	1,198.67
Control	6006	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	4	4	4	0.04%	26.90%	KALAAAGYDVEKNNSR	4.18	1,706.88
Control	6006	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	4	4	5	0.05%	17.50%	ILHVNGFNGEGGEEDPQAAR	3.6	2,110.00
Control	6006	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	4	4	5	0.05%	17.50%	LLLLGAGESGK	3.48	1,057.63
Control	6006	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	4	4	5	0.05%	17.50%	SKIEDYFPEFAR	2.24	1,501.73
Control	6006	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	4	4	5	0.05%	17.50%	VLTSGIFETK	2.78	1,094.61
Control	6006	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	4	4	5	0.05%	17.50%	YTTPEDATPEPGEDPR	2.31	1,774.78
Control	6006	PREDICTED: similar to Transmembrane 9 superfamily member 2 precursor (p76), partial	gi|194671915	72,962.00	99.80%	2	3	3	0.03%	5.19%	HTHIDKPDCSGPPMDISNK	3.61	2,107.95
Control	6006	PREDICTED: similar to Transmembrane 9 superfamily member 2 precursor (p76), partial	gi|194671915	72,962.00	99.80%	2	3	3	0.03%	5.19%	IYYHVVETGSMGAR	3.5	1,598.76

Control	6006	RecName: Full=60S acidic ribosomal protein P0; AltName: Full=L10E	gi|108935888,gi|2293577,gi|59858525,gi|60592767	34,353.40	99.80%	2	2	2	0.02%	6.92%	IIQLLDDYPK	3.31	1,217.68
Control	6006	RecName: Full=60S acidic ribosomal protein P0; AltName: Full=L10E	gi|108935888,gi|2293577,gi|59858525,gi|60592767	34,353.40	99.80%	2	2	2	0.02%	6.92%	TSFFQALGITTK	3.51	1,313.71
Control	6006	RPL12 protein	gi|148744191,gi|42564206,gi|45430019,gi|47117092,gi|74354972	17,801.10	99.80%	2	2	2	0.02%	15.20%	IGPLGLSPK	2.32	881.5457
Control	6006	RPL12 protein	gi|148744191,gi|42564206,gi|45430019,gi|47117092,gi|74354972	17,801.10	99.80%	2	2	2	0.02%	15.20%	QAQIEVVPSASALIIK	3.13	1,666.97
Control	6006	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	gi|111304648,gi|115496338,gi|121957506	27,838.90	99.80%	2	2	3	0.03%	11.20%	FKGPFTDVVTTNLK	3.88	1,566.85
Control	6006	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	gi|111304648,gi|115496338,gi|121957506	27,838.90	99.80%	2	2	3	0.03%	11.20%	GPFTDVVTTNLK	3.85	1,291.69
Control	6006	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	gi|111304648,gi|115496338,gi|121957506	27,838.90	99.80%	2	2	3	0.03%	11.20%	HEQILVLDPPTDLK	3	1,617.89

Control	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	15	16	17	0.19%	26.40%	AIMAQLPQEQK	2.66	1,272.66
Control	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	15	16	17	0.19%	26.40%	ALKPEVDKLNIMAAK	2.71	1,656.94
Control	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	15	16	17	0.19%	26.40%	ESQFLKEELVAAVEDVRK	4.43	2,090.11
Control	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	15	16	17	0.19%	26.40%	GKGPLKNTSDVISAAK	2.91	1,585.89
Control	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	15	16	17	0.19%	26.40%	HVNPVQALSEFKAMDSI	3.72	1,901.94
Control	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	15	16	17	0.19%	26.40%	IAEQVASFQEEK	3.84	1,378.68
Control	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	15	16	17	0.19%	26.40%	LLEPLVTQVTTLVNTNSK	3.5	1,970.12
Control	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	15	16	17	0.19%	26.40%	LLILADMADVYK	2.36	1,380.74
Control	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	15	16	17	0.19%	26.40%	NAGTEQDLGIQYK	3.35	1,436.70
Control	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	15	16	17	0.19%	26.40%	NLMNAVVQTVK	3.12	1,232.67
Control	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	15	16	17	0.19%	26.40%	QALQDLLSEYMGNAGRK	3.06	1,909.94
Control	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	15	16	17	0.19%	26.40%	QIIVDPLSFSEER	2.58	1,532.80
Control	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	15	16	17	0.19%	26.40%	TSVQTEDDQLIAGQSAR	2.58	1,818.88
Control	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	15	16	17	0.19%	26.40%	VIHVVTSEMDNYEPGVYTEK	3.76	2,326.09

Control	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	15	16	17	0.19%	26.40%	VLTDAVDDITSIDDFLAVSENHILEDVNK	3.28	3,200.58
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	AKFEELNMDLFR	4.61	1,528.75
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	DAGTIAGLNVMR	3.35	1,233.63
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	ELEEIVQPIISK	3.44	1,397.79
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	FEELNMDLFR	2.74	1,329.61
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	IDTRNELESYAYSLK	4.84	1,801.90
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	IINEPTAAAIAYGLDKR	4.1	1,816.00
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	ITITNDQNRLTPEEIER	3.19	2,042.05
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	ITPSYVAFTPEGER	3.83	1,566.78

Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	KKELEEIVQPIISK	4.71	1,653.98
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	KSQIFSTASDNQPTVTIK	3.8	1,965.03
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	KVTHAVVTVPAYFNDAQR	3.09	2,016.07
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	MVNDAEKFAEEDKK	2.8	1,669.77
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	NELESYAYSLK	3.19	1,316.64
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	NQLTSNPENTVFDAK	3.44	1,677.81
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	NQLTSNPENTVFDAKR	2.75	1,833.91
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	SQIFSTASDNQPTVTIK	4.18	1,836.93

Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	TFAPEEISAMVLTK	2.94	1,552.79
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	TKPYIQVDVGGGQTK	3.68	1,590.85
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	VLEDSDLKKSDIDEIVLVGGSTR	4.39	2,488.31
Control	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	32	37	0.40%	33.40%	VTHAVVTVPAYFNDAQR	3.45	1,887.97
Control	6006	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	4	4	4	0.04%	7.52%	LLNDEDPVVVTK	3.07	1,341.73
Control	6006	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	4	4	4	0.04%	7.52%	LNTIPLFVQLLYSSVENIQR	3.24	2,347.30
Control	6006	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	4	4	4	0.04%	7.52%	LVQLLVK	2.35	812.5605

Control	6006	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	4	4	4	0.04%	7.52%	NLSDVATKQEGLESVLK	2.64	1,830.98
Control	6006	PREDICTED: similar to histone, H2A	gi|76651181,gi|76689692	14,148.10	99.80%	2	3	4	0.04%	35.40%	AGLQFPVGR	3.1	944.5313
Control	6006	PREDICTED: similar to histone, H2A	gi|76651181,gi|76689692	14,148.10	99.80%	2	3	4	0.04%	35.40%	HLQLAIRNDEELNKLLGR	4.53	2,132.19
Control	6006	PREDICTED: similar to histone, H2A	gi|76651181,gi|76689692	14,148.10	99.80%	2	3	4	0.04%	35.40%	NDEELNKLLGR	3.2	1,300.69
Control	6006	PREDICTED: similar to histone, H2A	gi|76651181,gi|76689692	14,148.10	99.80%	2	3	4	0.04%	35.40%	VTIAQGGVLPNIQAVLLPK	4.93	1,931.17
Control	6006	syntaxin 7	gi|118150840,gi|122140829,gi|73586654	29,638.60	99.80%	2	2	2	0.02%	10.70%	EFGSLPTTPSDQR	3.28	1,434.69
Control	6006	syntaxin 7	gi|118150840,gi|122140829,gi|73586654	29,638.60	99.80%	2	2	2	0.02%	10.70%	TLNQLGTPQDSPELR	3.55	1,668.86
Control	6006	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	4	4	4	0.04%	19.60%	GDLLFLTNRVEDPIR	3.31	1,757.95
Control	6006	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	4	4	4	0.04%	19.60%	GDLLFLTNRVEDPIRVGEIVVFR	2.42	2,657.48
Control	6006	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	4	4	4	0.04%	19.60%	MLSLDFLDDVRR	1.88	1,495.76
Control	6006	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	4	4	4	0.04%	19.60%	VGEIVVFR	2.83	918.5407
Control	6006	PREDICTED: brain protein 44	gi|119889010,gi|194665199	14,264.40	99.80%	2	3	3	0.03%	18.90%	LRPLYNHPAGPR	3.07	1,390.77
Control	6006	PREDICTED: brain protein 44	gi|119889010,gi|194665199	14,264.40	99.80%	2	3	3	0.03%	18.90%	VLDKVELLLPEK	3.57	1,395.85

Control	6006	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	5	5	7	0.08%	9.44%	FTGLSKEELLK	3.74	1,264.71
Control	6006	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	5	5	7	0.08%	9.44%	LLIAGTDSSDLQQILR	3.59	1,742.97
Control	6006	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	5	5	7	0.08%	9.44%	SVSEDRLLIAGTDSSDLQQILR	3.58	2,416.27
Control	6006	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	5	5	7	0.08%	9.44%	VDLLLSTQPGR	3.33	1,198.68
Control	6006	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	5	5	7	0.08%	9.44%	VILDLTPNYK	3.31	1,175.67
Control	6006	MHC class I antigen	gi|84095083	40,657.50	100.00%	5	8	12	0.13%	12.60%	DYIALNEDLR	2.47	1,221.61
Control	6006	MHC class I antigen	gi|84095083	40,657.50	100.00%	5	8	12	0.13%	12.60%	FIAVGYVDDTQFVR	3.99	1,629.83
Control	6006	MHC class I antigen	gi|84095083	40,657.50	100.00%	5	8	12	0.13%	12.60%	GYRQDAYDGRDYIALNEDLR	3.98	2,403.13
Control	6006	MHC class I antigen	gi|84095083	40,657.50	100.00%	5	8	12	0.13%	12.60%	QDAYDGRDYIALNEDLR	3.28	2,026.95
Control	6006	MHC class I antigen	gi|84095083	40,657.50	100.00%	5	8	12	0.13%	12.60%	YLENGKDTLLR	2.31	1,321.71
Control	6006	RecName: Full=Serine palmitoyltransferase 1; AltName: Full=Serine-palmitoyl-CoA transferase 1; Short=SPT 1; Short=SPT1; AltName: Full=Long chain base biosynthesis protein 1; Short=L	gi|122139929,gi|75948211,gi|77736443	52,771.80	100.00%	3	5	5	0.05%	7.82%	ALQGIPGLK	2.6	896.5566

Control	6006	RecName: Full=Serine palmitoyltransferase 1; AltName: Full=Serine-palmitoyl-CoA transferase 1; Short=SPT 1; Short=SPT1; AltName: Full=Long chain base biosynthesis protein 1; Short=L	gi|122139929,gi|75948211,gi|77736443	52,771.80	100.00%	3	5	5	0.05%	7.82%	LLKEQEIEDQKNPR	3.47	1,739.93
Control	6006	RecName: Full=Serine palmitoyltransferase 1; AltName: Full=Serine-palmitoyl-CoA transferase 1; Short=SPT 1; Short=SPT1; AltName: Full=Long chain base biosynthesis protein 1; Short=L	gi|122139929,gi|75948211,gi|77736443	52,771.80	100.00%	3	5	5	0.05%	7.82%	VVVTVEQTEEDLEK	3.07	1,617.82
Control	6006	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	3	3	3	0.03%	4.90%	ALLELQLEPEELYQTFQR	3.07	2,220.15
Control	6006	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	3	3	3	0.03%	4.90%	VAVEAKNPADLPK	2.9	1,351.76

Control	6006	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	3	3	3	0.03%	4.90%	VFSGLVSTGLK	2.7	1,107.64
Control	6006	PREDICTED: similar to Calpain-5 (nCL-3) (htra-3) isoform 1	gi|76636134	72,988.00	100.00%	3	3	3	0.03%	6.25%	ANADDLQALHTLHLR	4.02	1,687.89
Control	6006	PREDICTED: similar to Calpain-5 (nCL-3) (htra-3) isoform 1	gi|76636134	72,988.00	100.00%	3	3	3	0.03%	6.25%	NSRQPSDLPGTVAVR	3.21	1,596.85
Control	6006	PREDICTED: similar to Calpain-5 (nCL-3) (htra-3) isoform 1	gi|76636134	72,988.00	100.00%	3	3	3	0.03%	6.25%	VLSSASLTAV	2.62	947.5407
Control	6006	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	3	4	5	0.05%	18.10%	LVLLGESAVGK	3.56	1,085.66
Control	6006	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	3	4	5	0.05%	18.10%	NRGVDLQENNPASR	4.62	1,569.77
Control	6006	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	3	4	5	0.05%	18.10%	QASPNIVIALAGNK	2.54	1,395.80
Control	6006	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	5	6	9	0.10%	23.10%	AKELNVMFIETSAK	3.2	1,596.83
Control	6006	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	5	6	9	0.10%	23.10%	ELNVMFIETSAK	2.91	1,397.70

Control	6006	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	5	6	9	0.10%	23.10%	GSDVIIMLVGNKTDLADKR	3.16	2,061.10
Control	6006	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	5	6	9	0.10%	23.10%	RVAAALPGMESTQDR	3.35	1,617.80
Control	6006	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	5	6	9	0.10%	23.10%	VAAALPGMESTQDR	2.83	1,461.70
Control	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	6	12	0.13%	28.50%	DLTDYLMK	1.83	1,014.48
Control	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	6	12	0.13%	28.50%	GYSFTTTAER	2.75	1,132.53
Control	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	6	12	0.13%	28.50%	GYSFTTTAEREIVR	2.92	1,629.82
Control	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	6	12	0.13%	28.50%	HQGVMVGMGQKDCYVGDEAQSK	3.73	2,383.05
Control	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	6	12	0.13%	28.50%	HQGVMVGMGQKDCYVGDEAQSKR	4.32	2,539.15

Control	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	6	12	0.13%	28.50%	IKIIAPPER	2.6	1,036.65
Control	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	6	12	0.13%	28.50%	IKIIAPPERK	2.61	1,164.75
Control	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	6	12	0.13%	28.50%	LDLAGRDLTDYLMK	3.38	1,639.84
Control	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	6	12	0.13%	28.50%	SYELPDGQVITIGNER	4.74	1,790.89
Control	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	6	12	0.13%	28.50%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	6.26	3,199.61
Control	6006	RecName: Full=Coiled-coil domain-containing protein 56	gi|108935963,gi|74268043,gi|77736311	11,689.70	99.80%	2	2	2	0.02%	18.90%	FLDELEDEAK	3.43	1,208.57
Control	6006	RecName: Full=Coiled-coil domain-containing protein 56	gi|108935963,gi|74268043,gi|77736311	11,689.70	99.80%	2	2	2	0.02%	18.90%	LTPAQLQFMR	2.48	1,220.65
Control	6006	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	9	12	12	0.13%	13.60%	FKASGVEGTDVVK	4.25	1,336.71
Control	6006	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	9	12	12	0.13%	13.60%	GKFNTSDVSAIEK	3.62	1,395.71
Control	6006	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	9	12	12	0.13%	13.60%	KIDKYLYAMR	2.92	1,316.70

Control	6006	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	9	12	12	0.13%	13.60%	LSDETLLDIMNR	3.3	1,435.71
Control	6006	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	9	12	12	0.13%	13.60%	QIEETLAHFSLTK	3	1,516.80
Control	6006	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	9	12	12	0.13%	13.60%	SANLVAATLGAILSR	3.92	1,456.85
Control	6006	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	9	12	12	0.13%	13.60%	SIPDGSEKGDFIALDLGGSSFR	3.26	2,268.11
Control	6006	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	9	12	12	0.13%	13.60%	TTVGVDGSLYK	2.56	1,139.59
Control	6006	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	9	12	12	0.13%	13.60%	YLSQIESDRLALLQVR	3.32	1,904.06
Control	6006	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	4	6	6	0.07%	9.12%	DIQGSLQDIFK	2.95	1,263.66
Control	6006	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	4	6	6	0.07%	9.12%	MTAFDADDPATDNALLR	2.64	1,852.84
Control	6006	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	4	6	6	0.07%	9.12%	SIVVSPILIPENQR	3.15	1,564.91
Control	6006	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	4	6	6	0.07%	9.12%	TLEGPVPLEVIVIDQNDNRPIFR	4.29	2,634.43
Control	6006	EGF, latrophilin and seven transmembrane domain containing 1	gi|115305144,gi|116004035	77,458.50	99.80%	2	2	2	0.02%	3.34%	IRHIEEPVALLR	3.75	1,445.86
Control	6006	EGF, latrophilin and seven transmembrane domain containing 1	gi|115305144,gi|116004035	77,458.50	99.80%	2	2	2	0.02%	3.34%	LIHTAEQATLR	3.4	1,252.70

Control	6006	PREDICTED: similar to ER lumen protein retaining receptor 3 (KDEL receptor 3) (KDEL endoplasmic reticulum protein retention receptor 3)	gi|119893224	24,969.50	99.80%	2	2	2	0.02%	11.20%	ILGDLSHLLAMILLLGK	3.73	1,836.10
Control	6006	PREDICTED: similar to ER lumen protein retaining receptor 3 (KDEL receptor 3) (KDEL endoplasmic reticulum protein retention receptor 3)	gi|119893224	24,969.50	99.80%	2	2	2	0.02%	11.20%	LSLPMPI	1.81	786.4432
Control	6006	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	5	7	7	0.08%	10.40%	GPFPQELVR	2.36	1,042.57

Control	6006	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	5	7	7	0.08%	10.40%	LDERPIHAEPQYPVR	2.43	1,819.95
Control	6006	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	5	7	7	0.08%	10.40%	MYVLTVAAENQVPLAK	3.27	1,762.94
Control	6006	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	5	7	7	0.08%	10.40%	SAAPHPGDIGDFINEGLK	4.18	1,837.91

Control	6006	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	5	7	7	0.08%	10.40%	YSVTGPGADQPPTGIFIINPISGQLSVTKPLDR	3.52	3,438.83
Control	6006	RecName: Full=Cytochrome c1, heme protein, mitochondrial; AltName: Full=Ubiquinol-cytochrome-c reductase complex cytochrome c1 subunit; Short=Cytochrome c-1; AltName: Full=Cytochrome b-c1 complex	gi|109940069,gi|114793904,gi|71042588,gi|75765182,gi|75765193,gi|82407279,gi|82407290,gi|83638779,gi|84000289	27,269.70	99.80%	2	3	5	0.05%	14.90%	LSDYFPKPYPNPEAAR	3.16	1,864.92

Control	6006	RecName: Full=Cytochrome c1, heme protein, mitochondrial; AltName: Full=Ubiquinol-cytochrome-c reductase complex cytochrome c1 subunit; Short=Cytochrome c-1; AltName: Full=Cytochrome b-c1 complex	gi|109940069,gi|114793904,gi|71042588,gi|75765182,gi|75765193,gi|82407279,gi|82407290,gi|83638779,gi|84000289	27,269.70	99.80%	2	3	5	0.05%	14.90%	MGLKMLLMMGLLLPLVYAMK	2.67	2,266.26
Control	6006	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	100.00%	4	5	7	0.08%	40.80%	ELAEAQEDTILK	3.42	1,359.70
Control	6006	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	100.00%	4	5	7	0.08%	40.80%	IERELAEAQEDTILK	5.39	1,757.93
Control	6006	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	100.00%	4	5	7	0.08%	40.80%	YSALFLGMAYGAK	4.56	1,407.70
Control	6006	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	100.00%	4	5	7	0.08%	40.80%	YSALFLGMAYGAKR	1.96	1,563.80
Control	6006	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	9	9	0.10%	28.00%	FDEGRNNFEGEVTK	3.37	1,641.75
Control	6006	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	9	9	0.10%	28.00%	FDEGRNNFEGEVTKEK	3.25	1,898.89
Control	6006	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	9	9	0.10%	28.00%	FLESGGQDGAGDDDDLEDLEEAEEPDLEEDDDQKAVKDEL	4.6	4,394.84
Control	6006	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	9	9	0.10%	28.00%	HNQLPLVIEFTEQTAPK	3.36	1,965.04
Control	6006	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	9	9	0.10%	28.00%	LITLEEEMTK	2.43	1,222.62
Control	6006	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	9	9	0.10%	28.00%	MDSTANEVEAVKVHSFPTLK	2.29	2,219.10

Control	6006	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	9	9	0.10%	28.00%	NFEEVAFDEKK	3.5	1,355.65
Control	6006	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	9	9	0.10%	28.00%	VDATEESDLAQQYGVR	2.91	1,780.83
Control	6006	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	9	9	0.10%	28.00%	YQLDKDGVVLFKK	3.18	1,552.87
Control	6006	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	6	7	0.08%	24.30%	FTRNEFNLESK	3.4	1,384.69
Control	6006	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	6	7	0.08%	24.30%	GAVGALLVYDIAK	3.07	1,289.75
Control	6006	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	6	7	0.08%	24.30%	NILTEIYR	2.23	1,021.57
Control	6006	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	6	7	0.08%	24.30%	STIGVEFATR	2.66	1,080.57
Control	6006	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	6	7	0.08%	24.30%	VVLIGDSGVGK	1.97	1,043.61
Control	6006	PREDICTED: ATP-binding cassette, sub-family B (MDR/TAP), member 1	gi|194685301	144,522.00	99.80%	2	2	2	0.02%	2.05%	IKEHGTHQQLLAQK	2.66	1,630.90
Control	6006	PREDICTED: ATP-binding cassette, sub-family B (MDR/TAP), member 1	gi|194685301	144,522.00	99.80%	2	2	2	0.02%	2.05%	YGREDVTMDEIQK	4.01	1,599.73
Control	6006	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	99.80%	2	2	2	0.02%	3.85%	GMGGLFSVGETTAK	3.21	1,370.66

Control	6006	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	99.80%	2	2	2	0.02%	3.85%	VTQSAYAQIVQFGMNEK	3.51	1,929.94
Control	6006	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	99.80%	2	2	2	0.02%	15.40%	TEEKPIFSLDTISSAESMSIYDDIDADVLR	6	3,376.60
Control	6006	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	99.80%	2	2	2	0.02%	15.40%	VYGVGSLALYEK	3.13	1,298.70
Control	6006	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	4	4	4	0.04%	24.10%	QMEQISQFLQAAER	2.73	1,694.82
Control	6006	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	4	4	4	0.04%	24.10%	TLMNLGGLAVAR	2.97	1,231.68
Control	6006	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	4	4	4	0.04%	24.10%	YFSDNQLQEGK	3.69	1,328.61
Control	6006	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	4	4	4	0.04%	24.10%	YFSDNQLQEGKNVIGLQMGTNR	4.51	2,528.22
Control	6006	PREDICTED: similar to Heparan sulfate 2-O-sulfotransferase 1 (2-O-sulfotransferase) (2OST), partial	gi|119889909	37,063.70	100.00%	3	3	3	0.03%	12.10%	EKDGDLYILAQNFFYEK	4.25	2,093.02

Control	6006	PREDICTED: similar to Heparan sulfate 2-O-sulfotransferase 1 (2-O-sulfotransferase) (2OST), partial	gi|119889909	37,063.70	100.00%	3	3	3	0.03%	12.10%	LVSYYYFLR	2.48	1,223.65
Control	6006	PREDICTED: similar to Heparan sulfate 2-O-sulfotransferase 1 (2-O-sulfotransferase) (2OST), partial	gi|119889909	37,063.70	100.00%	3	3	3	0.03%	12.10%	NNPVMSLQDQVR	3.23	1,416.69
Control	6006	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	6	8	8	0.09%	7.93%	AFTYINLDK	1.97	1,084.57
Control	6006	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	6	8	8	0.09%	7.93%	FVKEMNLFR	2.64	1,199.62
Control	6006	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	6	8	8	0.09%	7.93%	IMKVEYHLLSPYVSPR	3.86	1,948.04
Control	6006	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	6	8	8	0.09%	7.93%	LAADEEENVDSNMR	2.58	1,608.68
Control	6006	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	6	8	8	0.09%	7.93%	VEYHLLSPYVSPR	3.93	1,559.82
Control	6006	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	6	8	8	0.09%	7.93%	VSASPLLYSLIEK	4.08	1,419.81
Control	6006	Leucine rich repeat containing 8 family, member A	gi|115304767,gi|116003833	93,997.70	100.00%	3	3	3	0.03%	3.83%	IEAPALAFLR	2.81	1,100.65

Control	6006	Leucine rich repeat containing 8 family, member A	gi|115304767,gi|116003833	93,997.70	100.00%	3	3	3	0.03%	3.83%	MANLTELELIR	3.1	1,318.70
Control	6006	Leucine rich repeat containing 8 family, member A	gi|115304767,gi|116003833	93,997.70	100.00%	3	3	3	0.03%	3.83%	YFADTQPAYR	2.86	1,231.57
Control	6006	Caveolin 2	gi|157279219,gi|38322700,gi|51512145,gi|56119130,gi|66774044	18,142.30	99.80%	2	2	4	0.04%	18.50%	SFSSVSLQLSHD	2.5	1,306.63
Control	6006	Caveolin 2	gi|157279219,gi|38322700,gi|51512145,gi|56119130,gi|66774044	18,142.30	99.80%	2	2	4	0.04%	18.50%	VGFEDVIAEPVSTHSFDK	2.77	1,976.96
Control	6006	solute carrier family 29 (nucleoside transporters), member 1	gi|110331885,gi|73587285,gi|77735743	49,866.60	99.80%	2	2	2	0.02%	6.80%	LAFVPLLLLCNVQPR	3.92	1,696.00
Control	6006	solute carrier family 29 (nucleoside transporters), member 1	gi|110331885,gi|73587285,gi|77735743	49,866.60	99.80%	2	2	2	0.02%	6.80%	LEGPGEQETKLDLISK	3.17	1,756.93
Control	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	gi|146231724,gi|77736299	40,519.40	99.80%	2	2	2	0.02%	10.20%	ISQTNYIPTQQDVLR	2.7	1,775.93
Control	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	gi|146231724,gi|77736299	40,519.40	99.80%	2	2	2	0.02%	10.20%	LKIDFGEAAR	4.24	1,119.62

Control	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	gi|146231724,gi|77736299	40,519.40	99.80%	2	2	2	0.02%	10.20%	LLLLGAGESGK	3.48	1,057.63
Control	6006	Chromosome 9 open reading frame 46 ortholog	gi|74354529,gi|77735799	17,091.30	99.80%	2	2	3	0.03%	17.00%	GMITFESLEK	2.53	1,170.57
Control	6006	Chromosome 9 open reading frame 46 ortholog	gi|74354529,gi|77735799	17,091.30	99.80%	2	2	3	0.03%	17.00%	MKGEAENILETEKSK	4.28	1,722.86
Control	6006	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	5	6	6	0.07%	23.20%	IATSGYLPTQQDVLR	3.61	1,661.89

Control	6006	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	5	6	6	0.07%	23.20%	IIHGAGYSEEDKRGFTK	2.96	1,907.96
Control	6006	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	5	6	6	0.07%	23.20%	ILHSHLVDYFPEFDGPQR	4.01	2,170.07

Control	6006	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	5	6	6	0.07%	23.20%	LLLLGTGESGK	3.11	1,087.64
Control	6006	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	5	6	6	0.07%	23.20%	VRVPTTGIIEYPFDLENIIFR	4.98	2,492.36
Control	6006	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	3	4	4	0.04%	22.20%	IALMPLLQAEK	2.84	1,242.71
Control	6006	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	3	4	4	0.04%	22.20%	IALMPLLQAEKDRR	2.54	1,669.94

Control	6006	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	3	4	4	0.04%	22.20%	VKQDMPPVGGYGPIDYKR	5.46	2,036.03
Control	6006	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	3	3	3	0.03%	17.70%	FFVVSSESR	3.02	1,057.53
Control	6006	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	3	3	3	0.03%	17.70%	RKPDEVLDDEDIGSAPLK	4.9	1,997.02
Control	6006	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	3	3	3	0.03%	17.70%	VLKEDALPDLKTEYEVDSEDR	3.11	2,464.21
Control	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	10	11	15	0.16%	30.60%	AVLVDLEPGTMDSVR	3.33	1,617.82
Control	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	10	11	15	0.16%	30.60%	GHYTEGAELVDSVLDVVR	3.49	1,958.98
Control	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	10	11	15	0.16%	30.60%	GHYTEGAELVDSVLDVVRK	3.77	2,087.08
Control	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	10	11	15	0.16%	30.60%	IMNTFSVVPSPK	3.05	1,335.70
Control	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	10	11	15	0.16%	30.60%	IREEYPDRIMNTFSVVPSPK	2.98	2,394.21
Control	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	10	11	15	0.16%	30.60%	ISEQFTAMFR	2.73	1,245.59
Control	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	10	11	15	0.16%	30.60%	LAVNMVPFPR	3.44	1,159.63
Control	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	10	11	15	0.16%	30.60%	LHFFMPGFAPLTSR	3.02	1,636.83
Control	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	10	11	15	0.16%	30.60%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	5.68	4,479.06
Control	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	10	11	15	0.16%	30.60%	YLTVAAVFR	2.82	1,039.59
Control	6006	RAN binding protein 6	gi|78174362,gi|83715972	47,285.80	99.80%	2	2	2	0.02%	4.74%	ITFLLQAIR	3.16	1,074.67

Control	6006	RAN binding protein 6	gi|78174362,gi|83715972	47,285.80	99.80%	2	2	2	0.02%	4.74%	SLVEIADTVPK	3.1	1,171.66
Control	6006	RecName: Full=LAG1 longevity assurance homolog 2	gi|109892506,gi|73587265,gi|77736279	44,887.70	100.00%	2	2	2	0.02%	9.74%	LRAPPNPTLEHFYMTSGKQPK	3.63	2,428.24
Control	6006	RecName: Full=LAG1 longevity assurance homolog 2	gi|109892506,gi|73587265,gi|77736279	44,887.70	100.00%	2	2	2	0.02%	9.74%	NRPLANGHPILNNNHR	3.7	1,836.97
Control	6006	RecName: Full=Peptidyl-prolyl cis-trans isomerase B; Short=PPIase; Short=Rotamase; AltName: Full=Cyclophilin B; AltName: Full=S-cyclophilin; Short=SCYLP; Flags: Precursor	gi|215274238,gi|27806469,gi|529242,gi|59858297,gi|74268324	23,726.00	100.00%	3	3	3	0.03%	15.70%	TVDNFVALATGEK	3.27	1,364.71

Control	6006	RecName: Full=Peptidyl-prolyl cis-trans isomerase B; Short=PPIase; Short=Rotamase; AltName: Full=Cyclophilin B; AltName: Full=S-cyclophilin; Short=SCYLP; Flags: Precursor	gi|215274238,gi|27806469,gi|529242,gi|59858297,gi|74268324	23,726.00	100.00%	3	3	3	0.03%	15.70%	VIKDFMIQGGDFTR	3.34	1,642.83
Control	6006	RecName: Full=Peptidyl-prolyl cis-trans isomerase B; Short=PPIase; Short=Rotamase; AltName: Full=Cyclophilin B; AltName: Full=S-cyclophilin; Short=SCYLP; Flags: Precursor	gi|215274238,gi|27806469,gi|529242,gi|59858297,gi|74268324	23,726.00	100.00%	3	3	3	0.03%	15.70%	VIKDFMIQGGDFTRGDGTGGK	2.3	2,215.08
Control	6006	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	4	4	4	0.04%	12.40%	MALVLDALPR	3.57	1,114.63
Control	6006	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	4	4	4	0.04%	12.40%	NVVLQTLEGHLR	2.16	1,378.78
Control	6006	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	4	4	4	0.04%	12.40%	QVLLAQAEAEK	2.77	1,199.66
Control	6006	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	4	4	4	0.04%	12.40%	SILGTLTVEQIYQDRDQFAK	3.04	2,325.21

Control	6006	PREDICTED: similar to mCG10725 isoform 1	gi|119889261,gi|119912821,gi|194673249,gi|58760422,gi|70778964,gi|74354988,gi|75052080	13,725.00	99.80%	2	2	2	0.02%	15.20%	AALQELLSK	2.76	972.5725
Control	6006	PREDICTED: similar to mCG10725 isoform 1	gi|119889261,gi|119912821,gi|194673249,gi|58760422,gi|70778964,gi|74354988,gi|75052080	13,725.00	99.80%	2	2	2	0.02%	15.20%	LITPAVVSER	2.25	1,084.64
Control	6006	heterogeneous nuclear ribonucleoprotein A2/B1	gi|114051756,gi|122145945,gi|87578315	35,988.50	99.80%	2	2	2	0.02%	13.20%	GFGFVTFDDHDPVDKIVLQK	1.72	2,277.16
Control	6006	heterogeneous nuclear ribonucleoprotein A2/B1	gi|114051756,gi|122145945,gi|87578315	35,988.50	99.80%	2	2	2	0.02%	13.20%	NMGGPYGGGNYGPGGSGGSGGYGGR	3.82	2,205.90
Control	6006	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	8	8	8	0.09%	7.18%	AFMTADLPNELIELLEK	2.69	1,963.01
Control	6006	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	8	8	8	0.09%	7.18%	KFDVNTSAVQVLIEHIGNLDR	3.84	2,368.26

Control	6006	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	8	8	8	0.09%	7.18%	LASTLVHLGEYQAAVDGAR	2.81	1,971.03
Control	6006	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	8	8	8	0.09%	7.18%	LLYNNVSNFGR	3.2	1,296.67
Control	6006	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	8	8	8	0.09%	7.18%	NLQNLLILTAIK	3.26	1,353.85
Control	6006	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	8	8	8	0.09%	7.18%	NNLAGAEELFAR	3.46	1,304.66
Control	6006	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	8	8	8	0.09%	7.18%	RPISADSAIMNPASK	3.26	1,573.80

Control	6006	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	8	8	8	0.09%	7.18%	TLQIFNIEMK	2.66	1,252.66
Control	6006	PREDICTED: similar to Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase 4) (CCK-4) isoform 2	gi|119915291	126,668.70	100.00%	4	5	5	0.05%	5.74%	HPASEAAIQPLTQVTLR	3.27	1,832.00
Control	6006	PREDICTED: similar to Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase 4) (CCK-4) isoform 2	gi|119915291	126,668.70	100.00%	4	5	5	0.05%	5.74%	HTEAPLYVVDKPVLEESEGPGSPPPYK	2.97	2,935.47
Control	6006	PREDICTED: similar to Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase 4) (CCK-4) isoform 2	gi|119915291	126,668.70	100.00%	4	5	5	0.05%	5.74%	SEFGEVFLAK	2.37	1,126.58
Control	6006	PREDICTED: similar to Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase 4) (CCK-4) isoform 2	gi|119915291	126,668.70	100.00%	4	5	5	0.05%	5.74%	VVLAPQDVVVAR	2.49	1,265.76

Control	6006	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	4	6	6	0.07%	14.20%	FDAVIGYK	2.5	912.4826
Control	6006	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	4	6	6	0.07%	14.20%	KSVTGEIVLITGAGHGIGR	4.13	1,865.06
Control	6006	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	4	6	6	0.07%	14.20%	NPSTSLGPTLEPEEVVNK	3.6	1,910.97
Control	6006	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	4	6	6	0.07%	14.20%	SVTGEIVLITGAGHGIGR	3.31	1,736.97
Control	6006	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	5	5	5	0.05%	29.20%	AELNEFLTR	3.27	1,092.57
Control	6006	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	5	5	5	0.05%	29.20%	ELAEDGYSGVEVR	3.29	1,423.67
Control	6006	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	5	5	5	0.05%	29.20%	FVDGLMIHSGDPVNYYVDTAVR	4.88	2,484.19
Control	6006	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	5	5	5	0.05%	29.20%	GGKPEPPAMPQPVPTA	2.57	1,589.80
Control	6006	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	5	5	5	0.05%	29.20%	IRELTAVVQKR	3.74	1,312.81
Control	6006	Leucine zipper-EF hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	3	5	5	0.05%	5.74%	AMYLPETLSPADQLK	2.26	1,692.85
Control	6006	Leucine zipper-EF hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	3	5	5	0.05%	5.74%	FLQDTIEEMALK	3.54	1,453.72
Control	6006	Leucine zipper-EF hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	3	5	5	0.05%	5.74%	IRETGERPSNEEIMR	2.17	1,832.89

Control	6006	unnamed protein product	gi|117576085,gi|117576087,gi|119935998,gi|1902982,gi|27806503,gi|73621334	31,134.50	99.80%	2	2	3	0.03%	8.42%	EMIETLAHKLDEK	2.58	1,572.79
Control	6006	unnamed protein product	gi|117576085,gi|117576087,gi|119935998,gi|1902982,gi|27806503,gi|73621334	31,134.50	99.80%	2	2	3	0.03%	8.42%	QNLNLQEVLK	3.13	1,198.68
Control	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	12	15	23	0.25%	42.40%	GLKLTFDSSFSPNTGKK	4.54	1,826.96
Control	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	12	15	23	0.25%	42.40%	GYGFGLIK	2.13	854.4772
Control	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	12	15	23	0.25%	42.40%	LTFDSSFSPNTGK	3.61	1,400.67
Control	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	12	15	23	0.25%	42.40%	LTFDSSFSPNTGKK	2.77	1,528.76
Control	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	12	15	23	0.25%	42.40%	LTLSALLDGK	3.04	1,030.61
Control	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	12	15	23	0.25%	42.40%	LTLSALLDGKNVNAGGHK	4.14	1,808.00
Control	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	12	15	23	0.25%	42.40%	SRVTQSNFAVGYK	3.88	1,456.75
Control	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	12	15	23	0.25%	42.40%	TDEFQLHTNVNDGTEFGGSIYQK	4.56	2,600.19
Control	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	12	15	23	0.25%	42.40%	TKSENGLEFTSSGSANTETTK	4.12	2,189.02
Control	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	12	15	23	0.25%	42.40%	VNNSSLIGLGYTQTLKPGIK	3.15	2,103.18
Control	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	12	15	23	0.25%	42.40%	VTQSNFAVGYK	3.71	1,213.62
Control	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	12	15	23	0.25%	42.40%	VTQSNFAVGYKTDEFQLHTNVNDGTEFGGSIYQK	3.04	3,794.79

Control	6006	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	9	11	18	0.20%	34.00%	DIFNKGFGFGLVK	3.97	1,441.78
Control	6006	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	9	11	18	0.20%	34.00%	GFGFGLVK	1.78	824.4666
Control	6006	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	9	11	18	0.20%	34.00%	LTFDTTFSPNTGK	3.65	1,428.70
Control	6006	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	9	11	18	0.20%	34.00%	LTFDTTFSPNTGKK	2.17	1,556.80
Control	6006	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	9	11	18	0.20%	34.00%	LTLSALVDGK	3.34	1,016.60
Control	6006	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	9	11	18	0.20%	34.00%	NNFAVGYR	2.46	940.4634
Control	6006	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	9	11	18	0.20%	34.00%	TGDFQLHTNVNDGTEFGGSIYQK	5.54	2,528.17
Control	6006	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	9	11	18	0.20%	34.00%	VNNSSLIGVGYTQTLRPGVK	4.24	2,103.16
Control	6006	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	9	11	18	0.20%	34.00%	YQLDPTASISAK	2.84	1,293.67
Control	6006	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	4	7	8	0.09%	6.02%	GLGEHELDEDEEDYESSAK	4.52	2,151.88

Control	6006	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	4	7	8	0.09%	6.02%	IFGELSSYEDFLDAR	3.48	1,761.83
Control	6006	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	4	7	8	0.09%	6.02%	IKRDEQYTALSNMPK	4.41	1,809.92
Control	6006	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	4	7	8	0.09%	6.02%	KYFAATQFEPLAAR	3.71	1,612.85
Control	6006	CYB5B protein	gi|158455068,gi|76640228	26,782.70	99.80%	2	2	2	0.02%	22.40%	FLDEHPGGEEVLMEQAGGDATESFEDVGHSSDAR	5.99	3,634.55
Control	6006	CYB5B protein	gi|158455068,gi|76640228	26,782.70	99.80%	2	2	2	0.02%	22.40%	QYYIGDVHPNDLKPGGGSK	2.76	2,045.01
Control	6006	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	99.80%	2	2	2	0.02%	5.92%	QVAEQFLNIR	2.79	1,217.66
Control	6006	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	99.80%	2	2	2	0.02%	5.92%	TIAQGNLSNPDVQAAK	4.47	1,626.84
Control	6006	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	5	5	5	0.05%	15.50%	AQQVAVQEQEIAR	4.35	1,469.77
Control	6006	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	5	5	5	0.05%	15.50%	ISLNTLTLNVK	3.03	1,215.73

Control	6006	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	5	5	5	0.05%	15.50%	MRGEAEAFAIGAR	4.03	1,394.68
Control	6006	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	5	5	5	0.05%	15.50%	TEAEIAHIALETLEGHQR	3.3	2,018.03
Control	6006	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	5	5	5	0.05%	15.50%	VTGEVLDILSR	2.87	1,201.68
Control	6006	glutathione peroxidase 8	gi|114052907,gi|122143886,gi|84708688	23,965.80	99.80%	2	3	3	0.03%	11.00%	ILGSEAEPAFR	3.19	1,189.62
Control	6006	glutathione peroxidase 8	gi|114052907,gi|122143886,gi|84708688	23,965.80	99.80%	2	3	3	0.03%	11.00%	NNFGVTFPIFHK	3.19	1,420.74
Control	6006	ANXA6 protein	gi|154426044,gi|157151716,gi|160332337	75,893.80	100.00%	4	4	4	0.04%	9.21%	EMSGDVRDVFVAIVQSVK	3.76	1,995.02
Control	6006	ANXA6 protein	gi|154426044,gi|157151716,gi|160332337	75,893.80	100.00%	4	4	4	0.04%	9.21%	GLGTDEDTIIDIIAHR	2.84	1,738.90
Control	6006	ANXA6 protein	gi|154426044,gi|157151716,gi|160332337	75,893.80	100.00%	4	4	4	0.04%	9.21%	GTVRPAGDFNPDADAK	2.53	1,630.78
Control	6006	ANXA6 protein	gi|154426044,gi|157151716,gi|160332337	75,893.80	100.00%	4	4	4	0.04%	9.21%	NKPLFFADKLYK	4.46	1,483.83
Control	6006	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	7	9	0.10%	20.50%	GFVLTFK	2.04	811.4713
Control	6006	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	7	9	0.10%	20.50%	GVGMVADPDNPLVLDILTGSSTSYSFFPDKPITQYPHAVGK	5	4,350.16
Control	6006	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	7	9	0.10%	20.50%	LPDVYGVFQFK	2.73	1,312.69
Control	6006	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	7	9	0.10%	20.50%	SSLNPILFR	2.63	1,046.60

Control	6006	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	7	9	0.10%	20.50%	TADDPSLSLIK	2.95	1,159.62
Control	6006	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	7	9	0.10%	20.50%	TLVLLDNLNLR	3.4	1,283.77
Control	6006	reticulon 4 isoform 2	gi|164259354,gi|92096636	40,940.20	100.00%	3	4	4	0.04%	7.92%	GPLPAAPLAAPER	3.22	1,259.71
Control	6006	reticulon 4 isoform 2	gi|164259354,gi|92096636	40,940.20	100.00%	3	4	4	0.04%	7.92%	HQAQIDHYLGLANK	4.79	1,607.83
Control	6006	reticulon 4 isoform 2	gi|164259354,gi|92096636	40,940.20	100.00%	3	4	4	0.04%	7.92%	HQAQIDHYLGLANKNVK	3.47	1,949.04
Control	6006	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	5	7	8	0.09%	15.70%	ALASILLQDHIR	3.43	1,349.79
Control	6006	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	5	7	8	0.09%	15.70%	IYQGEDLPHPK	3.17	1,296.66
Control	6006	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	5	7	8	0.09%	15.70%	LKDIASEFKEQLQTLILHVLNPANLMEK	4.19	3,251.77
Control	6006	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	5	7	8	0.09%	15.70%	LQVKEHQHEEIQNVR	3.36	1,886.98
Control	6006	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	5	7	8	0.09%	15.70%	SMLQATAEANNLAAAASAK	5.43	1,848.91
Control	6006	RecName: Full=Glutathione S-transferase P; AltName: Full=GST class-pi	gi|121744,gi|29135329,gi|404,gi|74268086	23,595.90	99.80%	2	2	2	0.02%	15.70%	ALPQHLKPFETLLSQNK	3.19	1,964.10
Control	6006	RecName: Full=Glutathione S-transferase P; AltName: Full=GST class-pi	gi|121744,gi|29135329,gi|404,gi|74268086	23,595.90	99.80%	2	2	2	0.02%	15.70%	FQDGDLTLYQSNAILR	4.04	1,853.94

Control	6006	Poliovirus receptor-related 2 (herpesvirus entry mediator B)	gi|109658349,gi|115497936	43,243.10	99.80%	2	2	2	0.02%	5.46%	LLPVILSVR	2.12	1,009.68
Control	6006	Poliovirus receptor-related 2 (herpesvirus entry mediator B)	gi|109658349,gi|115497936	43,243.10	99.80%	2	2	2	0.02%	5.46%	YTVTPLSEADGVK	2.93	1,379.71
Control	6006	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	4	4	4	0.04%	9.09%	IRIDSLSAQLSQLQK	3.24	1,699.97
Control	6006	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	4	4	4	0.04%	9.09%	LADALQELR	2.49	1,028.57
Control	6006	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	4	4	4	0.04%	9.09%	LQEKEDLQELNDR	4.86	1,629.81
Control	6006	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	4	4	4	0.04%	9.09%	MQQQLDEYQELLDIK	2.44	1,909.92
Control	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	18	0.20%	38.80%	AVAISLPK	2.05	798.5084
Control	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	18	0.20%	38.80%	AVLSAEQLRDDEVHAGLGELLR	5.39	2,391.26

Control	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	18	0.20%	38.80%	DQAVENILLSPVVVASSLGLVSLGGK	4.61	2,565.45
Control	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	18	0.20%	38.80%	DTQSGSLLFIGR	2.35	1,293.68
Control	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	18	0.20%	38.80%	GVVEVTHDLQK	3.84	1,224.66
Control	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	18	0.20%	38.80%	HLAGLGLTEAIDKNK	4.99	1,579.88

Control	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	18	0.20%	38.80%	HLAGLGLTEAIDKNKADLSR	3.8	2,122.16
Control	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	18	0.20%	38.80%	KAVAISLPK	3.34	926.6034
Control	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	18	0.20%	38.80%	LFYADHPFIFLVR	2.86	1,637.88
Control	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	18	0.20%	38.80%	LSSLIIIMPHHVEPLER	2.64	2,000.10

Control	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	18	0.20%	38.80%	LSSLIIIMPHHVEPLERLEK	3.03	2,370.32
Control	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	18	0.20%	38.80%	LYGPSSVSFAEDFVR	3.29	1,673.82
Control	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	18	0.20%	38.80%	SAGLAFSLYQAMAK	3.44	1,473.74
Control	6006	PREDICTED: transmembrane emp24 protein transport domain containing 4	gi|194666384	37,465.50	100.00%	3	5	6	0.07%	7.76%	DKLTELQLR	2.87	1,115.64
Control	6006	PREDICTED: transmembrane emp24 protein transport domain containing 4	gi|194666384	37,465.50	100.00%	3	5	6	0.07%	7.76%	QLLDQVEQIQK	3.19	1,341.74

Control	6006	PREDICTED: transmembrane emp24 protein transport domain containing 4	gi|194666384	37,465.50	100.00%	3	5	6	0.07%	7.76%	QLLDQVEQIQKEQDYQR	3.74	2,161.09
Control	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	16	19	20	0.22%	19.70%	AQYPIADLVK	2.22	1,117.63
Control	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	16	19	20	0.22%	19.70%	AVVLAANHFGR	2.45	1,154.64
Control	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	16	19	20	0.22%	19.70%	EVLASDLVVK	2.25	1,072.62
Control	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	16	19	20	0.22%	19.70%	FFTGQITAAGK	3.37	1,140.60
Control	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	16	19	20	0.22%	19.70%	GTVVMKDGQVIFPAPTPK	3.16	1,901.02
Control	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	16	19	20	0.22%	19.70%	ILIVGGGVAGLASAGAAK	3.21	1,524.91
Control	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	16	19	20	0.22%	19.70%	MATQASTLYSNNITK	4.23	1,658.81
Control	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	16	19	20	0.22%	19.70%	RVALSPAGVQALVK	2.96	1,408.86
Control	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	16	19	20	0.22%	19.70%	SAPLLLPGR	2.04	923.5674
Control	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	16	19	20	0.22%	19.70%	SLGAEPLEVDLK	2.69	1,270.69

Control	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	16	19	20	0.22%	19.70%	SLGVGYAAVDNPIFYKPNTAMLLGDAK	4.34	2,841.45
Control	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	16	19	20	0.22%	19.70%	SLGVGYAAVDNPIFYKPNTAMLLGDAKK	3.72	2,969.54
Control	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	16	19	20	0.22%	19.70%	TSGTLISFIYPAQNPDLLNK	2.27	2,192.16
Control	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	16	19	20	0.22%	19.70%	TVAELEAEKAATITPFRK	3.05	1,975.09
Control	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	16	19	20	0.22%	19.70%	VALSPAGVQALVK	5.35	1,252.76
Control	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	16	19	20	0.22%	19.70%	VTIAQGYDALSSMANIAGYK	4.43	2,089.03
Control	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	16	22	0.24%	33.30%	IPDQLVILDMK	4.04	1,300.72
Control	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	16	22	0.24%	33.30%	IPDQLVILDMKHGVEAK	3.92	1,922.04
Control	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	16	22	0.24%	33.30%	ITDSAGHILYSK	3.66	1,304.68
Control	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	16	22	0.24%	33.30%	ITDSAGHILYSKEDATK	3.78	1,848.93

Control	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	16	22	0.24%	33.30%	ITDSAGHILYSKEDATKGK	3.88	2,034.05
Control	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	16	22	0.24%	33.30%	LKPLEVELR	3.58	1,096.67
Control	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	16	22	0.24%	33.30%	NYEEIAKVEK	2.49	1,222.63
Control	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	16	22	0.24%	33.30%	RLEDLSESIVNDFAYMK	3.26	2,045.99
Control	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	16	22	0.24%	33.30%	RLEDLSESIVNDFAYMKK	5.42	2,174.08
Control	6006	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	99.90%	2	2	2	0.02%	6.57%	LITVNTPDLVLFVGEALVGNEAVDQLVK	3.51	2,966.65
Control	6006	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	99.90%	2	2	2	0.02%	6.57%	NQGFDVVLVDTAGR	3.8	1,490.76
Control	6006	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	4	4	4	0.04%	6.16%	FLFLLLGPAGK	3.27	1,175.72
Control	6006	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	4	4	4	0.04%	6.16%	KIPSGAEASNVLVGEVDFLERPIIAFVR	3.3	3,026.67

Control	6006	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	4	4	4	0.04%	6.16%	LAPAVLLSGLTEVPVPTR	2.74	1,833.08
Control	6006	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	4	4	4	0.04%	6.16%	TSSTVNTKFEKEELESHR	2.4	2,122.04
Control	6006	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	7	7	0.08%	28.40%	FSDLDSASVDSDMYDLPK	2.87	2,020.87
Control	6006	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	7	7	0.08%	28.40%	FSDLDSASVDSDMYDLPKKEDALLYQSK	5.94	3,196.49
Control	6006	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	7	7	0.08%	28.40%	GFRQPSASLSDADPFHR	4.25	1,887.91
Control	6006	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	7	7	0.08%	28.40%	GYNDDYYEESYLTTR	3.21	1,888.79
Control	6006	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	7	7	0.08%	28.40%	QYNIPHGPVVGSTR	2.05	1,524.79
Control	6006	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	5	5	6	0.07%	24.20%	ATIGADFLTK	2.77	1,036.57
Control	6006	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	5	5	6	0.07%	24.20%	DPENFPFVVLGNK	3.58	1,475.75
Control	6006	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	5	5	6	0.07%	24.20%	DPENFPFVVLGNKIDLENR	4.27	2,216.13
Control	6006	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	5	5	6	0.07%	24.20%	FQSLGVAFYR	2.89	1,187.62

Control	6006	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	5	5	6	0.07%	24.20%	VIILGDSGVGK	2.63	1,057.63
Control	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	14	0.15%	24.20%	ARFEELNADLFR	3.83	1,480.75
Control	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	14	0.15%	24.20%	FEELNADLFR	3.11	1,253.62
Control	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	14	0.15%	24.20%	IINEPTAAAIAYGLDKK	2.97	1,787.99
Control	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	14	0.15%	24.20%	LDKSQIHDIVLVGGSTR	4.19	1,838.01
Control	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	14	0.15%	24.20%	NQVAMNPTNTVFDAK	3.34	1,665.79
Control	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	14	0.15%	24.20%	NSLESYAFNMK	3.42	1,319.59
Control	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	14	0.15%	24.20%	QTQTFTTYSDNQPGVLIQVYEGER	4.42	2,774.33
Control	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	14	0.15%	24.20%	SFYPEEVSSMVLTK	2.64	1,632.78
Control	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	14	0.15%	24.20%	STAGDTHLGGEDFDNR	3.13	1,691.73
Control	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	14	0.15%	24.20%	TTPSYVAFTDTER	2.87	1,487.70
Control	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	14	0.15%	24.20%	TVTNAVVTVPAYFNDSQR	3.03	1,982.00
Control	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	11	16	29	0.32%	32.60%	AAYFGIYDTAK	3.61	1,219.60
Control	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	11	16	29	0.32%	32.60%	DFLAGGIAAAISK	4.83	1,233.68
Control	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	11	16	29	0.32%	32.60%	DKYKQIFLGGVDK	3.69	1,510.83

Control	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	11	16	29	0.32%	32.60%	GLYQGFNVSVQGIIIYR	2.95	1,927.04
Control	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	11	16	29	0.32%	32.60%	GMGGAFVLVLYDELKK	3.66	1,755.94
Control	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	11	16	29	0.32%	32.60%	GMGGAFVLVLYDELKKVI	2.43	1,968.09
Control	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	11	16	29	0.32%	32.60%	QIFLGGVDKR	2.39	1,132.65
Control	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	11	16	29	0.32%	32.60%	VKLLLQVQHASK	4.01	1,363.84
Control	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	11	16	29	0.32%	32.60%	YFPTQALNFAFK	4.78	1,446.74
Control	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	11	16	29	0.32%	32.60%	YFPTQALNFAFKDK	3.72	1,689.86
Control	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	11	16	29	0.32%	32.60%	YFPTQALNFAFKDKYK	3.76	1,981.02
Control	6006	PREDICTED: insulin-like growth factor 1 receptor	gi|119913553	135,693.80	100.00%	3	4	4	0.04%	4.15%	ELGQGSFGMVYEGVAK	3.03	1,687.80
Control	6006	PREDICTED: insulin-like growth factor 1 receptor	gi|119913553	135,693.80	100.00%	3	4	4	0.04%	4.15%	SLRPEMENNPVLAPPSLSK	3.25	2,095.09
Control	6006	PREDICTED: insulin-like growth factor 1 receptor	gi|119913553	135,693.80	100.00%	3	4	4	0.04%	4.15%	TEAEKQAEKEEAEYR	2.01	1,810.85

Control	6006	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	9	9	9	0.10%	4.73%	EAFTNKPNVFTVVTR	3.01	1,722.92
Control	6006	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	9	9	9	0.10%	4.73%	FADEHVPGSPFTVK	2.89	1,530.76
Control	6006	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	9	9	9	0.10%	4.73%	IVGPGLGSGVR	2.57	1,011.59
Control	6006	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	9	9	9	0.10%	4.73%	LIALLEVLSQK	2.52	1,226.77
Control	6006	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	9	9	9	0.10%	4.73%	SPFTVGVAAPLDLSR	3.96	1,529.83
Control	6006	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	9	9	9	0.10%	4.73%	VLFASQEIPTSPFR	2.94	1,591.85
Control	6006	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	9	9	9	0.10%	4.73%	VSFAGDTIPK	2.64	1,034.55

Control	6006	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	9	9	9	0.10%	4.73%	VTEAEIVPVGK	2.88	1,141.65
Control	6006	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	9	9	9	0.10%	4.73%	YTPTQQGNMQVLVTYGGDPIPK	3.56	2,423.19
Control	6006	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	3	3	3	0.03%	7.05%	EAGHGTQKEEIPEEELAEDVEEIDHAER	3.88	3,189.45
Control	6006	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	3	3	3	0.03%	7.05%	GIIDSTVSEQR	2.88	1,204.62
Control	6006	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	3	3	3	0.03%	7.05%	KADVGFAMGIAGTDVAK	3.83	1,666.85
Control	6006	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	3	3	3	0.03%	7.05%	QVVAVTGDGTNDGPALK	3.97	1,641.84
Control	6006	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	3	3	3	0.03%	7.05%	QVVAVTGDGTNDGPALKK	2.95	1,769.94
Control	6006	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	3	3	3	0.03%	7.05%	SSLYEGLEKPESR	3.6	1,494.74
Control	6006	UNC84B protein	gi|151553917,gi|156121283	81,429.80	100.00%	2	3	3	0.03%	4.26%	IRPTAVTLEHVPK	3.88	1,460.86
Control	6006	UNC84B protein	gi|151553917,gi|156121283	81,429.80	100.00%	2	3	3	0.03%	4.26%	LEGQLAGLRQELAALTLK	3.07	1,924.12
Control	6006	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	3	5	5	0.05%	4.28%	DQAVMISGESGAGKTEATKR	3.01	2,052.00

Control	6006	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	3	5	5	0.05%	4.28%	HLGYKPEEYKMGR	2.58	1,623.80
Control	6006	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	3	5	5	0.05%	4.28%	MSLLELVEILK	2.77	1,303.75
Control	6006	PREDICTED: similar to Ras-interacting protein 1 isoform 2	gi|76642189	103,383.20	99.80%	2	2	2	0.02%	4.36%	AASGGAALASPGPGSGSGTPAGSGGKER	3.89	2,312.12
Control	6006	PREDICTED: similar to Ras-interacting protein 1 isoform 2	gi|76642189	103,383.20	99.80%	2	2	2	0.02%	4.36%	LSLTGPVTDDALHR	2.44	1,494.79
Control	6006	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	3	3	3	0.03%	3.27%	GQPLGPAGVQVSLR	2.55	1,378.78
Control	6006	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	3	3	3	0.03%	3.27%	SSIDSEPALVLGPLK	2.93	1,525.85
Control	6006	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	3	3	3	0.03%	3.27%	VQVMVPEAETR	3.13	1,274.64
Control	6006	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	6	10	10	0.11%	51.00%	ADALQAGASQFETSAAK	3.99	1,665.81
Control	6006	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	6	10	10	0.11%	51.00%	DQKLSELDDRADALQAGASQFETSAAK	5.68	2,865.39
Control	6006	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	6	10	10	0.11%	51.00%	LQQTQNQVDEVVDIMR	4.27	1,931.95
Control	6006	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	6	10	10	0.11%	51.00%	LSELDDRADALQAGASQFETSAAK	5.88	2,494.21

Control	6006	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	6	10	10	0.11%	51.00%	RLQQTQNQVDEVVDIMR	4.65	2,088.05
Control	6006	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	6	10	10	0.11%	51.00%	VNVDKVLER	2.49	1,071.62
Control	6006	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	5	8	11	0.12%	16.20%	DKLSELQLR	3.7	1,101.63
Control	6006	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	5	8	11	0.12%	16.20%	FSLFAGGMLR	3.01	1,114.57
Control	6006	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	5	8	11	0.12%	16.20%	QLVEQVEQIQK	3.52	1,341.74
Control	6006	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	5	8	11	0.12%	16.20%	QLVEQVEQIQKEQNYQR	4	2,160.10
Control	6006	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	5	8	11	0.12%	16.20%	VRQLVEQVEQIQKEQNYQR	3.64	2,415.27
Control	6006	PCDH1 protein	gi|134025143,gi|139947544	114,931.40	99.80%	2	2	2	0.02%	3.58%	NTGLITVQGPVDREDLSTLR	2.19	2,184.16
Control	6006	PCDH1 protein	gi|134025143,gi|139947544	114,931.40	99.80%	2	2	2	0.02%	3.58%	SPKPVKPVEDEDETGLQK	4.57	1,996.02
Control	6006	KRT4 protein	gi|134024768	58,029.30	99.80%	2	2	5	0.05%	5.10%	FASFIDKVR	1.63	1,082.60
Control	6006	KRT4 protein	gi|134024768	58,029.30	99.80%	2	2	5	0.05%	5.10%	LALDIEIATYR	4.18	1,277.71
Control	6006	KRT4 protein	gi|134024768	58,029.30	99.80%	2	2	5	0.05%	5.10%	NEISELNR	3.36	974.4901

Control	6006	PREDICTED: similar to solute carrier family 30 (zinc transporter), member 1 isoform 1	gi|76638149	55,359.70	99.80%	2	2	2	0.02%	7.51%	ESALILLQTVPK	2.12	1,311.79
Control	6006	PREDICTED: similar to solute carrier family 30 (zinc transporter), member 1 isoform 1	gi|76638149	55,359.70	99.80%	2	2	2	0.02%	7.51%	IIKDVFHNHGIHATTIQPEFASVGSK	2.43	2,846.50
Control	6006	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	5	7	0.08%	25.90%	EFADSLGIPFLETSAK	2.93	1,724.87
Control	6006	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	5	7	0.08%	25.90%	KVVDYTTAKEFADSLGIPFLETSAK	3.51	2,730.42
Control	6006	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	5	7	0.08%	25.90%	LLLIGDSGVGK	3.31	1,071.64
Control	6006	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	5	7	0.08%	25.90%	NATNVEQSFMTMAAEIK	3.66	1,900.88
Control	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	25	0.27%	32.30%	ALYETELADAR	2.29	1,251.62
Control	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	25	0.27%	32.30%	FKAEHDQLLLNYAK	2.6	1,689.90
Control	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	25	0.27%	32.30%	IESLSSQLSNLQK	3.69	1,446.78
Control	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	25	0.27%	32.30%	IQELEDLLAKER	2.44	1,456.80
Control	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	25	0.27%	32.30%	KLLEGEEERLK	3.53	1,343.75
Control	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	25	0.27%	32.30%	LALDMEISAYR	1.92	1,297.65
Control	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	25	0.27%	32.30%	LAQALHEMREQHDAQVK	3.32	2,020.00
Control	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	25	0.27%	32.30%	LAVYIDKVR	2.18	1,076.65

Control	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	25	0.27%	32.30%	LLEGEEERLK	3.12	1,215.66
Control	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	25	0.27%	32.30%	LREYEAALNSK	3.59	1,293.68
Control	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	25	0.27%	32.30%	LYKEELEQTYHAK	3.65	1,651.83
Control	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	25	0.27%	32.30%	MRIESLSSQLSNLQK	4.03	1,749.92
Control	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	25	0.27%	32.30%	NMYEEEINETR	3.25	1,443.61
Control	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	25	0.27%	32.30%	SLESDLEDLKDQIAQLEASLAAAK	5.77	2,558.32
Control	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	25	0.27%	32.30%	TTIPEEEEEEEEAAEVAVEEELFHQQGAPR	3.94	3,425.55
Control	6006	RecName: Full=40S ribosomal protein S27	gi|108860958,gi|148231402,gi|85812223,gi|86827527	9,442.90	99.80%	2	2	2	0.02%	31.00%	DLLHPSPEEEKRK	3.63	1,577.83
Control	6006	RecName: Full=40S ribosomal protein S27	gi|108860958,gi|148231402,gi|85812223,gi|86827527	9,442.90	99.80%	2	2	2	0.02%	31.00%	LVQSPNSYFMDVK	2.01	1,543.75
Control	6006	PREDICTED: similar to N-acetylgalactosaminyltransferase 7 (Protein-UDP acetylgalactosaminyltransferase 7) (UDP-GalNAc: polypeptide N-acetylgalactosaminyltransferase 7) (Polypeptide GalNAc transferas	gi|119896052	88,098.30	99.80%	2	2	2	0.02%	3.11%	AKPLVLGPEFK	2.53	1,198.72

Control	6006	PREDICTED: similar to N-acetylgalactosaminyltransferase 7 (Protein-UDP acetylgalactosaminyltransferase 7) (UDP-GalNAc: polypeptide N-acetylgalactosaminyltransferase 7) (Polypeptide GalNAc transferas	gi|119896052	88,098.30	99.80%	2	2	2	0.02%	3.11%	SPAMAGGLFAIER	2.9	1,335.67
Control	6006	CALM3 protein	gi|111308539,gi|114053089,gi|115305083,gi|157831834,gi|157879669,gi|194671098,gi|28189857,gi|49037473,gi|86822265	19,973.60	99.80%	2	2	2	0.02%	18.10%	EAFSLFDKDGDGTITTK	2.39	1,844.89
Control	6006	CALM3 protein	gi|111308539,gi|114053089,gi|115305083,gi|157831834,gi|157879669,gi|194671098,gi|28189857,gi|49037473,gi|86822265	19,973.60	99.80%	2	2	2	0.02%	18.10%	VFDKDGNGYISAAELR	2.62	1,754.87

Control	6006	RecName: Full=Cytochrome c oxidase polypeptide 7A2, mitochondrial; AltName: Full=Cytochrome c oxidase polypeptide VIIa-liver/heart; Short=Cytochrome c oxidase subunit VIIa-L; Short=VIIC; Flags: Precursor	gi|117120,gi|28461241,gi|488158,gi|74354141	9,305.40	99.80%	2	2	3	0.03%	27.70%	GGIADALLYR	3.36	1,048.58
Control	6006	RecName: Full=Cytochrome c oxidase polypeptide 7A2, mitochondrial; AltName: Full=Cytochrome c oxidase polypeptide VIIa-liver/heart; Short=Cytochrome c oxidase subunit VIIa-L; Short=VIIC; Flags: Precursor	gi|117120,gi|28461241,gi|488158,gi|74354141	9,305.40	99.80%	2	2	3	0.03%	27.70%	LFQEDNGIPVHLK	2.3	1,509.81
Control	6006	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	99.80%	2	2	2	0.02%	2.94%	NPFLAVVTTNR	3.32	1,231.68

Control	6006	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	99.80%	2	2	2	0.02%	2.94%	YAVFALGNK	2.34	982.5356
Control	6006	RecName: Full=Histone H2A.V; AltName: Full=H2A.F/Z	gi|109940032,gi|163150,gi|27807373,gi|410,gi|81674301,gi|81674755,gi|83288407,gi|84000371	13,535.20	99.80%	2	3	3	0.03%	33.60%	ATIAGGGVIPHIHK	4.05	1,370.79
Control	6006	RecName: Full=Histone H2A.V; AltName: Full=H2A.F/Z	gi|109940032,gi|163150,gi|27807373,gi|410,gi|81674301,gi|81674755,gi|83288407,gi|84000371	13,535.20	99.80%	2	3	3	0.03%	33.60%	VGATAAVYSAAILEYLTAEVLELAGNASK	2.6	2,895.54
Control	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	12	13	13	0.14%	25.80%	ALEEAMEQKAELER	2.61	1,662.80
Control	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	12	13	13	0.14%	25.80%	ANLQIDQLNTDLNLER	4.27	1,869.97
Control	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	12	13	13	0.14%	25.80%	ELEDATETADAMNREVSSLK	2.31	2,225.02
Control	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	12	13	13	0.14%	25.80%	IAQLEEELEEEQGNTELVNDR	2.88	2,458.16
Control	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	12	13	13	0.14%	25.80%	IAQLEEELEEEQGNTELVNDRLK	4.18	2,699.34
Control	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	12	13	13	0.14%	25.80%	IAQLEEQLDNETKER	4.43	1,815.91
Control	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	12	13	13	0.14%	25.80%	KFDQLLAEEK	2.85	1,220.65
Control	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	12	13	13	0.14%	25.80%	LKDVLLQVDDERR	2.63	1,598.89

Control	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	12	13	13	0.14%	25.80%	LQQELDDLLVDLDHQR	2.92	1,949.99
Control	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	12	13	13	0.14%	25.80%	QAQQERDELADEIANSSGK	4.72	2,088.98
Control	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	12	13	13	0.14%	25.80%	QISTLHAQVTDMR	2.8	1,515.76
Control	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	12	13	13	0.14%	25.80%	TRLQQELDDLLVDLDHQR	5.49	2,207.14
Control	6006	PREDICTED: similar to keratin 2 (epidermal ichthyosis bullosa of Siemens)	gi|119892108	64,293.10	99.80%	2	2	3	0.03%	3.89%	FLEQQNQVLQTK	4.04	1,475.79
Control	6006	PREDICTED: similar to keratin 2 (epidermal ichthyosis bullosa of Siemens)	gi|119892108	64,293.10	99.80%	2	2	3	0.03%	3.89%	TAAENEFVTLKK	3.75	1,350.73
Control	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	17	25	0.27%	35.80%	AASFLLALEPELEAR	4.56	1,629.88
Control	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	17	25	0.27%	35.80%	DTYIENEKLISGK	3.43	1,509.78
Control	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	17	25	0.27%	35.80%	FFTVKLPVALDPGAK	3.85	1,602.93
Control	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	17	25	0.27%	35.80%	HFDETVNRYK	3.18	1,308.63
Control	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	17	25	0.27%	35.80%	IDHILDAL	2.37	909.5042
Control	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	17	25	0.27%	35.80%	ISVIVEAVYTHVLQPYPTQITQSEK	2.58	2,843.52
Control	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	17	25	0.27%	35.80%	LPVALDPGAK	1.88	980.5777
Control	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	17	25	0.27%	35.80%	LVDHVFDEQVIDSLTVK	3.11	1,957.03
Control	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	17	25	0.27%	35.80%	NIQVDSPYEISR	3.61	1,420.71

Control	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	17	25	0.27%	35.80%	QFVVFEGNHYFYSPYPTK	2.86	2,223.05
Control	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	17	25	0.27%	35.80%	SEDLLDYGPFR	2.9	1,311.62
Control	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	17	25	0.27%	35.80%	THYIVGYNLPSYEYLYNLGDQYALK	2.7	2,997.47
Control	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	17	25	0.27%	35.80%	VHSENNSPFLTITSMTR	3.39	1,949.94
Control	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	17	25	0.27%	35.80%	VTAEVVLAHAGSGSSPR	5.68	1,637.86
Control	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	17	25	0.27%	35.80%	YDYQRQPDSGVSSVR	4.95	1,756.82
Control	6006	RecName: Full=60S ribosomal protein L8	gi|108860941,gi|154426156,gi|74267654,gi|77736197	28,006.80	99.80%	2	2	2	0.02%	6.61%	ASGNYATVISHNPETK	2.43	1,688.82
Control	6006	RecName: Full=60S ribosomal protein L8	gi|108860941,gi|154426156,gi|74267654,gi|77736197	28,006.80	99.80%	2	2	2	0.02%	6.61%	ASGNYATVISHNPETKK	2.51	1,816.92
Control	6006	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	4	4	4	0.04%	5.15%	LHVLEAQDLIAK	3.51	1,349.78
Control	6006	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	4	4	4	0.04%	5.15%	LLVPLVPDLQDVAQLR	3.83	1,789.06
Control	6006	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	4	4	4	0.04%	5.15%	LLYLDTSEVR	2.53	1,208.65

Control	6006	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	4	4	4	0.04%	5.15%	LTHSDSPPEAPAGPLGQVK	2.96	1,900.98
Control	6006	CD9 molecule	gi|151556398,gi|162821,gi|27806911,gi|399217	25,240.80	99.80%	2	3	5	0.05%	6.19%	EVQKFYEDTYNKLK	2.9	1,804.91
Control	6006	CD9 molecule	gi|151556398,gi|162821,gi|27806911,gi|399217	25,240.80	99.80%	2	3	5	0.05%	6.19%	FYEDTYNKLK	2.96	1,320.65
Control	6006	GANAB protein	gi|151553519,gi|194679898	109,455.80	99.90%	2	2	2	0.02%	3.31%	LSFQHDPETSVLILR	3.15	1,754.94
Control	6006	GANAB protein	gi|151553519,gi|194679898	109,455.80	99.90%	2	2	2	0.02%	3.31%	VVIIGAGKPATVVLQTK	3.52	1,694.06
Control	6006	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	3	4	4	0.04%	4.37%	DVIDKQHTEQEASYGR	5.01	1,875.88
Control	6006	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	3	4	4	0.04%	4.37%	LNQPQPDFTK	2.61	1,187.61
Control	6006	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	3	4	4	0.04%	4.37%	SFHSFYQLLQGGSDQMLR	3.2	2,130.01
Control	6006	Chromosome 20 open reading frame 3 ortholog	gi|74268319,gi|78369434	46,074.40	99.80%	2	2	2	0.02%	7.28%	GGADVFVENLPGFPDNIR	2.88	1,916.95
Control	6006	Chromosome 20 open reading frame 3 ortholog	gi|74268319,gi|78369434	46,074.40	99.80%	2	2	2	0.02%	7.28%	LLLSSETPIEGR	3.47	1,314.73

Control	6006	PREDICTED: similar to Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A	gi|119896006	130,855.40	100.00%	3	3	3	0.03%	2.88%	AEMLLDQYR	2.37	1,154.55
Control	6006	PREDICTED: similar to Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A	gi|119896006	130,855.40	100.00%	3	3	3	0.03%	2.88%	TQYIFNNMVVK	2.94	1,372.69

Control	6006	PREDICTED: similar to Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A	gi|119896006	130,855.40	100.00%	3	3	3	0.03%	2.88%	TTVVLAPLGDDFR	2.5	1,403.75
Control	6006	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	4	6	0.07%	21.30%	DYPLPDVAHVK	3.1	1,253.65

Control	6006	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	4	6	0.07%	21.30%	LKFKESFAEMNR	3.88	1,515.76
Control	6006	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	4	6	0.07%	21.30%	SEDYALPSYVDR	2.7	1,414.65

Control	6006	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	4	6	0.07%	21.30%	SEDYALPSYVDRR	2	1,570.75
Control	6006	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	5	6	7	0.08%	11.80%	APVPTGEVYFADSFDR	1.99	1,770.83
Control	6006	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	5	6	7	0.08%	11.80%	KIPNPDFFEDLEPFK	4.98	1,835.92
Control	6006	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	5	6	7	0.08%	11.80%	LPGDKGLVLMSR	2.16	1,301.72
Control	6006	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	5	6	7	0.08%	11.80%	TPELNLDQFHDKTPYTIMFGPDK	3.35	2,723.30
Control	6006	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	5	6	7	0.08%	11.80%	VTYKAPVPTGEVYFADSFDR	4.73	2,262.11
Control	6006	nicalin	gi|115494944,gi|94534903	63,091.10	99.80%	2	4	4	0.04%	6.23%	AAQLVDKDGTFLSTLEHYLSR	5.84	2,364.22
Control	6006	nicalin	gi|115494944,gi|94534903	63,091.10	99.80%	2	4	4	0.04%	6.23%	MQQYDLQGQPYGTR	2.85	1,700.77
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	GATYNIIVEAVK	2.96	1,277.71
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	GDSPASSKPVSINYR	3.49	1,577.79
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	GFNCESKPEPEETCFDKYTGNTYR	3.25	2,815.20

Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	GLAFTDVDVDSIK	3.7	1,379.71
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	GLRPGVVYEGQLISVQHYGQR	6.28	2,356.25
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	IHLYTLNDNAR	3.33	1,329.69
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	KKTDELPQLVTLPHPNLHGPEILDVPSTVQK	5.15	3,443.89
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	NLQPGSEYAVSLVAVK	4.19	1,674.91
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	NTFAEVTGLSPGVTYHFK	3.64	1,967.99
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	QYNVGPAASQYPLR	3.63	1,563.79
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	RPGAEPGNEGSTAHSYNQYSQR	4.16	2,406.08
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	SDKVPPPRDLQFVEVTDVK	2.64	2,169.16
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	SSPVVIDASTAIDAPSNLR	3.89	1,913.00
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	STATISGLKPGVDYTITVYAVTGR	3.41	2,470.32

Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	STTPDITGYR	2.25	1,110.54
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	SYTITGLQPGTDYK	3.57	1,543.76
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	SYTITGLQPGTDYKIHLYTLNDNAR	4.56	2,854.44
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	TEIDKPSQMQVTDVQDNSISVR	5.63	2,506.21
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	TKTETITGFQVDAIPANGQTPIQR	2.8	2,586.35
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	TPFITNPGYDTGNGIQLPGTSGQQPSLGQQMIFEEHGFRR	3.03	4,392.11
Control	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	28	30	0.33%	16.10%	VPGTSASATLTGLTR	4.35	1,431.78
Control	6006	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	5	7	8	0.09%	23.00%	KLPPLPLTLALGAFLNHR	3.25	1,971.19
Control	6006	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	5	7	8	0.09%	23.00%	KLPPLPLTLALGAFLNHRK	3.23	2,099.29
Control	6006	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	5	7	8	0.09%	23.00%	MQDTSVSFGYQLDLPK	2.52	1,844.87

Control	6006	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	5	7	8	0.09%	23.00%	QLSPTEAFPVLVGDMDNSGSLNAQVIHQLGPGLR	3.8	3,576.81
Control	6006	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	5	7	8	0.09%	23.00%	RPGEEGAVMSLAGK	3.68	1,417.71
Control	6006	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	7	8	8	0.09%	7.62%	AFHSSLHESIQKPK	2.95	1,608.85
Control	6006	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	7	8	8	0.09%	7.62%	KADVGFAMGIAGTDVAK	3.83	1,666.85
Control	6006	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	7	8	8	0.09%	7.62%	LKTNPVEGLSGNPADLEK	4.72	1,881.99
Control	6006	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	7	8	8	0.09%	7.62%	QVVAVTGDGTNDGPALK	3.97	1,641.84
Control	6006	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	7	8	8	0.09%	7.62%	QVVAVTGDGTNDGPALKK	2.95	1,769.94

Control	6006	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	7	8	8	0.09%	7.62%	TQDGVALEIQPLNSQEGIDSEEKEK	3.41	2,757.34
Control	6006	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	7	8	8	0.09%	7.62%	TQDGVALEIQPLNSQEGIDSEEKEKK	4.42	2,885.44
Control	6006	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	4	6	11	0.12%	35.40%	AGLQFPVGR	3.1	944.5313
Control	6006	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	4	6	11	0.12%	35.40%	HLQLAIRNDEELNKLLGK	2.94	2,104.19
Control	6006	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	4	6	11	0.12%	35.40%	NDEELNKLLGK	3.15	1,272.68
Control	6006	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	4	6	11	0.12%	35.40%	VTIAQGGVLPNIQAVLLPK	4.93	1,931.17
Control	6006	phosphatidic acid phosphatase type 2A	gi|122692411,gi|81674095	32,253.70	99.80%	2	4	4	0.04%	10.20%	KEEDSHTTLHETPTTGNHYR	3.88	2,353.08
Control	6006	phosphatidic acid phosphatase type 2A	gi|122692411,gi|81674095	32,253.70	99.80%	2	4	4	0.04%	10.20%	NNYIATIYK	2.47	1,099.58
Control	6006	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	100.00%	3	3	3	0.03%	9.42%	IIFGYKEIPVLVTQISSTNHPVK	2.81	2,583.45

Control	6006	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	100.00%	3	3	3	0.03%	9.42%	VGLSDAFVVVHR	4.43	1,298.72
Control	6006	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	100.00%	3	3	3	0.03%	9.42%	VNLSFDFPFYGHFLR	2.3	1,858.93
Control	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	16	21	0.23%	29.20%	ASLDRPFTSLESAFYSIVGLSSLGAQVPDVK	4.2	3,254.69
Control	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	16	21	0.23%	29.20%	FSSGYYDFSVK	2.74	1,299.59

Control	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	16	21	0.23%	29.20%	ISTEVGITNVDLSTVDKDQSIAPK	2.81	2,530.33
Control	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	16	21	0.23%	29.20%	LMDHVGTEPSIKEDQVIQLMNAIFSK	4.05	2,959.49

Control	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	16	21	0.23%	29.20%	LQVTNVLSQPLTQATVK	4.39	1,840.05
Control	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	16	21	0.23%	29.20%	LQVTNVLSQPLTQATVKLEHAK	2.57	2,418.37

Control	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	16	21	0.23%	29.20%	LSKEETVLATVQALQTASYLSQQADLR	4.93	2,963.57
Control	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	16	21	0.23%	29.20%	SIVEEIEDLVAR	3.72	1,372.73

Control	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	16	21	0.23%	29.20%	TGQEVVFVAEPDSK	3.13	1,505.75
Control	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	16	21	0.23%	29.20%	VEGDNRYIANTVELR	4.25	1,748.89

Control	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	16	21	0.23%	29.20%	VKISTEVGITNVDLSTVDKDQSIAPK	3.31	2,757.49
Control	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	16	21	0.23%	29.20%	YIANTVELR	2.85	1,078.59

Control	6006	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	99.80%	2	2	2	0.02%	7.85%	GLLPQLLGVAPEK	2.25	1,334.80
Control	6006	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	99.80%	2	2	2	0.02%	7.85%	ITLPAPNPDHVGGYK	2.21	1,578.83
Control	6006	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	99.80%	2	2	2	0.02%	7.85%	LQVAGEITTGPR	2.95	1,241.69

Control	6006	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	99.80%	2	2	2	0.02%	7.85%	YLNIFGESQPNPK	2.98	1,506.76
Control	6006	PREDICTED: integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	gi|119913150	148,911.70	99.90%	2	2	2	0.02%	2.20%	IFSGPSSEQFGYAVQQFINPK	2.87	2,344.16
Control	6006	PREDICTED: integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	gi|119913150	148,911.70	99.90%	2	2	2	0.02%	2.20%	VVFNLNTFK	2.42	1,081.60
Control	6006	STT3B protein	gi|146186621,gi|148235371	93,202.50	100.00%	4	4	4	0.04%	6.08%	ENPPVEDSSDEDDKRNPGNLYDK	2.25	2,633.16
Control	6006	STT3B protein	gi|146186621,gi|148235371	93,202.50	100.00%	4	4	4	0.04%	6.08%	FGEMQLDFR	2.91	1,158.53
Control	6006	STT3B protein	gi|146186621,gi|148235371	93,202.50	100.00%	4	4	4	0.04%	6.08%	HVTEQEKTEEGLGPNIK	3.28	1,908.97
Control	6006	STT3B protein	gi|146186621,gi|148235371	93,202.50	100.00%	4	4	4	0.04%	6.08%	KHVTEQEKTEEGLGPNIK	3.6	2,037.06
Control	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	12	18	28	0.30%	17.00%	ENPETEEDVGPVVQHIYELR	3.21	2,353.13
Control	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	12	18	28	0.30%	17.00%	FGSAIAPLGDLDQDGFNDIAIAAPYGGEDKK	5.87	3,165.54
Control	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	12	18	28	0.30%	17.00%	FSVHQQSEMDTSVK	4.41	1,638.74

Control	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	12	18	28	0.30%	17.00%	GALPTKLDFQVELLLDKLK	4.49	2,141.26
Control	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	12	18	28	0.30%	17.00%	GATDIDKNGYPDLIVGAFGVDR	4.36	2,293.15
Control	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	12	18	28	0.30%	17.00%	GIVYIFNGRPTGLNAVPSQILEGK	5.16	2,543.40
Control	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	12	18	28	0.30%	17.00%	IYIGDDNPLTLIVK	4.05	1,573.88
Control	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	12	18	28	0.30%	17.00%	KIYIGDDNPLTLIVK	2.71	1,701.98
Control	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	12	18	28	0.30%	17.00%	LNGFEVFAR	2.45	1,052.55
Control	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	12	18	28	0.30%	17.00%	MFLLVGAPK	3.36	991.5647
Control	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	12	18	28	0.30%	17.00%	SSASFNVIEFPYK	3.75	1,488.74
Control	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	12	18	28	0.30%	17.00%	YKENPETEEDVGPVVQHIYELR	4.42	2,644.29
Control	6006	RecName: Full=Monocarboxylate transporter 1; Short=MCT 1; AltName: Full=Solute carrier family 16 member 1	gi|122139973,gi|77567740,gi|82617542	54,281.70	99.80%	2	3	3	0.03%	3.79%	GASDANTDLIGGNPKEEK	3.42	1,815.87
Control	6006	RecName: Full=Monocarboxylate transporter 1; Short=MCT 1; AltName: Full=Solute carrier family 16 member 1	gi|122139973,gi|77567740,gi|82617542	54,281.70	99.80%	2	3	3	0.03%	3.79%	GASDANTDLIGGNPKEEKK	2.96	1,943.97

Control	6006	RecName: Full=L-lactate dehydrogenase B chain; Short=LDH-B	gi|118572666,gi|148744825,gi|154425698,gi|27806561,gi|59858383,gi|74353944,gi|8979739	36,606.70	99.80%	2	2	2	0.02%	7.49%	IVADKDYSVTANSK	2.45	1,510.77
Control	6006	RecName: Full=L-lactate dehydrogenase B chain; Short=LDH-B	gi|118572666,gi|148744825,gi|154425698,gi|27806561,gi|59858383,gi|74353944,gi|8979739	36,606.70	99.80%	2	2	2	0.02%	7.49%	MVVESAYEVIK	2.27	1,283.66
Control	6006	PREDICTED: similar to programmed cell death 6 interacting protein isoform 1	gi|119914274	96,862.00	99.80%	2	2	2	0.02%	2.63%	STPVNVPISQK	2.34	1,169.65
Control	6006	PREDICTED: similar to programmed cell death 6 interacting protein isoform 1	gi|119914274	96,862.00	99.80%	2	2	2	0.02%	2.63%	TMQGSEVVNVLK	3.93	1,320.68
Control	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	13	13	14	0.15%	35.90%	AVDSLVPIGR	2.98	1,026.59
Control	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	13	13	14	0.15%	35.90%	EAYPGDVFYLHSR	2.08	1,553.74
Control	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	13	13	14	0.15%	35.90%	EVAAFAQFGSDLDAATQQLLSR	3.28	2,338.17

Control	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	13	13	14	0.15%	35.90%	FENAFLSHVISQHQALLSK	2.31	2,169.15
Control	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	13	13	14	0.15%	35.90%	GMSLNLEPDNVGVVVFGNDKLIK	2.8	2,474.30
Control	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	13	13	14	0.15%	35.90%	HALIIYDDLSK	3.21	1,287.69
Control	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	13	13	14	0.15%	35.90%	ILGADTSVDLEETGR	3.64	1,575.79
Control	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	13	13	14	0.15%	35.90%	ISVREPMQTGIK	2.65	1,374.74
Control	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	13	13	14	0.15%	35.90%	ITKFENAFLSHVISQHQALLSK	4.69	2,511.37

Control	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	13	13	14	0.15%	35.90%	TGAIDVPVGEELLGR	3.28	1,624.89
Control	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	13	13	14	0.15%	35.90%	VGLKAPGIIPR	2.89	1,120.72
Control	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	13	13	14	0.15%	35.90%	VLSIGDGIAR	2.36	1,000.58
Control	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	13	13	14	0.15%	35.90%	VVDALGNAIDGKGPIGSK	4.41	1,710.94
Control	6006	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	10	10	0.11%	41.80%	IMVANIEEVLQR	4.13	1,430.77
Control	6006	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	10	10	0.11%	41.80%	IMVANIEEVLQRGEALSALDSK	2.72	2,402.26
Control	6006	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	10	10	0.11%	41.80%	KLAFAYLEDLHSEFDEQHGK	4.16	2,377.15
Control	6006	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	10	10	0.11%	41.80%	KVPTVSRPYSFIEFDTYIQK	2.88	2,418.27

Control	6006	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	10	10	0.11%	41.80%	NLGSINTELQDVQR	4.02	1,586.81
Control	6006	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	10	10	0.11%	41.80%	VADGLPLAASMQEDEQSGR	2.91	1,989.92
Control	6006	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	10	10	0.11%	41.80%	VADGLPLAASMQEDEQSGRDLQQYQSQAK	5.46	3,179.49
Control	6006	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	4	4	5	0.05%	19.60%	INVNEIFYDLVR	3.75	1,494.80
Control	6006	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	4	4	5	0.05%	19.60%	LVVLGSGGVGK	2.97	985.6042
Control	6006	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	4	4	5	0.05%	19.60%	SKINVNEIFYDLVR	3.72	1,709.92
Control	6006	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	4	4	5	0.05%	19.60%	YDPTIEDSYRK	2.31	1,386.65
Control	6006	RecName: Full=ATP synthase subunit g, mitochondrial; Short=ATPase subunit g	gi|2493093,gi|74354012,gi|7579922,gi|94400870	11,604.00	99.80%	2	4	6	0.07%	19.20%	APALVNAAVTYSKPR	3.18	1,557.87
Control	6006	RecName: Full=ATP synthase subunit g, mitochondrial; Short=ATPase subunit g	gi|2493093,gi|74354012,gi|7579922,gi|94400870	11,604.00	99.80%	2	4	6	0.07%	19.20%	NLAEKAPALVNAAVTYSKPR	7.01	2,113.18
Control	6006	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	100.00%	3	3	3	0.03%	15.30%	LLLLGTGESGK	3.11	1,087.64

Control	6006	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	100.00%	3	3	3	0.03%	15.30%	VADPAYLPTQQDVLR	2.62	1,685.89
Control	6006	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	100.00%	3	3	3	0.03%	15.30%	VRVPTTGIIEYPFDLQSVIFR	5.74	2,450.34
Control	6006	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	100.00%	3	3	3	0.03%	15.30%	YYLNDLDRVADPAYLPTQQDVLR	3.17	2,738.38
Control	6006	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	100.00%	3	3	3	0.03%	6.25%	LPVPASAPIPFFHR	3.43	1,548.87
Control	6006	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	100.00%	3	3	3	0.03%	6.25%	NAELEAIPNSGMDHTHR	2.55	1,907.87
Control	6006	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	100.00%	3	3	3	0.03%	6.25%	VLMEFVENSR	3.13	1,239.60
Control	6006	RecName: Full=60S ribosomal protein L7a	gi|108860939,gi|146231828,gi|83638795,gi|94966839	30,008.40	99.90%	2	2	2	0.02%	10.20%	LKVPPAINQFTQALDR	5.39	1,811.02
Control	6006	RecName: Full=60S ribosomal protein L7a	gi|108860939,gi|146231828,gi|83638795,gi|94966839	30,008.40	99.90%	2	2	2	0.02%	10.20%	NFGIGQDIQPK	2.88	1,216.63

Control	6006	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	5	5	5	0.05%	16.50%	GFKDQIYDIFQK	3.3	1,501.77
Control	6006	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	5	5	5	0.05%	16.50%	GIYAYGFEKPSAIQQR	2.59	1,827.94
Control	6006	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	5	5	5	0.05%	16.50%	GYDVIAQAQSGTGK	3.5	1,394.69

Control	6006	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	5	5	5	0.05%	16.50%	LQMEAPHIIVGTPGR	3.66	1,634.87
Control	6006	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	5	5	5	0.05%	16.50%	VLITTDLLAR	3.04	1,114.68
Control	6006	PREDICTED: similar to rat bone marrow stromal cell antigen 1 (BST-1)	gi|119894230	35,126.70	99.80%	2	2	2	0.02%	4.72%	GFFADFEIPYLQK	2.77	1,574.79
Control	6006	PREDICTED: similar to rat bone marrow stromal cell antigen 1 (BST-1)	gi|119894230	35,126.70	99.80%	2	2	2	0.02%	4.72%	GFFADFEIPYLQKDK	1.93	1,817.91
Control	6006	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	6	8	8	0.09%	23.60%	GPPDFSSDEEREPTPVLGSGAAVAGR	4.98	2,598.24
Control	6006	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	6	8	8	0.09%	23.60%	HAAPILPITEFSDIPR	2.92	1,776.96
Control	6006	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	6	8	8	0.09%	23.60%	LKSELVANNVTLPAGEQR	3.39	1,939.06

Control	6006	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	6	8	8	0.09%	23.60%	LKSELVANNVTLPAGEQRK	3.92	2,067.16
Control	6006	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	6	8	8	0.09%	23.60%	SSTPLPTISSSVENTR	2.65	1,675.85
Control	6006	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	6	8	8	0.09%	23.60%	YGVNPGPIVGTTR	3.29	1,330.71
Control	6006	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	6	6	6	0.07%	4.01%	GLAGAVSELLR	2.97	1,085.63
Control	6006	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	6	6	6	0.07%	4.01%	LAQAAQSSVATITR	4.28	1,416.78
Control	6006	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	6	6	6	0.07%	4.01%	LLAALLEDEGGSGRPLLQAAK	3.18	2,122.19
Control	6006	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	6	6	6	0.07%	4.01%	LNEAAAGLNQAATELVQASR	3.07	2,027.05
Control	6006	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	6	6	6	0.07%	4.01%	QAAASATQTIAAAQHATSTPK	3.49	2,025.04
Control	6006	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	6	6	6	0.07%	4.01%	TLSHPQQMALLDQTK	3.96	1,726.88
Control	6006	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	7	7	7	0.08%	15.00%	FKPPSVAVVQPK	3.67	1,296.77
Control	6006	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	7	7	7	0.08%	15.00%	GLIPQLIGVAPEK	2.25	1,334.80
Control	6006	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	7	7	7	0.08%	15.00%	IAPLAEGALPYNLAELQR	3.27	1,939.06
Control	6006	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	7	7	7	0.08%	15.00%	LQVAGEITTGPR	2.95	1,241.69
Control	6006	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	7	7	7	0.08%	15.00%	LTLADIER	2.34	930.5256
Control	6006	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	7	7	7	0.08%	15.00%	NIFLQYASTEVDGEHYMTPEDFVQR	3.71	3,005.36
Control	6006	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	7	7	7	0.08%	15.00%	YLGLYNDPNSNPK	3.23	1,494.72
Control	6006	ALDH3A2 protein	gi|151557095,gi|156120617	54,059.30	99.80%	2	3	3	0.03%	4.95%	IAFGGEMDEATR	2.17	1,312.58
Control	6006	ALDH3A2 protein	gi|151557095,gi|156120617	54,059.30	99.80%	2	3	3	0.03%	4.95%	NADEAIQFINER	3	1,419.69
Control	6006	IKK interacting protein	gi|126010633,gi|126165284,gi|193806036	39,199.60	100.00%	3	3	3	0.03%	13.80%	METSEFQGLQSK	3.48	1,400.64
Control	6006	IKK interacting protein	gi|126010633,gi|126165284,gi|193806036	39,199.60	100.00%	3	3	3	0.03%	13.80%	MSGLVTDVTSLTDSVQELENKIEK	3.04	2,652.33

Control	6006	IKK interacting protein	gi|126010633,gi|126165284,gi|193806036	39,199.60	100.00%	3	3	3	0.03%	13.80%	NIGDLLSSSIDR	3.35	1,289.67
Control	6006	defender against cell death 1	gi|59858361,gi|73918963,gi|74354770,gi|77736467,gi|83286811	12,477.50	99.80%	2	2	4	0.04%	19.50%	ADFQGISPER	3.16	1,119.54
Control	6006	defender against cell death 1	gi|59858361,gi|73918963,gi|74354770,gi|77736467,gi|83286811	12,477.50	99.80%	2	2	4	0.04%	19.50%	FLEEYLSATPQR	2.39	1,453.73
Control	6006	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	5	5	6	0.07%	7.62%	ESVEQQADSFK	2.76	1,267.58
Control	6006	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	5	5	6	0.07%	7.62%	GNSSESIEAIRDYEEEFFQNSK	3.96	2,579.15
Control	6006	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	5	5	6	0.07%	7.62%	MLAITANTLR	3.07	1,119.62
Control	6006	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	5	5	6	0.07%	7.62%	VDLAEKNVTSPSR	3.12	1,415.75
Control	6006	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	5	5	6	0.07%	7.62%	VSDKEKIDQLQEELLHTQLK	2.73	2,394.29
Control	6006	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	5	5	5	0.05%	9.73%	AFITNIPFDVK	2.9	1,264.69
Control	6006	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	5	5	5	0.05%	9.73%	GGNRFEPYANPTKR	4.15	1,606.81

Control	6006	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	5	5	5	0.05%	9.73%	GNFGGSFAGSFGGAGGHAPGVAR	3.68	2,034.95
Control	6006	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	5	5	5	0.05%	9.73%	INEILSNALK	2.61	1,114.65
Control	6006	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	5	5	5	0.05%	9.73%	LKEVFSMAGVVVR	3.54	1,450.81
Control	6006	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	6	8	9	0.10%	16.20%	ELQALTDAMYTNLR	3.34	1,654.81
Control	6006	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	6	8	9	0.10%	16.20%	LLLFPFLSPQKDPEIYTDPEVFK	4.01	2,736.45
Control	6006	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	6	8	9	0.10%	16.20%	LLLFPFLSPQKDPEIYTDPEVFKYNR	3.88	3,169.66
Control	6006	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	6	8	9	0.10%	16.20%	LTAAPFITR	2.64	989.5779
Control	6006	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	6	8	9	0.10%	16.20%	VLDSMPVLDSVLSESLR	3.09	1,875.97
Control	6006	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	6	8	9	0.10%	16.20%	YGFGLMQPEHDVPVR	2.35	1,760.84
Control	6006	metalloproteinase	gi|1044811,gi|157742933,gi|27806209,gi|29839751	84,171.20	99.80%	2	2	2	0.02%	4.01%	AIDTIYQTTDFSGIR	2.86	1,700.85
Control	6006	metalloproteinase	gi|1044811,gi|157742933,gi|27806209,gi|29839751	84,171.20	99.80%	2	2	2	0.02%	4.01%	HYEGLSYDVDSLHQK	3.81	1,790.83

Control	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	5	0.05%	36.70%	AILVDLEPGTMDSVR	3.4	1,631.83
Control	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	5	0.05%	36.70%	ALTVPELTQQVFDAK	2.17	1,659.90
Control	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	5	0.05%	36.70%	GHYTEGAELVDSVLDVVR	3.49	1,958.98
Control	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	5	0.05%	36.70%	GHYTEGAELVDSVLDVVRK	3.77	2,087.08
Control	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	5	0.05%	36.70%	IMNTFSVVPSPK	3.05	1,335.70
Control	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	5	0.05%	36.70%	IREEYPDRIMNTFSVVPSPK	2.98	2,394.21
Control	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	5	0.05%	36.70%	ISEQFTAMFR	2.73	1,245.59
Control	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	5	0.05%	36.70%	ISVYYNEATGGK	3.54	1,301.64
Control	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	5	0.05%	36.70%	LAVNMVPFPR	3.44	1,159.63
Control	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	5	0.05%	36.70%	LHFFMPGFAPLTSR	3.02	1,636.83
Control	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	5	0.05%	36.70%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	5.68	4,479.06
Control	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	5	0.05%	36.70%	YLTVAAVFR	2.82	1,039.59
Control	6006	RAP2B protein	gi|134025188,gi|154425870,gi|156523174	20,470.40	99.80%	2	2	2	0.02%	7.65%	ASVDELFAEIVR	2.41	1,348.71
Control	6006	RAP2B protein	gi|134025188,gi|154425870,gi|156523174	20,470.40	99.80%	2	2	2	0.02%	7.65%	NKASVDELFAEIVR	4.2	1,590.85
Control	6006	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	7	9	416	4.52%	62.80%	AAVTSLFAK	2.69	907.5247
Control	6006	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	7	9	416	4.52%	62.80%	FFESFGDLSSADAILGNPK	2.52	2,014.98

Control	6006	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	7	9	416	4.52%	62.80%	LLGNVLVVVLAR	4.74	1,265.83
Control	6006	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	7	9	416	4.52%	62.80%	LLVVYPWTQR	3.19	1,274.73
Control	6006	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	7	9	416	4.52%	62.80%	RFGSEFSPELQASFQK	2.82	1,857.91
Control	6006	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	7	9	416	4.52%	62.80%	VKVDEVGGEALGR	4.12	1,328.72
Control	6006	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	7	9	416	4.52%	62.80%	VVTGVANALAHR	4.1	1,207.69
Control	6006	Ribosomal protein L6	gi|126717393,gi|58760432,gi|61553343,gi|61553350,gi|67461090,gi|72534798	32,672.90	99.80%	2	2	2	0.02%	10.50%	AVPQLQGYLR	2.46	1,144.65
Control	6006	Ribosomal protein L6	gi|126717393,gi|58760432,gi|61553343,gi|61553350,gi|67461090,gi|72534798	32,672.90	99.80%	2	2	2	0.02%	10.50%	HQEGEIFDTEREKYEITEQR	3.76	2,537.19
Control	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	11	12	12	0.13%	7.49%	AFGPGLQGGSAGSPAR	4.02	1,429.72
Control	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	11	12	12	0.13%	7.49%	ANLPQSFQVDTSK	2.85	1,434.72
Control	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	11	12	12	0.13%	7.49%	AYGPGIEPTGNMVK	3.64	1,449.70

Control	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	11	12	12	0.13%	7.49%	FNEEHIPDSPFVVPVASPSGDAR	2.76	2,467.19
Control	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	11	12	12	0.13%	7.49%	GAGTGGLGLAVEGPSEAK	4.38	1,570.81
Control	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	11	12	12	0.13%	7.49%	IANLQTDLSDGLR	3.27	1,415.75
Control	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	11	12	12	0.13%	7.49%	LIALLEVLSQK	2.52	1,226.77
Control	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	11	12	12	0.13%	7.49%	SPFEVYVDKSQGDASK	3.71	1,756.84
Control	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	11	12	12	0.13%	7.49%	SPFSVGVSPSLDLSK	4.05	1,519.80
Control	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	11	12	12	0.13%	7.49%	VAQPAITDNKDGTVTVR	2.38	1,784.95
Control	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	11	12	12	0.13%	7.49%	VTAQGPGLEPSGNIANK	4.79	1,652.86

Control	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	11	12	12	0.13%	7.49%	YTPVQQGPVGINVTYGGDAIPK	3.21	2,274.18
Control	6006	NRAS protein	gi|146186548,gi|148226664	21,211.30	99.80%	2	2	2	0.02%	12.20%	SFADINLYR	2.57	1,098.56
Control	6006	NRAS protein	gi|146186548,gi|148226664	21,211.30	99.80%	2	2	2	0.02%	12.20%	TRQGVEDAFYTLVR	3.22	1,654.85
Control	6006	PI4K2A protein	gi|151554868,gi|154152033	54,067.10	99.80%	2	2	2	0.02%	6.89%	ERNEFPEDPEFEAVVR	4.67	1,962.92
Control	6006	PI4K2A protein	gi|151554868,gi|154152033	54,067.10	99.80%	2	2	2	0.02%	6.89%	IYQGSSGSYFVKDPQGK	2.14	1,860.91
Control	6006	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	6	8	12	0.13%	29.40%	ANQVTDESLESTR	3.34	1,449.68
Control	6006	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	6	8	12	0.13%	29.40%	ILGLAIESQDAGIK	4.34	1,427.81
Control	6006	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	6	8	12	0.13%	29.40%	TITMLDEQGEQLK	3.68	1,521.75
Control	6006	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	6	8	12	0.13%	29.40%	TITMLDEQGEQLKR	2.54	1,677.85
Control	6006	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	6	8	12	0.13%	29.40%	VTNGQPQQATAGAASGGYIK	3.45	1,918.96
Control	6006	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	6	8	12	0.13%	29.40%	VTNGQPQQATAGAASGGYIKR	2.96	2,075.06
Control	6006	LBR protein	gi|151557087,gi|154152031	71,240.40	100.00%	3	4	4	0.04%	7.41%	FHLSQESSYIPTQYSLR	2.71	2,056.01
Control	6006	LBR protein	gi|151557087,gi|154152031	71,240.40	100.00%	3	4	4	0.04%	7.41%	LTPLVLKPFGNSINR	2.07	1,668.98
Control	6006	LBR protein	gi|151557087,gi|154152031	71,240.40	100.00%	3	4	4	0.04%	7.41%	SASASYQADLKEAR	3.24	1,496.73
Control	6006	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	gi|124828540,gi|126158903,gi|145566947	55,991.00	99.80%	2	2	2	0.02%	4.53%	ETVDSFLDLTR	2.79	1,295.65

Control	6006	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	gi|124828540,gi|126158903,gi|145566947	55,991.00	99.80%	2	2	2	0.02%	4.53%	NLFPSNLVVAAFR	2.74	1,447.81
Control	6006	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	5	8	13	0.14%	7.68%	ESTLHLVLR	3.07	1,067.62
Control	6006	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	5	8	13	0.14%	7.68%	IQDKEGIPPDQQR	2.68	1,523.78
Control	6006	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	5	8	13	0.14%	7.68%	QLEDGRTLSDYNIQK	2.93	1,779.89
Control	6006	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	5	8	13	0.14%	7.68%	TITLEVEPSDTIENVK	3.02	1,787.93
Control	6006	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	5	8	13	0.14%	7.68%	TLSDYNIQKESTLHLVLR	2.54	2,130.16
Control	6006	TPA: predicted NADPH oxidase-5	gi|151427572,gi|155372001	86,454.40	99.80%	2	2	3	0.03%	4.90%	MAALHIVEVNLLPSK	3.8	1,650.92
Control	6006	TPA: predicted NADPH oxidase-5	gi|151427572,gi|155372001	86,454.40	99.80%	2	2	3	0.03%	4.90%	RPPLFHYRPGDYLYLNIPSIAR	2.43	2,658.43
Control	6006	RecName: Full=Small nuclear ribonucleoprotein Sm D1; Short=Sm-D1; AltName: Full=snRNP core protein D1	gi|109894869,gi|73586929,gi|78050059	13,263.90	99.80%	2	2	2	0.02%	27.70%	NREPVQLETLSIR	3.7	1,554.86

Control	6006	RecName: Full=Small nuclear ribonucleoprotein Sm D1; Short=Sm-D1; AltName: Full=snRNP core protein D1	gi|109894869,gi|73586929,gi|78050059	13,263.90	99.80%	2	2	2	0.02%	27.70%	YFILPDSLPLDTLLVDVEPK	3.14	2,287.25
Control	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	16	20	21	0.23%	23.20%	AFTGREFDELSPSAQR	4.08	1,810.87
Control	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	16	20	21	0.23%	23.20%	AKDIVPGDIVEIAVGDKVPADIR	3.53	2,390.33
Control	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	16	20	21	0.23%	23.20%	AMGVVVATGVNTEIGK	4.1	1,561.83
Control	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	16	20	21	0.23%	23.20%	EEMNLEDSANFIK	2.82	1,555.69

Control	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	16	20	21	0.23%	23.20%	EFTLEFSR	1.87	1,028.50
Control	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	16	20	21	0.23%	23.20%	IGIFRQDEDVTAK	3.03	1,491.78
Control	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	16	20	21	0.23%	23.20%	IRDEMVATEQERTPLQQK	2.42	2,188.10
Control	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	16	20	21	0.23%	23.20%	ISLPVILMDETLK	2.65	1,487.84
Control	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	16	20	21	0.23%	23.20%	KSEIGIAMGSGTAVAK	4.63	1,535.81
Control	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	16	20	21	0.23%	23.20%	MNVFDTELKGLSK	2.95	1,497.76

Control	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	16	20	21	0.23%	23.20%	NAENAIEALKEYEPEMGK	3.19	2,051.96
Control	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	16	20	21	0.23%	23.20%	NMLFSGTNIAAGK	2.86	1,339.67
Control	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	16	20	21	0.23%	23.20%	SEIGIAMGSGTAVAK	5.27	1,407.72
Control	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	16	20	21	0.23%	23.20%	TASEMVLADDNFSTIVAAVEEGR	2.91	2,441.15
Control	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	16	20	21	0.23%	23.20%	VDQSILTGESVSVIK	3.97	1,574.86
Control	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	16	20	21	0.23%	23.20%	VGSTKVPMTPGVK	2.29	1,316.72

Control	6006	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	99.80%	2	4	4	0.04%	6.08%	HSLEGNPRDEEDDDEDMYSDNINAATEEK	5.28	3,354.35
Control	6006	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	99.80%	2	4	4	0.04%	6.08%	NLSLPFIFHEK	1.94	1,344.73
Control	6006	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	100.00%	3	3	3	0.03%	7.20%	DREVIEDVMLRDLEK	1.92	1,875.95
Control	6006	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	100.00%	3	3	3	0.03%	7.20%	ILEVVNQVQDEER	4.32	1,570.81
Control	6006	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	100.00%	3	3	3	0.03%	7.20%	IPVYSAFR	2.18	952.525
Control	6006	PREDICTED: similar to hCG1980844	gi|194674945	298,419.90	99.80%	2	2	2	0.02%	0.87%	QLQPNEEADYLGVR	3.54	1,631.80
Control	6006	PREDICTED: similar to hCG1980844	gi|194674945	298,419.90	99.80%	2	2	2	0.02%	0.87%	YLLTQELLR	2.95	1,148.67
Control	6006	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	99.80%	2	2	2	0.02%	6.27%	LRDPLQVHLPLR	3.61	1,456.87
Control	6006	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	99.80%	2	2	2	0.02%	6.27%	VAIYSPDGVR	2.31	1,076.57

Control	6006	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	7	0.08%	8.51%	EKDGEFSVLQLVGMLR	3.43	1,836.95
Control	6006	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	7	0.08%	8.51%	FADIVSILDK	2.92	1,120.63
Control	6006	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	7	0.08%	8.51%	IDTIAPDEITGSSDFEAR	3.35	1,936.91
Control	6006	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	7	0.08%	8.51%	TYVDPHTYEDPNQAVLK	2.26	1,989.96
Control	6006	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	7	0.08%	8.51%	VIGAGEFGEVYK	3.28	1,268.65
Control	6006	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	7	0.08%	8.51%	YSEPPLGLTR	2.45	1,132.60
Control	6006	Fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	gi|75773587,gi|78045491	54,768.00	100.00%	3	3	3	0.03%	7.71%	LINRPIIVFR	2.42	1,240.79
Control	6006	Fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	gi|75773587,gi|78045491	54,768.00	100.00%	3	3	3	0.03%	7.71%	LVAHPEPATGYTLEFR	3.91	1,800.93
Control	6006	Fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	gi|75773587,gi|78045491	54,768.00	100.00%	3	3	3	0.03%	7.71%	YLAPSGPSGTLK	2.48	1,190.64

Control	6006	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	3	3	4	0.04%	19.10%	FYGPEGPYGVFAGR	3.82	1,516.72
Control	6006	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	3	3	4	0.04%	19.10%	IVRGDQPAASDSDDDEPPPLPR	4.86	2,347.12
Control	6006	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	3	3	4	0.04%	19.10%	KFYGPEGPYGVFAGR	3.55	1,644.82
Control	6006	PTPN1 protein	gi|151556032,gi|154152077	49,019.80	99.80%	2	2	2	0.02%	5.18%	FSYLAVIEGAK	3.45	1,197.65
Control	6006	PTPN1 protein	gi|151556032,gi|154152077	49,019.80	99.80%	2	2	2	0.02%	5.18%	YRDVSPFDHSR	3.38	1,378.65
Control	6006	similar to ribosomal protein L27	gi|28189717,gi|47117099,gi|74268027,gi|77404275	15,780.40	99.80%	2	2	2	0.02%	14.70%	VYNYNHLMPTR	1.5	1,423.68
Control	6006	similar to ribosomal protein L27	gi|28189717,gi|47117099,gi|74268027,gi|77404275	15,780.40	99.80%	2	2	2	0.02%	14.70%	YSVDIPLDK	2.52	1,049.55
Control	6006	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.08%	13.40%	ISSVQSIVPALEIANAHR	3.26	1,905.06
Control	6006	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.08%	13.40%	LVQDVANNTNEEAGDGTTTATVLAR	4.5	2,560.25
Control	6006	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.08%	13.40%	TLKIPAMTIAK	2.23	1,202.72
Control	6006	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.08%	13.40%	TLNDELEIIEGMKFDR	2.24	1,938.95

Control	6006	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.08%	13.40%	VGEVIVTKDDAMLLK	3.07	1,646.90
Control	6006	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.08%	13.40%	VGLQVVAVK	2.34	912.5877
Control	6006	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	8	15	21	0.23%	36.70%	GPNGLLVYQGK	4	1,145.63
Control	6006	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	8	15	21	0.23%	36.70%	IDGNLVIRPYTPVSSDDDKGFVDLVIK	4.94	2,975.57
Control	6006	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	8	15	21	0.23%	36.70%	IGDTIEFR	2.64	950.4943
Control	6006	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	8	15	21	0.23%	36.70%	LIDKEVISHDTR	2.8	1,425.77
Control	6006	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	8	15	21	0.23%	36.70%	LIDKEVISHDTRR	3.26	1,581.87
Control	6006	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	8	15	21	0.23%	36.70%	STPAITLENPDIKYPLR	2.57	1,928.05
Control	6006	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	8	15	21	0.23%	36.70%	SVGMIAGGTGITPMLQVIR	4.06	1,917.03
Control	6006	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	8	15	21	0.23%	36.70%	VYFKDTHPKFPAGGK	2.5	1,691.89
Control	6006	endothelial cell adhesion molecule	gi|118151218,gi|119919027,gi|86823868	41,779.80	99.80%	2	2	2	0.02%	8.84%	ALEEPANDIKEDAIAPR	2.57	1,851.94
Control	6006	endothelial cell adhesion molecule	gi|118151218,gi|119919027,gi|86823868	41,779.80	99.80%	2	2	2	0.02%	8.84%	GSDTISKNGTLSSVTSAR	3.04	1,780.90
Control	6006	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	99.80%	2	2	2	0.02%	0.98%	GTLEPVQRPDVVLVGAGHR	4.07	2,000.10

Control	6006	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	99.80%	2	2	2	0.02%	0.98%	LRSPVISIDPPSSTVQQGQDASFK	4.44	2,557.33
Control	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	9	12	16	0.17%	23.10%	ALEEANADLEVK	2.45	1,301.66
Control	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	9	12	16	0.17%	23.10%	ASLENSLEETKGR	3.27	1,433.72
Control	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	9	12	16	0.17%	23.10%	LASYLDKVR	3.24	1,064.61
Control	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	9	12	16	0.17%	23.10%	LLEGEDAHLSSSQFSSGSQSSR	3.81	2,309.06
Control	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	9	12	16	0.17%	23.10%	QRPAEIKDYSPYFK	3.31	1,741.89
Control	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	9	12	16	0.17%	23.10%	TEELNREVATNSELVQSGK	5.6	2,104.05
Control	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	9	12	16	0.17%	23.10%	TRLEQEIATYR	3.56	1,379.73
Control	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	9	12	16	0.17%	23.10%	TRLEQEIATYRR	3.71	1,535.83
Control	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	9	12	16	0.17%	23.10%	VLDELTLAR	4.52	1,029.59
Control	6006	Transmembrane protein 49	gi|111307060,gi|115496266,gi|122133514	46,165.40	99.80%	2	2	3	0.03%	12.60%	LSGAEPDDEEYQEFEEMLEHAETAQDFASR	5.08	3,489.46
Control	6006	Transmembrane protein 49	gi|111307060,gi|115496266,gi|122133514	46,165.40	99.80%	2	2	3	0.03%	12.60%	VAMNKEQYNGNFTDPSSVNEK	5.36	2,388.08
Control	6006	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	5	6	8	0.09%	9.65%	FASFIDKVR	1.63	1,082.60
Control	6006	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	5	6	8	0.09%	9.65%	NKYEDEINKR	2.51	1,308.65
Control	6006	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	5	6	8	0.09%	9.65%	SLDLDSIIAEVK	3.05	1,302.72

Control	6006	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	5	6	8	0.09%	9.65%	SRTEAESWYQTKYEELQQTAGR	2.49	2,661.25
Control	6006	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	5	6	8	0.09%	9.65%	TLNNKFASFIDKVR	2.14	1,652.91
Control	6006	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	6	6	7	0.08%	11.40%	ALVQTEDHLLLFLQQLAGR	3.66	2,165.21
Control	6006	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	6	6	7	0.08%	11.40%	AQFFLQLSPSHYALLHYR	3.43	2,191.14
Control	6006	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	6	6	7	0.08%	11.40%	HLLVGLPSGAILSLPK	3.94	1,614.99
Control	6006	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	6	6	7	0.08%	11.40%	QLHELAPSIFFYLVDADQGR	3.41	2,319.18
Control	6006	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	6	6	7	0.08%	11.40%	RPEIPTEQSREENLIPYSPDVQIHAER	3.29	3,203.61
Control	6006	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	6	6	7	0.08%	11.40%	RPVLQSLLLPIMDQDYAK	3.23	2,116.15
Control	6006	A2M protein	gi|157743038,gi|157954061	167,557.60	99.80%	2	2	2	0.02%	2.98%	ASFSVLGDILGSAMR	3.28	1,523.79
Control	6006	A2M protein	gi|157743038,gi|157954061	167,557.60	99.80%	2	2	2	0.02%	2.98%	GGVDDEVTLSAYITIALLEMPLPVTHPVVR	4.02	3,205.72
Control	6006	chloride intracellular channel 1	gi|59858371,gi|62751970,gi|74268283,gi|75040226	26,974.50	100.00%	3	3	3	0.03%	23.70%	GVTFNVTTVDTK	3.02	1,281.67
Control	6006	chloride intracellular channel 1	gi|59858371,gi|62751970,gi|74268283,gi|75040226	26,974.50	100.00%	3	3	3	0.03%	23.70%	LAALNPESNTAGLDIFAK	3.79	1,844.98
Control	6006	chloride intracellular channel 1	gi|59858371,gi|62751970,gi|74268283,gi|75040226	26,974.50	100.00%	3	3	3	0.03%	23.70%	VLDNYLTSPLPDEVDETSAEDEGISQR	3.98	2,992.39
Control	6006	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	100.00%	4	4	4	0.04%	14.60%	AQIQEQNPSIEVVYYNK	2.86	2,023.01

Control	6006	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	100.00%	4	4	4	0.04%	14.60%	ELQVGIPVTNEQGQR	2.84	1,667.87
Control	6006	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	100.00%	4	4	4	0.04%	14.60%	NLLLSGAQLEASR	4.27	1,371.76
Control	6006	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	100.00%	4	4	4	0.04%	14.60%	QRELQVGIPVTNEQGQR	1.95	1,952.03
Control	6006	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	100.00%	2	3	4	0.04%	11.10%	LNQAVEFDVLPAFDALGQLTK	4.05	2,289.21
Control	6006	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	100.00%	2	3	4	0.04%	11.10%	QLAKPRPVILDPADPTGNVAGK	3.77	2,257.27
Control	6006	RecName: Full=GTP-binding protein SAR1a	gi|115311863,gi|74354052,gi|77735989	22,391.90	99.80%	2	2	2	0.02%	16.70%	LVFLGLDNAGK	2.95	1,146.65
Control	6006	RecName: Full=GTP-binding protein SAR1a	gi|115311863,gi|74354052,gi|77735989	22,391.90	99.80%	2	2	2	0.02%	16.70%	TDAISEEKLREIFGLYGQTTGK	2.99	2,456.27
Control	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	15	23	48	0.52%	42.70%	AVFPSIVGRPR	3.21	1,198.71
Control	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	15	23	48	0.52%	42.70%	DLTDYLMK	1.83	1,014.48
Control	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	15	23	48	0.52%	42.70%	DLYANTVLSGGTTMYPGIADR	4.35	2,231.07
Control	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	15	23	48	0.52%	42.70%	EITALAPSTMK	2.93	1,161.62
Control	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	15	23	48	0.52%	42.70%	GYSFTTTAER	2.75	1,132.53
Control	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	15	23	48	0.52%	42.70%	GYSFTTTAEREIVR	2.92	1,629.82
Control	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	15	23	48	0.52%	42.70%	IKIIAPPER	2.6	1,036.65

Control	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	15	23	48	0.52%	42.70%	IKIIAPPERK	2.61	1,164.75
Control	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	15	23	48	0.52%	42.70%	KDLYANTVLSGGTTMYPGIADR	6.1	2,359.16
Control	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	15	23	48	0.52%	42.70%	LDLAGRDLTDYLMK	3.38	1,639.84
Control	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	15	23	48	0.52%	42.70%	QEYDESGPSIVHR	1.87	1,516.70
Control	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	15	23	48	0.52%	42.70%	QEYDESGPSIVHRK	2.61	1,644.80
Control	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	15	23	48	0.52%	42.70%	SYELPDGQVITIGNER	4.74	1,790.89
Control	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	15	23	48	0.52%	42.70%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	6.26	3,199.61
Control	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	15	23	48	0.52%	42.70%	VAPEEHPVLLTEAPLNPK	4.81	1,954.06
Control	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	15	18	19	0.21%	33.70%	EATNPPVIQEEKPK	2.52	1,579.83
Control	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	15	18	19	0.21%	33.70%	ELSDFISYLK	2.17	1,214.63
Control	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	15	18	19	0.21%	33.70%	FLEDYFDGNLKR	3.47	1,516.74
Control	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	15	18	19	0.21%	33.70%	FVMQEEFSR	2.72	1,188.54
Control	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	15	18	19	0.21%	33.70%	FVMQEEFSRDGK	2.46	1,488.68
Control	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	15	18	19	0.21%	33.70%	GFPTIYFSPANK	2.8	1,341.68
Control	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	15	18	19	0.21%	33.70%	IFRDGEESGAYDGPR	5.47	1,668.76
Control	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	15	18	19	0.21%	33.70%	KLHFAVASR	3.02	1,028.60
Control	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	15	18	19	0.21%	33.70%	KTFSHELSDFGLESTTGEIPVVAVR	4.38	2,719.39
Control	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	15	18	19	0.21%	33.70%	LRKDPNIVIAK	3.41	1,266.79
Control	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	15	18	19	0.21%	33.70%	MDATANDVPSPYEVR	3.88	1,680.75

Control	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	15	18	19	0.21%	33.70%	SEPIPESNDGPVK	2.12	1,368.66
Control	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	15	18	19	0.21%	33.70%	TFSHELSDFGLESTTGEIPVVAVR	3.58	2,591.30
Control	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	15	18	19	0.21%	33.70%	VDCTANTNTCNKYGVSGYPTLK	2.77	2,349.09
Control	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	15	18	19	0.21%	33.70%	YGVSGYPTLK	2.27	1,084.57
Control	6006	GPR56 protein	gi|134024611,gi|139949073	76,936.90	99.80%	2	2	2	0.02%	3.35%	LPISSGSTSSSRI	3.65	1,291.69
Control	6006	GPR56 protein	gi|134024611,gi|139949073	76,936.90	99.80%	2	2	2	0.02%	3.35%	VLGIVVQNTK	2.7	1,070.66
Control	6006	PREDICTED: similar to Cyclin-Y-like protein 1	gi|76610508	41,110.50	99.80%	2	2	2	0.02%	6.89%	SLADDNNLNFLFAPLSK	2.6	1,878.96
Control	6006	PREDICTED: similar to Cyclin-Y-like protein 1	gi|76610508	41,110.50	99.80%	2	2	2	0.02%	6.89%	SLDIFDER	2.27	994.4841
Control	6006	PECAM1 protein	gi|111308531	82,597.50	100.00%	6	11	16	0.17%	8.81%	APVHFTIEK	2.94	1,041.57
Control	6006	PECAM1 protein	gi|111308531	82,597.50	100.00%	6	11	16	0.17%	8.81%	APVHFTIEKFELNIR	3	1,814.00
Control	6006	PECAM1 protein	gi|111308531	82,597.50	100.00%	6	11	16	0.17%	8.81%	FHIIPEGK	2.66	940.5252
Control	6006	PECAM1 protein	gi|111308531	82,597.50	100.00%	6	11	16	0.17%	8.81%	GTETVYSEIR	2.91	1,154.57
Control	6006	PECAM1 protein	gi|111308531	82,597.50	100.00%	6	11	16	0.17%	8.81%	QMPVEMSRPAVPLLNSNNEK	3.26	2,270.13
Control	6006	PECAM1 protein	gi|111308531	82,597.50	100.00%	6	11	16	0.17%	8.81%	RNTESYLIPHVR	3.1	1,484.80
Control	6006	RecName: Full=40S ribosomal protein S16	gi|108860953,gi|74354274,gi|75812950	16,427.90	100.00%	3	3	3	0.03%	15.80%	EIKDILIQYDR	3.05	1,405.77
Control	6006	RecName: Full=40S ribosomal protein S16	gi|108860953,gi|74354274,gi|75812950	16,427.90	100.00%	3	3	3	0.03%	15.80%	LLEPVLLLGK	2.21	1,094.72
Control	6006	RecName: Full=40S ribosomal protein S16	gi|108860953,gi|74354274,gi|75812950	16,427.90	100.00%	3	3	3	0.03%	15.80%	LLEPVLLLGKER	2.13	1,379.86
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	DGQVINETSQHHDDLE	2.54	1,836.80

Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	EEAESTLQSFRQDVDNASLAR	3.4	2,366.12
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	EMEENFSVEAANYQDTIGR	3.2	2,218.96
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	ETNLDSLPLVDTHSK	3.18	1,668.84
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	ETNLDSLPLVDTHSKR	2.96	1,824.95
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	EYQDLLNVK	2.07	1,121.58
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	FADLSEAANR	4.14	1,093.53
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	FADLSEAANRNNDALR	2.92	1,776.86
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	FANYIDKVR	2.97	1,125.61
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	HLREYQDLLNVK	4.6	1,527.83
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	ILLAELEQLK	3.48	1,169.71
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	ILLAELEQLKGQGK	4.43	1,539.91
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	ISLPLPNFSSLNLR	3.21	1,570.90
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	ISLPLPNFSSLNLRETNLDSLPLVDTHSKR	3.48	3,376.82
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	KLHDEEIQELQAQIQEQHVQIDMDVSKPDLTAALR	4.55	4,085.06
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	KVESLQEEIAFLK	5.02	1,533.85
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	KVESLQEEIAFLKK	4.4	1,661.95
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	LHDEEIQELQAQIQEQHVQIDMDVSKPDLTAALR	4.55	3,956.97
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	LQDEIQNMKEEMAR	2.59	1,750.81
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	LQEEMLQREEAESTLQSFR	5.04	2,340.11
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	LQEEMLQREEAESTLQSFRQDVDNASLAR	4.05	3,409.63

Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	MALDIEIATYR	3.82	1,311.66
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	TLYTSSPGGVYATR	4.43	1,472.74
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	TNEKVELQELNDR	4.13	1,587.80
Control	6006	vimentin	gi|110347570	53,710.80	100.00%	25	38	52	0.57%	55.60%	VEVERDNLAEDIMR	4.22	1,688.83
Control	6006	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	4	7	9	0.10%	20.60%	DKLDGNELDLSLSDLNEVPVKELAALPK	5.04	3,035.62
Control	6006	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	4	7	9	0.10%	20.60%	LRQLPADFGR	2.53	1,172.65
Control	6006	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	4	7	9	0.10%	20.60%	LVNLQHLDLLNNR	3.13	1,561.88
Control	6006	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	4	7	9	0.10%	20.60%	LVTLPVSFAQLK	4.93	1,315.80
Control	6006	RecName: Full=CDGSH iron sulfur domain-containing protein 1; AltName: Full=MitoNEET	gi|110825757,gi|73587067,gi|77404223	11,964.80	99.70%	2	2	2	0.02%	26.40%	HNEETGDNVGPLIIK	4.69	1,635.83
Control	6006	RecName: Full=CDGSH iron sulfur domain-containing protein 1; AltName: Full=MitoNEET	gi|110825757,gi|73587067,gi|77404223	11,964.80	99.70%	2	2	2	0.02%	26.40%	VVHAFDMEDLGDK	2.51	1,491.68

Control	6006	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	3	3	3	0.03%	5.45%	DAGQISGLNVLR	3.77	1,242.68
Control	6006	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	3	3	3	0.03%	5.45%	TTPSVVAFTADGER	3.36	1,450.72

Control	6006	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	3	3	3	0.03%	5.45%	VQQTVQDLFGR	2.92	1,290.68
Control	6006	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	5	7	7	0.08%	47.40%	ADLEAQRDVTYEEAKQFAEENGLLFLEASAK	3.27	3,485.71
Control	6006	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	5	7	7	0.08%	47.40%	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	3.95	3,150.56
Control	6006	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	5	7	7	0.08%	47.40%	NLTNPNTVIILIGNK	3.82	1,623.94
Control	6006	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	5	7	7	0.08%	47.40%	TGENVEDAFLEAAKK	3.04	1,621.81
Control	6006	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	5	7	7	0.08%	47.40%	YIIIGDMGVGK	2.91	1,181.62
Control	6006	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	2	3	5	0.05%	13.20%	EHGLIFMETSAK	2.91	1,378.67
Control	6006	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	2	3	5	0.05%	13.20%	GAAGALLVYDITR	2.11	1,319.73
Control	6006	RAB5A, member RAS oncogene family	gi|113911876,gi|115495947,gi|122144200	23,670.90	100.00%	3	4	5	0.05%	18.10%	GRGVDLTEPTQPTR	2.72	1,526.79
Control	6006	RAB5A, member RAS oncogene family	gi|113911876,gi|115495947,gi|122144200	23,670.90	100.00%	3	4	5	0.05%	18.10%	GVDLTEPTQPTR	2.51	1,313.67

Control	6006	RAB5A, member RAS oncogene family	gi|113911876,gi|115495947,gi|122144200	23,670.90	100.00%	3	4	5	0.05%	18.10%	LVLLGESAVGK	3.56	1,085.66
Control	6006	RAB5A, member RAS oncogene family	gi|113911876,gi|115495947,gi|122144200	23,670.90	100.00%	3	4	5	0.05%	18.10%	TSMNVNEIFMAIAK	2.82	1,584.78
Control	6006	nucleoside-diphosphate kinase NBR-A	gi|1064895,gi|1064897,gi|115311823,gi|115496892,gi|119224069,gi|151556410,gi|169658382,gi|169658384,gi|1709243,gi|74354800	17,307.40	99.80%	2	2	2	0.02%	19.10%	TFIAIKPDGVQR	2.21	1,344.76
Control	6006	nucleoside-diphosphate kinase NBR-A	gi|1064895,gi|1064897,gi|115311823,gi|115496892,gi|119224069,gi|151556410,gi|169658382,gi|169658384,gi|1709243,gi|74354800	17,307.40	99.80%	2	2	2	0.02%	19.10%	VMLGETNPADSKPGTIR	3.35	1,801.91
Control	6006	RecName: Full=Vesicle-associated membrane protein 8; Short=VAMP-8	gi|122140420,gi|74353894,gi|77735533	11,339.40	100.00%	3	3	4	0.04%	33.00%	NKTEDLEATSEHFK	5.13	1,648.78
Control	6006	RecName: Full=Vesicle-associated membrane protein 8; Short=VAMP-8	gi|122140420,gi|74353894,gi|77735533	11,339.40	100.00%	3	3	4	0.04%	33.00%	NLRDEVEGVK	2.94	1,158.61
Control	6006	RecName: Full=Vesicle-associated membrane protein 8; Short=VAMP-8	gi|122140420,gi|74353894,gi|77735533	11,339.40	100.00%	3	3	4	0.04%	33.00%	NLRDEVEGVKNIMTQNVER	3.08	2,260.14

Control	6006	RecName: Full=Annexin A1; AltName: Full=Annexin-1; AltName: Full=Annexin I; AltName: Full=Lipocortin I; AltName: Full=Calpactin II; AltName: Full=Chromobindin-9; AltName: Full=p35; AltName: Full=Phospholipase A2	gi|118597373,gi|264182,gi|61553085,gi|73587269,gi|73853762,gi|74	38,881.20	100.00%	4	4	5	0.05%	20.20%	GDRSEELAVNDDLADSDAR	5.21	2,047.92
Control	6006	RecName: Full=Annexin A1; AltName: Full=Annexin-1; AltName: Full=Annexin I; AltName: Full=Lipocortin I; AltName: Full=Calpactin II; AltName: Full=Chromobindin-9; AltName: Full=p35; AltName: Full=Phospholipase A2	gi|118597373,gi|264182,gi|61553085,gi|73587269,gi|73853762,gi|74	38,881.20	100.00%	4	4	5	0.05%	20.20%	GGPGSAVSPYPTFNPSSDVEALHK	2.32	2,414.16

Control	6006	RecName: Full=Annexin A1; AltName: Full=Annexin-1; AltName: Full=Annexin I; AltName: Full=Lipocortin I; AltName: Full=Calpactin II; AltName: Full=Chromobindin-9; AltName: Full=p35; AltName: Full=Phospholipase A2	gi|118597373,gi|264182,gi|61553085,gi|73587269,gi|73853762,gi|74	38,881.20	100.00%	4	4	5	0.05%	20.20%	GLGTDEDTLNEILASR	4.22	1,703.84
Control	6006	RecName: Full=Annexin A1; AltName: Full=Annexin-1; AltName: Full=Annexin I; AltName: Full=Lipocortin I; AltName: Full=Calpactin II; AltName: Full=Chromobindin-9; AltName: Full=p35; AltName: Full=Phospholipase A2	gi|118597373,gi|264182,gi|61553085,gi|73587269,gi|73853762,gi|74	38,881.20	100.00%	4	4	5	0.05%	20.20%	TPAQFDAEELR	3.57	1,276.62
Control	6006	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	5	6	6	0.07%	8.97%	IPQAVVDVSSHLQK	3.65	1,520.84
Control	6006	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	5	6	6	0.07%	8.97%	NLEELYLVGSLSHDISR	3.29	1,945.00
Control	6006	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	5	6	6	0.07%	8.97%	SIEEIVSFQHLR	2.04	1,457.77
Control	6006	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	5	6	6	0.07%	8.97%	SNTTQSGPEGSLVNSQSLK	4.69	1,933.95
Control	6006	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	5	6	6	0.07%	8.97%	YLDLSYNDIR	2.74	1,271.63

Control	6006	MGAT1 protein	gi|154426138,gi|59858237,gi|62751783	51,684.70	100.00%	3	3	3	0.03%	8.05%	GIVSFLYR	2.36	954.5407
Control	6006	MGAT1 protein	gi|154426138,gi|59858237,gi|62751783	51,684.70	100.00%	3	3	3	0.03%	8.05%	LAQDAEVELER	2.57	1,272.64
Control	6006	MGAT1 protein	gi|154426138,gi|59858237,gi|62751783	51,684.70	100.00%	3	3	3	0.03%	8.05%	LNQHFVPFTQLDLSYLR	5.12	2,091.10
Control	6006	Chain A, Structure Of Mammalian C3 With An Intact Thioester At 3a Resolution	gi|110590846,gi|110590847,gi|124056491,gi|83764016,gi|86438252,gi|99028969	187,214.10	100.00%	3	4	8	0.09%	3.49%	LYNVEATSYALLALLAR	3.54	1,881.05
Control	6006	Chain A, Structure Of Mammalian C3 With An Intact Thioester At 3a Resolution	gi|110590846,gi|110590847,gi|124056491,gi|83764016,gi|86438252,gi|99028969	187,214.10	100.00%	3	4	8	0.09%	3.49%	RPYTVAIAAYALALLGK	4.95	1,791.05
Control	6006	Chain A, Structure Of Mammalian C3 With An Intact Thioester At 3a Resolution	gi|110590846,gi|110590847,gi|124056491,gi|83764016,gi|86438252,gi|99028969	187,214.10	100.00%	3	4	8	0.09%	3.49%	YYGGGYGSTQATFMVFQALAQYQK	2.73	2,679.25
Control	6006	PREDICTED: similar to Thioredoxin domain-containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein ERp46) isoform 1	gi|119915902	45,792.10	99.80%	2	2	2	0.02%	4.55%	FFKPGQEAVK	2.47	1,150.63

Control	6006	PREDICTED: similar to Thioredoxin domain-containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein ERp46) isoform 1	gi|119915902	45,792.10	99.80%	2	2	2	0.02%	4.55%	GYPTLLLFR	2.58	1,079.62
Control	6006	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	5	8	11	0.12%	29.70%	FFDEESYSLLR	3.04	1,405.66

Control	6006	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	5	8	11	0.12%	29.70%	NNEDVSVIPPLFTVSVDHR	3.46	2,138.09
Control	6006	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	5	8	11	0.12%	29.70%	NRVQNMALYADVSGK	3.74	1,681.83

Control	6006	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	5	8	11	0.12%	29.70%	VQNMALYADVSGK	3.82	1,411.69
Control	6006	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	5	8	11	0.12%	29.70%	VQNMALYADVSGKQFPVTR	3.33	2,140.09
Control	6006	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	99.80%	2	3	3	0.03%	3.78%	LRPESALAQAQK	4.13	1,311.74

Control	6006	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	99.80%	2	3	3	0.03%	3.78%	NVDLSTFYQNR	2.94	1,356.65
Control	6006	RecName: Full=Elongation factor 1-gamma; Short=EF-1-gamma; AltName: Full=eEF-1B gamma	gi|122146155,gi|74268360,gi|94966781,gi|95769122	50,360.80	100.00%	3	4	4	0.04%	7.50%	AKDPFAHLPK	3.12	1,123.63
Control	6006	RecName: Full=Elongation factor 1-gamma; Short=EF-1-gamma; AltName: Full=eEF-1B gamma	gi|122146155,gi|74268360,gi|94966781,gi|95769122	50,360.80	100.00%	3	4	4	0.04%	7.50%	ALIAAQYSGAQVR	2.68	1,347.74
Control	6006	RecName: Full=Elongation factor 1-gamma; Short=EF-1-gamma; AltName: Full=eEF-1B gamma	gi|122146155,gi|74268360,gi|94966781,gi|95769122	50,360.80	100.00%	3	4	4	0.04%	7.50%	ILGLLDAHLK	3.04	1,092.68
Control	6006	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	3	3	5	0.05%	5.16%	IPLNDIFR	3.21	987.5623
Control	6006	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	3	3	5	0.05%	5.16%	VALKIPLNDIFR	4.32	1,398.85

Control	6006	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	3	3	5	0.05%	5.16%	YLDFVFAVK	1.93	1,101.60
Control	6006	Nicastrin	gi|74267600,gi|77735901	79,055.00	99.80%	2	2	2	0.02%	3.63%	ALAGVATVLAR	2.95	1,041.64
Control	6006	Nicastrin	gi|74267600,gi|77735901	79,055.00	99.80%	2	2	2	0.02%	3.63%	MATAGGGCVADPGSR	3.12	1,349.59
Control	6006	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	5	6	0.07%	18.80%	DFSLEQLR	2.51	1,007.52
Control	6006	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	5	6	0.07%	18.80%	FYGPAGPYGIFAGR	3.97	1,472.73
Control	6006	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	5	6	0.07%	18.80%	GLGAGAGAGEESPAASLPR	3.77	1,667.83
Control	6006	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	5	6	0.07%	18.80%	RGLGAGAGAGEESPAASLPR	3.28	1,823.94
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	FGKPDPIVSVIFKDEK	3.49	1,819.00
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	FKGFPPPVLSEDGSSIR	3.95	1,832.95
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	GNNPFFDELFFYNVHLTPSELMDEIISIR	3.11	3,473.67
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	HKDGSNLPILPSQR	3.52	1,561.84
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	ILHQHLGPPEER	3.2	1,425.76
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	ILVELSTLLEK	3.25	1,257.77
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	IPAHQVLYSTSGGDASGK	2.42	1,787.89

Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	ISVYDYDTFTR	2.36	1,379.65
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	ISVYDYDTFTRDEK	2.24	1,751.81
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	IYRAEDIPQMDDAFSQTVK	3.91	2,243.07
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	NLMALDKDSFSDPYAHVSFLHR	2.78	2,579.23
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	NLVDPFVEVSFAGK	2.76	1,521.79
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	SLLTEADAGHTEFTDEVYQNESR	4.46	2,612.17
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	TLHSSFQPNISQGR	3.72	1,571.79
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	TQGLVPEHVETR	2.72	1,365.71
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	VEMTLEVLNEKEADERPAGK	2.44	2,274.13
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	VFLPKEELYMPPLVIK	3.18	1,932.09
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	VIEDRDNYIPNTLNPVFGR	3.9	2,232.14

Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	VIIELFDNDQVGKDEFLGR	2.53	2,207.13
Control	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	25	28	0.30%	15.50%	VIVESASNIPK	3.06	1,156.66
Control	6006	TXNDC13 protein	gi|148878448,gi|149642897	38,865.40	99.80%	2	2	2	0.02%	7.18%	FFVTTLPAFFHAK	3.85	1,525.82
Control	6006	TXNDC13 protein	gi|148878448,gi|149642897	38,865.40	99.80%	2	2	2	0.02%	7.18%	VDVIQEPGLSGR	3.48	1,269.68
Control	6006	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	4	4	4	0.04%	17.80%	FKNLENSPLGEALR	4	1,587.85
Control	6006	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	4	4	4	0.04%	17.80%	NLENSPLGEALR	2.76	1,312.69
Control	6006	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	4	4	4	0.04%	17.80%	NRESYEVTLTHK	3.19	1,476.74
Control	6006	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	4	4	4	0.04%	17.80%	SVPLAATSMLITQGLISK	2.88	1,846.04
Control	6006	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	99.80%	2	2	2	0.02%	7.76%	GSYGDLGGPIITTQVTIPK	3.67	1,917.03
Control	6006	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	99.80%	2	2	2	0.02%	7.76%	TDYNASVSVPDSSGPER	3.21	1,780.80
Control	6006	myristoylated alanine-rich protein kinase C substrate	gi|115495497,gi|148872484,gi|163340,gi|94534743	31,960.80	99.80%	2	3	5	0.05%	6.87%	GEATAERPGEAAVASSPSK	4.27	1,814.89
Control	6006	myristoylated alanine-rich protein kinase C substrate	gi|115495497,gi|148872484,gi|163340,gi|94534743	31,960.80	99.80%	2	3	5	0.05%	6.87%	TAAKGEATAERPGEAAVASSPSK	3.18	2,186.10

Control	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	14	16	0.17%	13.90%	FKMLAELYGSDPQEELVY	1.74	2,148.02
Control	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	14	16	0.17%	13.90%	NLESPSSFTIK	2.63	1,222.63
Control	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	14	16	0.17%	13.90%	PSLYAQVQKPPR	2.28	1,383.77
Control	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	14	16	0.17%	13.90%	RTSDKGQFFGITK	3.49	1,484.79
Control	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	14	16	0.17%	13.90%	TSDKGQFFGITK	3.23	1,328.68
Control	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	14	16	0.17%	13.90%	VDKNTGDVYALER	4.32	1,479.74
Control	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	14	16	0.17%	13.90%	VFRVDKNTGDVYALER	3.5	1,881.98
Control	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	14	16	0.17%	13.90%	VGSPLGSLFVEDPDEPQNR	3.35	2,056.00
Control	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	14	16	0.17%	13.90%	VGSPLGSLFVEDPDEPQNRK	2.09	2,184.09
Control	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	14	16	0.17%	13.90%	YSFVQGEYR	2.9	1,148.54
Control	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	14	16	0.17%	13.90%	YTFSVPEDIR	2.21	1,226.61
Control	6006	LOC515309 protein	gi|148878460,gi|149773584	31,548.40	100.00%	3	4	4	0.04%	13.40%	KEEEEEEEEYDEGSNLKR	5.84	2,241.96

Control	6006	LOC515309 protein	gi|148878460,gi|149773584	31,548.40	100.00%	3	4	4	0.04%	13.40%	LYIEFVK	2.21	911.5237
Control	6006	LOC515309 protein	gi|148878460,gi|149773584	31,548.40	100.00%	3	4	4	0.04%	13.40%	SNPEDQILYQTER	2.44	1,592.76
Control	6006	acyl-CoA synthetase long-chain family member 5	gi|115497154,gi|152941112,gi|94534758	76,013.10	100.00%	3	3	3	0.03%	5.86%	ALVLISNVEK	2.82	1,085.66
Control	6006	acyl-CoA synthetase long-chain family member 5	gi|115497154,gi|152941112,gi|94534758	76,013.10	100.00%	3	3	3	0.03%	5.86%	GAMLTHANIVSNASGFLK	2.53	1,846.95
Control	6006	acyl-CoA synthetase long-chain family member 5	gi|115497154,gi|152941112,gi|94534758	76,013.10	100.00%	3	3	3	0.03%	5.86%	PQPALPHVDLNK	2.78	1,328.73
Control	6006	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	99.80%	2	2	2	0.02%	4.31%	LQTVQSADQVLVLR	3.85	1,569.90
Control	6006	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	99.80%	2	2	2	0.02%	4.31%	QVVLVGQEPVLFSGSVR	3.99	1,814.02
Control	6006	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	gi|165973956,gi|2493087,gi|81294315	10,254.50	99.80%	2	3	4	0.04%	25.00%	DFTPSGIAGAFQR	3.67	1,366.68
Control	6006	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	gi|165973956,gi|2493087,gi|81294315	10,254.50	99.80%	2	3	4	0.04%	25.00%	YYNKYVNVK	3.02	1,190.62

Control	6006	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	5	6	6	0.07%	25.10%	ANAFVAELKDLDPAR	3.15	1,629.86
Control	6006	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	5	6	6	0.07%	25.10%	LTLYDIAHTPGVAADLSHIETR	2.64	2,393.25
Control	6006	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	5	6	6	0.07%	25.10%	VAVLGASGGIGQPLSLLLK	4.22	1,793.09
Control	6006	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	5	6	6	0.07%	25.10%	VNVPVIGGHAGK	2.91	1,147.66
Control	6006	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	5	6	6	0.07%	25.10%	VSPFEEKMIAEAIPELK	3.39	1,947.01
Control	6006	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	5	9	0.10%	26.60%	HYLFDVQR	2.86	1,077.55

Control	6006	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	5	9	0.10%	26.60%	IAQLEEVKQASIK	4.05	1,456.84
Control	6006	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	5	9	0.10%	26.60%	LNEQKIAQLEEVK	3.3	1,541.85
Control	6006	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	5	9	0.10%	26.60%	NNIAMALEVTYR	3.67	1,410.70
Control	6006	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	5	9	0.10%	26.60%	QIQDAIDMEKSQQALVQKR	3.4	2,245.16
Control	6006	Ribosomal protein S8	gi|119224110,gi|58760384,gi|59858489,gi|70778956,gi|74268417,gi|75070020	24,188.40	99.90%	2	3	3	0.03%	14.90%	ADGYVLEGKELEFYLR	3.28	1,901.96
Control	6006	Ribosomal protein S8	gi|119224110,gi|58760384,gi|59858489,gi|70778956,gi|74268417,gi|75070020	24,188.40	99.90%	2	3	3	0.03%	14.90%	IIDVVYNASNNELVR	5.12	1,718.91
Control	6006	PREDICTED: similar to oxysterol 7alpha-hydroxylase	gi|194672764	90,479.20	100.00%	2	2	2	0.02%	4.34%	AMAVLRDEIDHLLQSTGQK	2.86	2,141.10
Control	6006	PREDICTED: similar to oxysterol 7alpha-hydroxylase	gi|194672764	90,479.20	100.00%	2	2	2	0.02%	4.34%	YITFILDPFHYTSVAK	2.15	1,915.00

Control	6006	p33/41 (annexin IV)	gi|1063258,gi|113956,gi|14278334,gi|157829985,gi|157830000,gi|163030,gi|216,gi|48374083,gi|74353976	35,872.70	100.00%	3	3	3	0.03%	11.90%	GLGTDDDTLIR	3.33	1,175.59
Control	6006	p33/41 (annexin IV)	gi|1063258,gi|113956,gi|14278334,gi|157829985,gi|157830000,gi|163030,gi|216,gi|48374083,gi|74353976	35,872.70	100.00%	3	3	3	0.03%	11.90%	GLGTDEDAIINVLAYR	3.01	1,719.89
Control	6006	p33/41 (annexin IV)	gi|1063258,gi|113956,gi|14278334,gi|157829985,gi|157830000,gi|163030,gi|216,gi|48374083,gi|74353976	35,872.70	100.00%	3	3	3	0.03%	11.90%	INQTYQLQYGR	3.59	1,383.70
Control	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	11	14	19	0.21%	33.70%	AVFVDLEPTVIDEVR	4.6	1,701.91
Control	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	11	14	19	0.21%	33.70%	DVNAAIATIK	3.19	1,015.58
Control	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	11	14	19	0.21%	33.70%	EIIDLVLDR	2.32	1,085.62
Control	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	11	14	19	0.21%	33.70%	FDGALNVDLTEFQTNLVPYPR	2.72	2,409.21
Control	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	11	14	19	0.21%	33.70%	IHFPLATYAPVISAEK	3.67	1,756.96
Control	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	11	14	19	0.21%	33.70%	LDHKFDLMYAK	2.29	1,396.69
Control	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	11	14	19	0.21%	33.70%	LISQIVSSITASLR	3.38	1,487.88
Control	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	11	14	19	0.21%	33.70%	NLDIERPTYTNLNR	2.64	1,718.88
Control	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	11	14	19	0.21%	33.70%	QLFHPEQLITGKEDAANNYAR	3.26	2,415.21
Control	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	11	14	19	0.21%	33.70%	RNLDIERPTYTNLNR	2.32	1,874.98
Control	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	11	14	19	0.21%	33.70%	TIGGGDDSFNTFFSETGAGK	2.54	2,007.89

Control	6006	RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8; AltName: Full=NADH-ubiquinone oxidoreductase 19 kDa subunit; AltName: Full=Complex I-19kD;	gi|1171870, gi|28461275,gi|5996815,gi|86827664	20,073.10	99.90%	2	4	4	0.04%	18.60%	ARPEPNPEVEGDLKPAR	4.29	1,874.97
Control	6006	RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8; AltName: Full=NADH-ubiquinone oxidoreductase 19 kDa subunit; AltName: Full=Complex I-19kD;	gi|1171870, gi|28461275,gi|5996815,gi|86827664	20,073.10	99.90%	2	4	4	0.04%	18.60%	VKTDRPLPENPYHSR	3.6	1,808.94

Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	AAAQDIFSPKR	2.62	1,203.65
Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	ATILYASETGR	3.14	1,181.62

Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	AVDTRLEELGGER	3.34	1,444.74
Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	DFINQYYSSIK	2.9	1,377.67

Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	DFINQYYSSIKR	2.2	1,533.77
Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	ESSNTDSAGALGTLR	3.84	1,478.71

Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	IRTQSFSLQER	2.96	1,364.73
Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	KLQTRPSPGPPPAEQLLSQAR	4.89	2,271.26

Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	KMFQATVLSVENLQSSK	3.91	1,926.00
Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	LLSTLAEEPSEQQELETLSQDPR	3.68	2,613.29

Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	LLSTLAEEPSEQQELETLSQDPRR	3.71	2,769.39
Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	LSTQAEGLQLLPGLIHVHR	3.83	2,082.18

Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	MFQATVLSVENLQSSK	3.13	1,797.91
Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	RKESSNTDSAGALGTLR	3.55	1,762.90

Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	SAITVFPQRAPGR	3	1,399.78
Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	TYVQDILR	2.62	1,007.55

Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	VEDPPPPTESVAVEQLEK	3.34	1,963.99
Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	VLTAFSREPDSPK	2.57	1,446.76

Control	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	19	27	31	0.34%	18.20%	YHEDIFGLTLR	2.78	1,363.70
Control	6006	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	8	10	11	0.12%	21.40%	EHALLAYTLGVK	3.51	1,314.74
Control	6006	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	8	10	11	0.12%	21.40%	IGGIGTVPVGR	2.25	1,025.61
Control	6006	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	8	10	11	0.12%	21.40%	LPLQDVYK	2.52	975.5511
Control	6006	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	8	10	11	0.12%	21.40%	TIEKFEKEAAEMGK	2.72	1,626.80

Control	6006	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	8	10	11	0.12%	21.40%	VETGVLKPGMVVTFAPVNVTTEVK	3.9	2,531.38
Control	6006	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	8	10	11	0.12%	21.40%	YEEIVKEVSTYIKK	2.67	1,728.94
Control	6006	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	8	10	11	0.12%	21.40%	YYVTIIDAPGHR	2.58	1,404.73
Control	6006	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	8	10	11	0.12%	21.40%	YYVTIIDAPGHRDFIK	2.02	1,908.00
Control	6006	cell division cycle 42 (GTP binding protein, 25kDa)	gi|114052486,gi|122063301,gi|86821687	21,240.70	100.00%	2	3	4	0.04%	19.90%	NVFDEAILAALEPPEPK	3.38	1,852.97
Control	6006	cell division cycle 42 (GTP binding protein, 25kDa)	gi|114052486,gi|122063301,gi|86821687	21,240.70	100.00%	2	3	4	0.04%	19.90%	TPFLLVGTQIDLRDDPSTIEK	2.86	2,358.26
Control	6006	minor histocompatibility antigen 13	gi|164448616	41,537.10	100.00%	3	3	5	0.05%	10.90%	GEVTEMFSYEESNPKDPAAVTETR	3.31	2,703.21
Control	6006	minor histocompatibility antigen 13	gi|164448616	41,537.10	100.00%	3	3	5	0.05%	10.90%	LVFPQDLLEK	2.11	1,201.68

Control	6006	minor histocompatibility antigen 13	gi|164448616	41,537.10	100.00%	3	3	5	0.05%	10.90%	SFEAPIKLVFPQDLLEK	3.09	1,974.09
Control	6006	Interleukin 1 receptor accessory protein	gi|111305355,gi|115495597	41,650.00	99.90%	2	2	2	0.02%	5.83%	QIQVYEDEPAR	3.05	1,347.65
Control	6006	Interleukin 1 receptor accessory protein	gi|111305355,gi|115495597	41,650.00	99.90%	2	2	2	0.02%	5.83%	VAFPLEVVQK	2.29	1,129.66
Control	6006	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	99.80%	2	2	2	0.02%	18.20%	NYQQNYQNSESGEKNEGSESAPEGQAQQR	5.28	3,257.40
Control	6006	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	99.80%	2	2	2	0.02%	18.20%	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	5.49	3,239.53
Control	6006	RecName: Full=Apolipoprotein A-I; Short=Apo-AI; Short=ApoA-I; Flags: Precursor	gi|113988,gi|146186566,gi|162678,gi|74268269,gi|75832056	30,253.70	99.80%	2	2	3	0.03%	9.81%	DYVAQFEASALGK	3.62	1,398.69
Control	6006	RecName: Full=Apolipoprotein A-I; Short=Apo-AI; Short=ApoA-I; Flags: Precursor	gi|113988,gi|146186566,gi|162678,gi|74268269,gi|75832056	30,253.70	99.80%	2	2	3	0.03%	9.81%	VSILAAIDEASKK	2.82	1,344.77
Control	6006	PREDICTED: similar to vesicle amine transport protein 1 isoform 1	gi|76671278	42,822.00	100.00%	4	4	4	0.04%	14.70%	GVDIVMDPLGGSDTAK	4.07	1,590.77
Control	6006	PREDICTED: similar to vesicle amine transport protein 1 isoform 1	gi|76671278	42,822.00	100.00%	4	4	4	0.04%	14.70%	LLALYNQGHIKPR	2.05	1,522.89

Control	6006	PREDICTED: similar to vesicle amine transport protein 1 isoform 1	gi|76671278	42,822.00	100.00%	4	4	4	0.04%	14.70%	LQTRPAAPPAPGTGQLTLR	3.52	1,945.10
Control	6006	PREDICTED: similar to vesicle amine transport protein 1 isoform 1	gi|76671278	42,822.00	100.00%	4	4	4	0.04%	14.70%	VLLVPGPEKEN	2.76	1,194.67
Control	6006	PREDICTED: similar to Feline leukemia virus subgroup C receptor-related protein 1 (Feline leukemia virus subgroup C receptor) (hFLVCR)	gi|194674242	59,731.10	99.80%	2	2	2	0.02%	7.73%	ATASGTPDGPKTPLAPEEETQAR	3.97	2,324.14
Control	6006	PREDICTED: similar to Feline leukemia virus subgroup C receptor-related protein 1 (Feline leukemia virus subgroup C receptor) (hFLVCR)	gi|194674242	59,731.10	99.80%	2	2	2	0.02%	7.73%	LLPKDPGEETPGGEGTLVPR	3.31	2,062.08
Control	6006	RecName: Full=Hemoglobin subunit beta; AltName: Full=Hemoglobin beta chain; AltName: Full=Beta-globin	gi|122572,gi|27819608,gi|395	15,936.20	99.80%	2	5	17	0.19%	35.20%	LLGNVLVVVLAR	4.74	1,265.83

Control	6006	RecName: Full=Hemoglobin subunit beta; AltName: Full=Hemoglobin beta chain; AltName: Full=Beta-globin	gi|122572,gi|27819608,gi|395	15,936.20	99.80%	2	5	17	0.19%	35.20%	LLGNVLVVVLARNFGKEFTPVLQADFQK	3.81	3,115.77
Control	6006	RecName: Full=Hemoglobin subunit beta; AltName: Full=Hemoglobin beta chain; AltName: Full=Beta-globin	gi|122572,gi|27819608,gi|395	15,936.20	99.80%	2	5	17	0.19%	35.20%	LLVVYPWTQR	3.19	1,274.73
Control	6006	RecName: Full=Hemoglobin subunit beta; AltName: Full=Hemoglobin beta chain; AltName: Full=Beta-globin	gi|122572,gi|27819608,gi|395	15,936.20	99.80%	2	5	17	0.19%	35.20%	NFGKEFTPVLQADFQK	2.84	1,868.95
Control	6006	RecName: Full=Hemoglobin subunit beta; AltName: Full=Hemoglobin beta chain; AltName: Full=Beta-globin	gi|122572,gi|27819608,gi|395	15,936.20	99.80%	2	5	17	0.19%	35.20%	VKVDEVGGEALGR	4.12	1,328.72

Control	6006	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	99.80%	2	2	2	0.02%	5.57%	FTSLGLLPR	2.73	1,003.59
Control	6006	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	99.80%	2	2	2	0.02%	5.57%	VFRLPEDQAIINR	3.07	1,570.87
Control	6006	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	3	4	5	0.05%	7.01%	AENLGEVLRGDR	2.67	1,328.69
Control	6006	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	3	4	5	0.05%	7.01%	ISEDYYVHLIADNLPVATR	3.08	2,189.12
Control	6006	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	3	4	5	0.05%	7.01%	IVNTPFQVLMNSEK	4.08	1,635.84
Control	6006	PREDICTED: plexin A2	gi|194674254	210,938.30	100.00%	3	3	3	0.03%	2.27%	FVDDLFETLFSTVHR	3.8	1,825.91
Control	6006	PREDICTED: plexin A2	gi|194674254	210,938.30	100.00%	3	3	3	0.03%	2.27%	LLQAAYLAKPGDALAR	2.79	1,670.96
Control	6006	PREDICTED: plexin A2	gi|194674254	210,938.30	100.00%	3	3	3	0.03%	2.27%	LNTLMHYQVSDR	2.66	1,492.72
Control	6006	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	99.90%	2	3	5	0.05%	11.70%	GAAQNIIPASTGAAK	3.7	1,369.74
Control	6006	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	99.90%	2	3	5	0.05%	11.70%	VIHDHFGIVEGLMTTVHAITATQK	3.73	2,634.37
Control	6006	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	100.00%	3	3	3	0.03%	12.70%	FFLSAGLIDKVDNFK	2.29	1,713.92
Control	6006	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	100.00%	3	3	3	0.03%	12.70%	LEDPHVDIIR	2.36	1,206.65

Control	6006	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	100.00%	3	3	3	0.03%	12.70%	VSFSYAGLSSDDPDLGPAHVVTVIAR	3.43	2,673.35
Control	6006	Myeloid-associated differentiation marker	gi|111308557,gi|115497460	35,291.10	100.00%	3	5	11	0.12%	14.60%	ARPGEITGYMATVPGLLK	4.83	1,890.02
Control	6006	Myeloid-associated differentiation marker	gi|111308557,gi|115497460	35,291.10	100.00%	3	5	11	0.12%	14.60%	LVFVRV	1.79	732.4766
Control	6006	Myeloid-associated differentiation marker	gi|111308557,gi|115497460	35,291.10	100.00%	3	5	11	0.12%	14.60%	TTVTTTMSSSSGLGSPTIVGSPR	4.57	2,240.11
Control	6006	ribosomal protein L24	gi|27806129,gi|28189314,gi|28189753,gi|28189757,gi|28189765,gi|3132823,gi|41019240,gi|74267598	17,630.30	99.80%	2	2	2	0.02%	16.00%	AITGASLADIMAK	3.66	1,277.68
Control	6006	ribosomal protein L24	gi|27806129,gi|28189314,gi|28189753,gi|28189757,gi|28189765,gi|3132823,gi|41019240,gi|74267598	17,630.30	99.80%	2	2	2	0.02%	16.00%	TDGKVFQFLNAK	3.43	1,367.73
Control	6006	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	12	0.13%	14.10%	DAEAWFNEK	2.58	1,109.49

Control	6006	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	12	0.13%	14.10%	IRLENEIQTYR	4.51	1,434.77
Control	6006	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	12	0.13%	14.10%	LASYLDKVR	3.24	1,064.61
Control	6006	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	12	0.13%	14.10%	QSLEASLAETEGR	4.32	1,390.68
Control	6006	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	12	0.13%	14.10%	QSVEADINGLRR	1.62	1,357.72
Control	6006	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	12	0.13%	14.10%	RVLDELTLTK	3.14	1,187.70

Control	6006	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	12	0.13%	14.10%	SQYEQLAEKNR	3.56	1,365.68
Control	6006	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	12	0.13%	14.10%	VLDELTLTK	3.63	1,031.60
Control	6006	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	5	5	5	0.05%	11.40%	DLDELSRYPEDKITPENLPQILLQLK	3.32	3,080.65
Control	6006	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	5	5	5	0.05%	11.40%	DSFDDRGPSLNPVLDYDHGSR	3.3	2,362.07
Control	6006	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	5	5	5	0.05%	11.40%	VIHLSNLPHSGYSDSAVLK	3.12	2,037.08
Control	6006	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	5	5	5	0.05%	11.40%	VVHIMDFQR	2.8	1,160.59
Control	6006	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	5	5	5	0.05%	11.40%	YQLLQLVEPFGVISNHLILNK	3.15	2,438.38
Control	6006	Transferrin	gi|113911795,gi|114326282	77,721.80	100.00%	6	8	102	1.11%	16.80%	AISNNEADAVTLDGGLVYEAGLKPNNLKPVVAEFHGTK	3.46	3,952.05
Control	6006	Transferrin	gi|113911795,gi|114326282	77,721.80	100.00%	6	8	102	1.11%	16.80%	GEADAMSLDGGYLYIAGK	3.06	1,846.85
Control	6006	Transferrin	gi|113911795,gi|114326282	77,721.80	100.00%	6	8	102	1.11%	16.80%	MDFELYLGYEYVTALQNLR	4.77	2,338.14
Control	6006	Transferrin	gi|113911795,gi|114326282	77,721.80	100.00%	6	8	102	1.11%	16.80%	TVGGKEDVIWELLNHAQEHFGK	3.91	2,507.27
Control	6006	Transferrin	gi|113911795,gi|114326282	77,721.80	100.00%	6	8	102	1.11%	16.80%	TYDSYLGDDYVR	2.9	1,466.64

Control	6006	Transferrin	gi|113911795,gi|114326282	77,721.80	100.00%	6	8	102	1.11%	16.80%	YYGYTGAFR	2.53	1,097.51
Control	6006	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	4	7	8	0.09%	19.70%	GVGDDQLGEESEERDDHLLPM	2.98	2,357.02
Control	6006	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	4	7	8	0.09%	19.70%	HTLADNFNPVSEER	4.37	1,628.77
Control	6006	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	4	7	8	0.09%	19.70%	HTLADNFNPVSEERGK	2.98	1,813.88
Control	6006	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	4	7	8	0.09%	19.70%	SFESTVGQSPDMYSYVFR	4.1	2,115.93
Control	6006	ADP-ribosylation-like factor 6 interacting protein 5	gi|59858163,gi|62460474,gi|74354855,gi|75057806	21,648.60	99.80%	2	3	4	0.04%	13.80%	FARPDFR	1.73	908.4737
Control	6006	ADP-ribosylation-like factor 6 interacting protein 5	gi|59858163,gi|62460474,gi|74354855,gi|75057806	21,648.60	99.80%	2	3	4	0.04%	13.80%	TPMGIVLDALEQQEETITK	3.61	2,132.08
Control	6006	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	5	5	7	0.08%	12.50%	EKPYFPIPEDYTFIQNVPLEDR	3.98	2,710.34
Control	6006	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	5	5	7	0.08%	12.50%	KAEVEGKDLPEHAVLK	3.66	1,762.97

Control	6006	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	5	5	7	0.08%	12.50%	LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR	5.39	3,142.43
Control	6006	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	5	5	7	0.08%	12.50%	NFILDQTNVSAAAQR	3.44	1,647.84
Control	6006	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	5	5	7	0.08%	12.50%	SSGPTSLFAVTVAPPGAR	2.47	1,714.91
Control	6006	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	gi|124829038,gi|125630707,gi|171769867	51,147.90	100.00%	3	3	3	0.03%	9.27%	ADYLQNYEFPHLQNFIK	2.48	2,140.05
Control	6006	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	gi|124829038,gi|125630707,gi|171769867	51,147.90	100.00%	3	3	3	0.03%	9.27%	LLLVSFDGFR	2.7	1,166.66
Control	6006	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	gi|124829038,gi|125630707,gi|171769867	51,147.90	100.00%	3	3	3	0.03%	9.27%	VLEEIDEHIGELVHR	2.36	1,787.93
Control	6006	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	3	3	3	0.03%	7.89%	EESREPAPASPAPAGVEIR	3.46	1,962.99
Control	6006	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	3	3	3	0.03%	7.89%	IMLEDGNLHVTQGAGR	2.59	1,726.85
Control	6006	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	3	3	3	0.03%	7.89%	NLHQSGFSLSGTQVDEGVR	3.27	2,030.99

Control	6006	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	8	11	36	0.39%	30.30%	AIAELGIYPAVDPLDSTSR	3.17	1,988.03
Control	6006	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	8	11	36	0.39%	30.30%	FTQAGSEVSALLGR	3.82	1,435.75
Control	6006	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	8	11	36	0.39%	30.30%	IMDPNIVGSEHYDVAR	2.8	1,831.86
Control	6006	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	8	11	36	0.39%	30.30%	IVAVIGAVVDVQFDEGLPPILNALEVQGR	4.36	3,031.68
Control	6006	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	8	11	36	0.39%	30.30%	SLQDIIAILGMDELSEEDKLTVSR	3.77	2,691.38

Control	6006	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	8	11	36	0.39%	30.30%	TIAMDGTEGLVR	3.24	1,278.64
Control	6006	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	8	11	36	0.39%	30.30%	TVLIMELINNVAK	2.46	1,473.83
Control	6006	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	8	11	36	0.39%	30.30%	VLDSGAPIRIPVGPETLGR	3.62	1,947.10
Control	6006	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	99.80%	2	2	2	0.02%	11.80%	QAQILASEAEKAEQINQAAGEASAVLAK	3.35	2,839.48
Control	6006	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	99.80%	2	2	2	0.02%	11.80%	STDASLDEELDRVK	2.68	1,577.77
Control	6006	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	99.80%	2	3	3	0.03%	3.29%	LGEVPITVTAVSPAASDAVTQR	3.35	2,182.17
Control	6006	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	99.80%	2	3	3	0.03%	3.29%	SYSQSILLDLTDSTLQTTLK	3.02	2,227.17

Control	6006	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	gi|27806793,gi|296576,gi|730944	124,936.20	99.80%	2	2	2	0.02%	1.85%	NVLVGENLASK	2.58	1,143.64
Control	6006	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	gi|27806793,gi|296576,gi|730944	124,936.20	99.80%	2	2	2	0.02%	1.85%	VLETDPAFAR	2.78	1,118.58
Control	6006	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	99.80%	2	2	3	0.03%	6.64%	FLVGFTNK	2.58	925.5142
Control	6006	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	99.80%	2	2	3	0.03%	6.64%	GEDFPANNIVK	3.25	1,203.60
Control	6006	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	7	7	8	0.09%	18.60%	FGTFHSPALEDADFDGKPMVLVAGQYSTGK	4.99	3,201.52
Control	6006	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	7	7	8	0.09%	18.60%	GYDFPAVLR	2.13	1,037.54
Control	6006	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	7	7	8	0.09%	18.60%	KLNPFGNTFLNR	4.51	1,420.77
Control	6006	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	7	7	8	0.09%	18.60%	LFELEEQDLFR	3.18	1,438.72
Control	6006	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	7	7	8	0.09%	18.60%	LFELEEQDLFRDIQGLPR	4.02	2,218.15
Control	6006	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	7	7	8	0.09%	18.60%	SKYDEIFYNLAPADGK	3.33	1,830.89
Control	6006	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	7	7	8	0.09%	18.60%	TSFIQYLLEQEVPGSR	3.84	1,866.96
Control	6006	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	3	3	3	0.03%	8.87%	ALGVEQDLALPAIAVIGDQSSGK	3.22	2,252.21
Control	6006	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	3	3	3	0.03%	8.87%	ATEELQQYGDDIPSDEGDKMFFLIEK	2.64	3,034.39
Control	6006	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	3	3	3	0.03%	8.87%	SSVLEALSGVALPR	4.6	1,398.80

Control	6006	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	7	10	10	0.11%	33.50%	ELDAEKAFANEQLTR	3.18	1,734.87
Control	6006	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	7	10	10	0.11%	33.50%	KQDAFYKEQLAR	4.45	1,496.79
Control	6006	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	7	10	10	0.11%	33.50%	LSENVIDRMKETSPSGPK	3.7	2,004.01
Control	6006	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	7	10	10	0.11%	33.50%	QNTQQTLSCSALASQYMR	3.42	2,045.94
Control	6006	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	7	10	10	0.11%	33.50%	RVAEELALEQAKK	4.65	1,484.84
Control	6006	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	7	10	10	0.11%	33.50%	VAEELALEQAK	3.21	1,200.65
Control	6006	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	7	10	10	0.11%	33.50%	VAEELALEQAKK	4.15	1,328.74
Control	6006	integrin beta 1	gi|111183155,gi|218563327	88,051.70	100.00%	11	17	27	0.29%	15.80%	GTAEKLQPEDITQIQPQQLVLQLR	3.87	2,746.51
Control	6006	integrin beta 1	gi|111183155,gi|218563327	88,051.70	100.00%	11	17	27	0.29%	15.80%	IGFGSFVEK	2.48	983.5197
Control	6006	integrin beta 1	gi|111183155,gi|218563327	88,051.70	100.00%	11	17	27	0.29%	15.80%	LLVFSTDAGFHFAGDGK	4.23	1,781.89
Control	6006	integrin beta 1	gi|111183155,gi|218563327	88,051.70	100.00%	11	17	27	0.29%	15.80%	LPEGVTINYK	3.09	1,133.62
Control	6006	integrin beta 1	gi|111183155,gi|218563327	88,051.70	100.00%	11	17	27	0.29%	15.80%	LQPEDITQIQPQQLVLQLR	5.01	2,260.27
Control	6006	integrin beta 1	gi|111183155,gi|218563327	88,051.70	100.00%	11	17	27	0.29%	15.80%	LSENNIQTIFAVTEEFQPVYK	3.84	2,470.25

Control	6006	integrin beta 1	gi|111183155,gi|218563327	88,051.70	100.00%	11	17	27	0.29%	15.80%	LSENNIQTIFAVTEFQPVYKELK	3.05	2,840.47
Control	6006	integrin beta 1	gi|111183155,gi|218563327	88,051.70	100.00%	11	17	27	0.29%	15.80%	NVLSLTDKGEVFNELVGK	4.64	1,962.05
Control	6006	integrin beta 1	gi|111183155,gi|218563327	88,051.70	100.00%	11	17	27	0.29%	15.80%	SGEPQTFTLK	2.24	1,107.57
Control	6006	integrin beta 1	gi|111183155,gi|218563327	88,051.70	100.00%	11	17	27	0.29%	15.80%	SKGTAEKLQPEDITQIQPQQLVLQLR	2.72	2,961.64
Control	6006	integrin beta 1	gi|111183155,gi|218563327	88,051.70	100.00%	11	17	27	0.29%	15.80%	TVMPYISTTPAK	3.01	1,324.68
Control	6006	RecName: Full=Thymopoietin-2; AltName: Full=Thymopoietin II	gi|135801,gi|135803,gi|226446	5,620.60	99.80%	2	2	2	0.02%	67.30%	LKSELVANNVTLPAGEQR	3.39	1,939.06
Control	6006	RecName: Full=Thymopoietin-2; AltName: Full=Thymopoietin II	gi|135801,gi|135803,gi|226446	5,620.60	99.80%	2	2	2	0.02%	67.30%	LKSELVANNVTLPAGEQRK	3.92	2,067.16
Control	6006	RecName: Full=Thymopoietin-2; AltName: Full=Thymopoietin II	gi|135801,gi|135803,gi|226446	5,620.60	99.80%	2	2	2	0.02%	67.30%	PEFLEDPSVLTK	3.06	1,374.72
Control	6006	RecName: Full=Thymopoietin-2; AltName: Full=Thymopoietin II	gi|135801,gi|135803,gi|226446	5,620.60	99.80%	2	2	2	0.02%	67.30%	PEFLEDPSVLTKEK	3.61	1,631.85
Control	6006	TPM3 protein	gi|79153472	29,015.30	99.80%	2	2	2	0.02%	12.10%	HIAEEADRKYEEVAR	3.16	1,815.90
Control	6006	TPM3 protein	gi|79153472	29,015.30	99.80%	2	2	2	0.02%	12.10%	RIQLVEEELDRAQER	3.55	1,883.99

Control	6006	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	5	6	7	0.08%	20.40%	DVFNKGYGFGMVK	2.47	1,477.71
Control	6006	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	5	6	7	0.08%	20.40%	LSQNNFALGYK	2.52	1,254.65
Control	6006	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	5	6	7	0.08%	20.40%	LTLDTIFVPNTGKK	2.9	1,546.88

Control	6006	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	5	6	7	0.08%	20.40%	LTLSALIDGK	3.04	1,030.61
Control	6006	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	5	6	7	0.08%	20.40%	LTLSALIDGKNFNAGGHK	3.57	1,856.00
Control	6006	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	5	6	7	0.08%	20.40%	SKLSQNNFALGYK	3.67	1,469.77
Control	6006	SLC25A3 protein	gi|151556064	39,986.50	100.00%	5	8	12	0.13%	11.40%	IQTQPGYANTLR	3.96	1,361.72
Control	6006	SLC25A3 protein	gi|151556064	39,986.50	100.00%	5	8	12	0.13%	11.40%	LPRPPPPEMPESLK	4.36	1,603.85

Control	6006	SLC25A3 protein	gi|151556064	39,986.50	100.00%	5	8	12	0.13%	11.40%	LPRPPPPEMPESLKK	4.77	1,731.95
Control	6006	SLC25A3 protein	gi|151556064	39,986.50	100.00%	5	8	12	0.13%	11.40%	MYKEEGLKAFYK	3.98	1,522.76
Control	6006	SLC25A3 protein	gi|151556064	39,986.50	100.00%	5	8	12	0.13%	11.40%	VRIQTQPGYANTLR	2.98	1,616.89
Control	6006	FKBP8 protein	gi|115545478,gi|119894476,gi|194668654	44,616.30	99.70%	2	2	2	0.02%	7.52%	TAVDGPDLEMLTGQER	3.34	1,747.82
Control	6006	FKBP8 protein	gi|115545478,gi|119894476,gi|194668654	44,616.30	99.70%	2	2	2	0.02%	7.52%	VDMTFEEEQLLQLK	2.28	1,867.90
Control	6006	ALCAM/CD166	gi|13111304,gi|41386784,gi|47605539	64,749.10	99.80%	2	2	2	0.02%	4.29%	SSNTYTLTDVKR	2.38	1,384.71
Control	6006	ALCAM/CD166	gi|13111304,gi|41386784,gi|47605539	64,749.10	99.80%	2	2	2	0.02%	4.29%	VFKQPSKPEIVSK	2.95	1,486.86
Control	6006	Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	gi|109659140,gi|27806841,gi|28372116,gi|2920652,gi|3046232,gi|33111880,gi|68067472	75,368.60	100.00%	3	4	4	0.04%	6.30%	GRELPGFVNYK	3.29	1,279.68
Control	6006	Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	gi|109659140,gi|27806841,gi|28372116,gi|2920652,gi|3046232,gi|33111880,gi|68067472	75,368.60	100.00%	3	4	4	0.04%	6.30%	IEDIRLEQENEAEK	2.33	1,715.84
Control	6006	Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	gi|109659140,gi|27806841,gi|28372116,gi|2920652,gi|3046232,gi|33111880,gi|68067472	75,368.60	100.00%	3	4	4	0.04%	6.30%	SKIEDIRLEQENEAEK	3.02	1,930.97
Control	6006	Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	gi|109659140,gi|27806841,gi|28372116,gi|2920652,gi|3046232,gi|33111880,gi|68067472	75,368.60	100.00%	3	4	4	0.04%	6.30%	SSVLEALSGVALPR	4.6	1,398.80

Control	6006	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor 1; AltName: Full=p40; AltName: Full=Protein C10	gi|122066007,gi|28189773,gi|73587277	18,591.70	100.00%	3	4	4	0.04%	22.20%	AIVAIENPADVSVISSR	3.86	1,740.95
Control	6006	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor 1; AltName: Full=p40; AltName: Full=Protein C10	gi|122066007,gi|28189773,gi|73587277	18,591.70	100.00%	3	4	4	0.04%	22.20%	FAAATGATPIAGR	3.81	1,203.65
Control	6006	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor 1; AltName: Full=p40; AltName: Full=Protein C10	gi|122066007,gi|28189773,gi|73587277	18,591.70	100.00%	3	4	4	0.04%	22.20%	LLVVTDPR	2.49	912.5514
Control	6006	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,053.70	100.00%	4	4	4	0.04%	16.90%	IALTDNALIAR	3.88	1,170.68

Control	6006	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,053.70	100.00%	4	4	4	0.04%	16.90%	KTTHFVEGGDAGNREDQINR	2.97	2,244.08
Control	6006	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,053.70	100.00%	4	4	4	0.04%	16.90%	KVPAVPETLKK	3.29	1,209.76
Control	6006	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,053.70	100.00%	4	4	4	0.04%	16.90%	TTHFVEGGDAGNREDQINR	2.33	2,115.98
Control	6006	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	4	4	4	0.04%	10.40%	ADLINNLGTIAK	3.47	1,242.71
Control	6006	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	4	4	4	0.04%	10.40%	ALLFVPR	1.85	815.5138
Control	6006	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	4	4	4	0.04%	10.40%	GVVDSEDLPLNISR	3.57	1,513.79
Control	6006	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	4	4	4	0.04%	10.40%	HLEINPDHSIIETLR	4.14	1,786.94
Control	6006	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	4	4	4	0.04%	10.40%	NPDDITNEEYGEFYK	3.28	1,833.78
Control	6006	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	4	4	4	0.04%	10.40%	TLTIVDTGIGMTK	4.22	1,365.73
Control	6006	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	3	4	5	0.05%	9.52%	ESYSVYVYK	1.99	1,137.55
Control	6006	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	3	4	5	0.05%	9.52%	KESYSVYVYK	2.77	1,265.64
Control	6006	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	3	4	5	0.05%	9.52%	SRKESYSVYVYK	4.25	1,508.77

Control	6006	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	5	6	6	0.07%	11.90%	GDLGIEIPAEK	2.6	1,141.61
Control	6006	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	5	6	6	0.07%	11.90%	IISKIENHEGVR	2.84	1,394.78
Control	6006	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	5	6	6	0.07%	11.90%	IYVDDGLISLLVK	3.19	1,447.84
Control	6006	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	5	6	6	0.07%	11.90%	LDIDSPPITAR	3.43	1,197.65
Control	6006	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	5	6	6	0.07%	11.90%	QKGPDFLVTEVENGGSLGSK	2.98	2,062.05
Control	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	7	12	22	0.24%	22.50%	AMGNLQIDFADPSR	4.17	1,550.73
Control	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	7	12	22	0.24%	22.50%	AMGNLQIDFADPSRADDAR	2.66	2,078.96
Control	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	7	12	22	0.24%	22.50%	AVVYSNTIQSIMAIVK	3.83	1,752.96
Control	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	7	12	22	0.24%	22.50%	EYQLNDSAAYYLNDLER	3.32	2,076.95

Control	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	7	12	22	0.24%	22.50%	IAQSDYIPTQQDVLR	3.3	1,746.90
Control	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	7	12	22	0.24%	22.50%	LLLLGAGESGK	3.48	1,057.63
Control	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	7	12	22	0.24%	22.50%	SREYQLNDSAAYYLNDLER	4.1	2,320.08
Control	6006	FOLH1 protein	gi|151553958,gi|156120365	84,574.90	100.00%	4	4	5	0.05%	6.93%	AFTDPLGLPDRPFYR	2.01	1,764.91
Control	6006	FOLH1 protein	gi|151553958,gi|156120365	84,574.90	100.00%	4	4	5	0.05%	6.93%	IPHLAGTEQNFQLAK	3.37	1,666.89
Control	6006	FOLH1 protein	gi|151553958,gi|156120365	84,574.90	100.00%	4	4	5	0.05%	6.93%	IYNVIGTLR	2.47	1,048.62
Control	6006	FOLH1 protein	gi|151553958,gi|156120365	84,574.90	100.00%	4	4	5	0.05%	6.93%	LQDLDKNNPILLR	2.35	1,551.89
Control	6006	Na/K-ATPase beta 1 subunit [synthetic construct]	gi|22094876	35,156.20	100.00%	3	4	5	0.05%	10.50%	AYGENIGYSEKDR	3.64	1,501.69
Control	6006	Na/K-ATPase beta 1 subunit [synthetic construct]	gi|22094876	35,156.20	100.00%	3	4	5	0.05%	10.50%	AYGENIGYSEKDRFQGR	2.78	1,989.94
Control	6006	Na/K-ATPase beta 1 subunit [synthetic construct]	gi|22094876	35,156.20	100.00%	3	4	5	0.05%	10.50%	SYMTYVDNIDNFLKK	3.44	1,866.89
Control	6006	plastin 3	gi|152941116	70,782.90	99.80%	2	2	2	0.02%	4.60%	IDINMSGFNETDDLKR	2.74	1,883.88

Control	6006	plastin 3	gi|152941116	70,782.90	99.80%	2	2	2	0.02%	4.60%	MINLSVPDTIDER	3.85	1,518.75
Control	6006	ARF1 protein	gi|146327384,gi|28603778,gi|59858233,gi|62751462	20,583.70	100.00%	3	3	3	0.03%	30.90%	ILMVGLDAAGK	2.95	1,103.61
Control	6006	ARF1 protein	gi|146327384,gi|28603778,gi|59858233,gi|62751462	20,583.70	100.00%	3	3	3	0.03%	30.90%	LKLGEIVTTIPTIGFNVETVEYK	3.38	2,564.42
Control	6006	ARF1 protein	gi|146327384,gi|28603778,gi|59858233,gi|62751462	20,583.70	100.00%	3	3	3	0.03%	30.90%	QDLPNAMNAAEITDKLGLHSLR	2.64	2,423.24
Control	6006	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	100.00%	7	7	7	0.08%	21.10%	ALLILANGR	2.32	940.5939
Control	6006	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	100.00%	7	7	7	0.08%	21.10%	GAGTDEFTLNR	2.98	1,180.56
Control	6006	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	100.00%	7	7	7	0.08%	21.10%	GIGTDEKTLISILTER	3.92	1,745.96
Control	6006	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	100.00%	7	7	7	0.08%	21.10%	LTFDEYR	1.73	943.452

Control	6006	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	100.00%	7	7	7	0.08%	21.10%	SEIDLLDIR	3.26	1,073.58
Control	6006	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	100.00%	7	7	7	0.08%	21.10%	SLGDEISSETSGDFRK	3.14	1,727.81
Control	6006	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	100.00%	7	7	7	0.08%	21.10%	TLISILTER	2.49	1,045.63
Control	6006	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	9	10	0.11%	14.20%	GLNTIPLFVQLLYSPIENIQR	4.13	2,428.36
Control	6006	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	9	10	0.11%	14.20%	HAVVNLINYQDDAELATR	3.82	2,042.03
Control	6006	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	9	10	0.11%	14.20%	LHYGLPVVVK	3.09	1,124.68
Control	6006	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	9	10	0.11%	14.20%	LLNDEDQVVVNK	3.37	1,385.73

Control	6006	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	9	10	0.11%	14.20%	LVQLLVR	2.33	840.5666
Control	6006	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	9	10	0.11%	14.20%	MLGSPVDSVLFYAITTLHNLLLHQEGAK	4.21	3,083.62
Control	6006	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	9	10	0.11%	14.20%	TSMGGTQQQFVEGVR	2.3	1,640.77
Control	6006	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	gi|117306519,gi|118151180,gi|158512477	51,340.60	99.80%	2	2	2	0.02%	7.87%	SHLTDKGMLTAATEDK	2.47	1,733.84
Control	6006	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	gi|117306519,gi|118151180,gi|158512477	51,340.60	99.80%	2	2	2	0.02%	7.87%	VAREPEAPPEDKESESEAK	2.36	2,097.99
Control	6006	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	4	5	5	0.05%	1.70%	GLTSSEPVSIMEK	2.88	1,393.69
Control	6006	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	4	5	5	0.05%	1.70%	ITYQPSTGEGNEQTTTIGGR	3.36	2,110.01
Control	6006	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	4	5	5	0.05%	1.70%	IVEVFEIGPK	2.37	1,130.65
Control	6006	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	4	5	5	0.05%	1.70%	NIGVEVFSLGIK	3.3	1,275.73

Control	6006	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	3	4	4	0.04%	13.10%	ANVDKVFFDLMR	3.76	1,470.74
Control	6006	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	3	4	4	0.04%	13.10%	VFFDLMR	1.93	943.4707
Control	6006	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	3	4	4	0.04%	13.10%	VKEDENVPFLLVGNK	3.87	1,700.92
Control	6006	hemoglobin alpha chain	gi|116812902,gi|126717493,gi|13634094,gi|194678485,gi|197724899,gi|197724901,gi|197724903,gi|6006421,gi|74268120	15,035.40	100.00%	5	8	22	0.24%	48.20%	AVEHLDDLPGALSELSDLHAHK	4.43	2,367.19
Control	6006	hemoglobin alpha chain	gi|116812902,gi|126717493,gi|13634094,gi|194678485,gi|197724899,gi|197724901,gi|197724903,gi|6006421,gi|74268120	15,035.40	100.00%	5	8	22	0.24%	48.20%	FLANVSTVLTSK	4.81	1,279.73
Control	6006	hemoglobin alpha chain	gi|116812902,gi|126717493,gi|13634094,gi|194678485,gi|197724899,gi|197724901,gi|197724903,gi|6006421,gi|74268120	15,035.40	100.00%	5	8	22	0.24%	48.20%	LRVDPVNFK	2.71	1,087.63

Control	6006	hemoglobin alpha chain	gi|116812902,gi|126717493,gi|13634094,gi|194678485,gi|197724899,gi|197724901,gi|197724903,gi|6006421,gi|74268120	15,035.40	100.00%	5	8	22	0.24%	48.20%	MFLSFPTTK	2.53	1,087.55
Control	6006	hemoglobin alpha chain	gi|116812902,gi|126717493,gi|13634094,gi|194678485,gi|197724899,gi|197724901,gi|197724903,gi|6006421,gi|74268120	15,035.40	100.00%	5	8	22	0.24%	48.20%	TYFPHFDLSHGSAQVK	2.94	1,833.89
Control	6006	RecName: Full=Transmembrane emp24 domain-containing protein 1; Flags: Precursor	gi|114152289,gi|83638714,gi|84370158	25,119.90	99.80%	2	2	2	0.02%	11.50%	KADGVHTVEPTEAGDYK	3.06	1,816.87
Control	6006	RecName: Full=Transmembrane emp24 domain-containing protein 1; Flags: Precursor	gi|114152289,gi|83638714,gi|84370158	25,119.90	99.80%	2	2	2	0.02%	11.50%	SIQVLTLLR	3.02	1,042.66
Control	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	8	10	12	0.13%	20.80%	IIGAVDQIQLTQAQLEER	4.92	2,025.10
Control	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	8	10	12	0.13%	20.80%	IREGQVEVLK	4.27	1,170.68
Control	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	8	10	12	0.13%	20.80%	KLEVNEAELLR	4.41	1,313.74

Control	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	8	10	12	0.13%	20.80%	KSFTPDHVVYAR	3.52	1,419.74
Control	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	8	10	12	0.13%	20.80%	LEVNEAELLR	2.77	1,185.65
Control	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	8	10	12	0.13%	20.80%	QAEMEGAVQSIQGELSK	4.35	1,820.87
Control	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	8	10	12	0.13%	20.80%	SFTPDHVVYAR	2.83	1,291.64
Control	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	8	10	12	0.13%	20.80%	VMIYQDEVKLPAK	3.15	1,549.83
Control	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	11	15	76	0.83%	20.80%	DAFLGSFLYEYSR	3.34	1,567.74
Control	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	11	15	76	0.83%	20.80%	FKDLGEEHFK	4.42	1,249.62
Control	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	11	15	76	0.83%	20.80%	HLVDEPQNLIK	2.96	1,305.72
Control	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	11	15	76	0.83%	20.80%	KQTALVELLK	4.41	1,142.71

Control	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	11	15	76	0.83%	20.80%	KVPQVSTPTLVEVSR	4.04	1,639.94
Control	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	11	15	76	0.83%	20.80%	LVNELTEFAK	2.85	1,163.63
Control	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	11	15	76	0.83%	20.80%	LVVSTQTALA	2.54	1,002.58
Control	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	11	15	76	0.83%	20.80%	RHPEYAVSVLLR	5.3	1,439.81
Control	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	11	15	76	0.83%	20.80%	RHPYFYAPELLYANK	4.53	2,045.03
Control	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	11	15	76	0.83%	20.80%	TVMENFVAFVDK	3.34	1,399.69
Control	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	11	15	76	0.83%	20.80%	YLYEIAR	2.05	927.4934

Control	6006	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	99.80%	2	4	4	0.04%	11.00%	KYMEENDLLKK	3.04	1,426.72
Control	6006	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	99.80%	2	4	4	0.04%	11.00%	VNLQNNPGAVEHFHMK	3.29	1,850.90
Control	6006	PREDICTED: similar to ribosomal protein S4, X-linked X	gi|119901281,gi|119930307,gi|119934106,gi|194668343,gi|76660997	29,599.10	99.80%	2	2	2	0.02%	8.75%	ERHPGSFDVVHVK	3.21	1,506.78
Control	6006	PREDICTED: similar to ribosomal protein S4, X-linked X	gi|119901281,gi|119930307,gi|119934106,gi|194668343,gi|76660997	29,599.10	99.80%	2	2	2	0.02%	8.75%	TIRYPDPLIK	2.36	1,215.71
Control	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	12	16	20	0.22%	44.80%	AQVSLLIR	2.4	899.5673
Control	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	12	16	20	0.22%	44.80%	DLQMVNISLR	2.69	1,204.64
Control	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	12	16	20	0.22%	44.80%	FNASQLITQR	3.12	1,177.63
Control	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	12	16	20	0.22%	44.80%	IGGVQQDTILAEGLHFR	3.12	1,853.99
Control	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	12	16	20	0.22%	44.80%	ISSPTGSKDLQMVNISLR	3.1	1,962.03
Control	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	12	16	20	0.22%	44.80%	IVQAEGEAEAAR	2.25	1,243.63
Control	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	12	16	20	0.22%	44.80%	IYLTADNLVLNLQDESFTR	5.4	2,225.15
Control	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	12	16	20	0.22%	44.80%	LGLDYEER	2.55	994.4841
Control	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	12	16	20	0.22%	44.80%	LLLGAGAVAYGIR	4.44	1,273.76
Control	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	12	16	20	0.22%	44.80%	QKIVQAEGEAEAAR	3.93	1,499.78
Control	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	12	16	20	0.22%	44.80%	VLPSIVNEVLK	2.6	1,210.74

Control	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	12	16	20	0.22%	44.80%	VLSRPNAMELPSMYQR	2.51	1,907.95
Control	6006	TAP1 protein	gi|151557007	81,933.30	100.00%	5	6	6	0.07%	10.70%	GVVGAALGFR	3.32	946.5469
Control	6006	TAP1 protein	gi|151557007	81,933.30	100.00%	5	6	6	0.07%	10.70%	QVAAVGQEPLLFGR	4.23	1,484.82
Control	6006	TAP1 protein	gi|151557007	81,933.30	100.00%	5	6	6	0.07%	10.70%	SFANEEGEAQKFR	3.34	1,512.71
Control	6006	TAP1 protein	gi|151557007	81,933.30	100.00%	5	6	6	0.07%	10.70%	SSQVAIEVLSAMPTVR	2.58	1,703.90
Control	6006	TAP1 protein	gi|151557007	81,933.30	100.00%	5	6	6	0.07%	10.70%	STVAALLQNLYQPTEGQVLLDGEPLPK	4.38	2,894.55
Control	6006	signal sequence receptor, gamma (translocon-associated protein gamma)	gi|116004307,gi|122140189,gi|74268139	21,057.60	99.80%	2	3	3	0.03%	9.73%	GGPKQQSEEDLLLQDFSR	3.5	2,047.01
Control	6006	signal sequence receptor, gamma (translocon-associated protein gamma)	gi|116004307,gi|122140189,gi|74268139	21,057.60	99.80%	2	3	3	0.03%	9.73%	QQSEEDLLLQDFSR	3.36	1,707.82
Control	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	11	17	18	0.20%	44.00%	AYTNFDAERDALNIETAIK	4.46	2,155.07

Control	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	11	17	18	0.20%	44.00%	GVDEVTIVNILTNR	4.17	1,542.85
Control	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	11	17	18	0.20%	44.00%	LSLEGDHSTPPSAYGSVK	4.45	1,844.90

Control	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	11	17	18	0.20%	44.00%	QDIAFAYQR	2.71	1,111.55
Control	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	11	17	18	0.20%	44.00%	RAEDGSVIDYELIDQDAR	4.53	2,064.98

Control	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	11	17	18	0.20%	44.00%	SALSGHLETVILGLLK	3.9	1,650.98
Control	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	11	17	18	0.20%	44.00%	SLYYYIQQDTKGDYQK	2.6	2,012.96

Control	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	11	17	18	0.20%	44.00%	SNEQRQDIAFAYQR	5.14	1,725.83
Control	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	11	17	18	0.20%	44.00%	TDLEKDIVSDTSGDFRK	3.71	1,925.95

Control	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	11	17	18	0.20%	44.00%	TKGVDEVTIVNILTNR	4.24	1,771.99
Control	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	11	17	18	0.20%	44.00%	TPAQYDASELKASMK	3.15	1,655.79
Control	6006	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	3	3	3	0.03%	9.05%	ELIEVLQPLIAEHQAR	2.45	1,859.04

Control	6006	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	3	3	3	0.03%	9.05%	GIDYDKLIVR	2.45	1,191.67
Control	6006	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	3	3	3	0.03%	9.05%	MSASDPNSSIFLTDTAK	3.64	1,800.83
Control	6006	PREDICTED: similar to Transmembrane protein 16F	gi|119892265	106,290.10	100.00%	3	3	3	0.03%	5.60%	LLQVDESIIKPEQEFFTAPFEK	1.95	2,608.35
Control	6006	PREDICTED: similar to Transmembrane protein 16F	gi|119892265	106,290.10	100.00%	3	3	3	0.03%	5.60%	MNDFYIQDRDTFFNPATR	2.36	2,267.02
Control	6006	PREDICTED: similar to Transmembrane protein 16F	gi|119892265	106,290.10	100.00%	3	3	3	0.03%	5.60%	SLVDDKLVFVK	2.43	1,262.74
Control	6006	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	5	6	7	0.08%	16.90%	ALSSSLDDTEVK	2.97	1,264.63
Control	6006	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	5	6	7	0.08%	16.90%	ALSSSLDDTEVKK	3.29	1,392.72
Control	6006	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	5	6	7	0.08%	16.90%	FRGPFTDVVTTNLK	2.97	1,594.86

Control	6006	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	5	6	7	0.08%	16.90%	GPFTDVVTTNLK	3.85	1,291.69
Control	6006	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	5	6	7	0.08%	16.90%	VEQVLSLEPQHELK	4.23	1,648.89
Control	6006	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	5	5	5	0.05%	13.50%	APDFVFYAPR	3.27	1,182.59
Control	6006	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	5	5	5	0.05%	13.50%	FYPEDVSEELIQDITQR	2.77	2,082.00
Control	6006	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	5	5	5	0.05%	13.50%	KAPDFVFYAPR	2.78	1,310.69
Control	6006	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	5	5	5	0.05%	13.50%	TAMSTPHVAEPAENEQDEQDENGAEASAELR	6.09	3,342.43
Control	6006	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	5	5	5	0.05%	13.50%	VTTMDAELEFAIQPNTTGK	3.2	2,082.01
Control	6006	PREDICTED: similar to Keratin, type I cytoskeletal 24 (Cytokeratin-24) (Keratin-24) (Type I keratin-24)	gi|194676109	55,111.70	100.00%	2	2	2	0.02%	5.33%	KVLDDLTMTR	3.29	1,207.64
Control	6006	PREDICTED: similar to Keratin, type I cytoskeletal 24 (Cytokeratin-24) (Keratin-24) (Type I keratin-24)	gi|194676109	55,111.70	100.00%	2	2	2	0.02%	5.33%	SDLEMQIESLTEELAYLK	2.63	2,112.04
Control	6006	PREDICTED: transmembrane protein 33 isoform 2	gi|119893815,gi|119922774	27,968.00	99.80%	2	2	2	0.02%	8.10%	ALLANALTSALR	3.77	1,213.73

Control	6006	PREDICTED: transmembrane protein 33 isoform 2	gi|119893815,gi|119922774	27,968.00	99.80%	2	2	2	0.02%	8.10%	LPHFQLSR	2.33	997.5578
Control	6006	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	4	5	7	0.08%	43.60%	DSLLQDGEFTMDLR	3.39	1,655.76
Control	6006	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	4	5	7	0.08%	43.60%	SSFFVNGLTLGGQK	3.78	1,454.76
Control	6006	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	4	5	7	0.08%	43.60%	STGGAPTFNITVTMTAK	3.32	1,712.85
Control	6006	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	4	5	7	0.08%	43.60%	TFVNITPAEVGILVGK	2.82	1,657.95

Control	6006	Brain abundant, membrane attached signal protein 1	gi|115304757,gi|1930063,gi|27807507,gi|6686271	22,992.60	99.80%	2	2	2	0.02%	28.20%	AQAPAAPADEVKPAETPAANSDQTVAVKE	3.39	2,876.43
Control	6006	Brain abundant, membrane attached signal protein 1	gi|115304757,gi|1930063,gi|27807507,gi|6686271	22,992.60	99.80%	2	2	2	0.02%	28.20%	SDGAPASDSKPSSTEAAPSSKETPAATEAPSSTPK	3.54	3,344.56
Control	6006	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	99.80%	2	3	4	0.04%	14.50%	ALNLPSSGEGLAFFTFPNIASATK	3.75	2,453.27
Control	6006	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	99.80%	2	3	4	0.04%	14.50%	NKENPVYTPLYFPEELHR	5.27	2,246.12
Control	6006	HADHA protein	gi|74268185	83,232.60	100.00%	3	3	3	0.03%	5.77%	GFYIYQEGVK	2.84	1,203.60
Control	6006	HADHA protein	gi|74268185	83,232.60	100.00%	3	3	3	0.03%	5.77%	HVAENLGKEFGER	3.13	1,485.74
Control	6006	HADHA protein	gi|74268185	83,232.60	100.00%	3	3	3	0.03%	5.77%	TVLGSPEVLLGILPGAGTQR	3.02	2,049.17
Control	6006	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	3	3	4	0.04%	2.91%	FQDLVDAVR	2.55	1,062.56
Control	6006	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	3	3	4	0.04%	2.91%	KVTEENKELANELR	3.11	1,672.89
Control	6006	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	3	3	4	0.04%	2.91%	TIVTTLQDSIR	3.15	1,246.70
Control	6006	annexin 5	gi|119936560,gi|120474983,gi|260137,gi|73586525	36,057.60	100.00%	4	5	5	0.05%	17.80%	DLLDDLKSELTGKFEK	2.93	1,850.98
Control	6006	annexin 5	gi|119936560,gi|120474983,gi|260137,gi|73586525	36,057.60	100.00%	4	5	5	0.05%	17.80%	GLGTDEESILTLLTSR	3.41	1,704.90

Control	6006	annexin 5	gi|119936560,gi|120474983,gi|260137,gi|73586525	36,057.60	100.00%	4	5	5	0.05%	17.80%	MLVVLLQANRDPDAR	2.46	1,726.93
Control	6006	annexin 5	gi|119936560,gi|120474983,gi|260137,gi|73586525	36,057.60	100.00%	4	5	5	0.05%	17.80%	SEIDLYNIRK	2.47	1,250.67
Control	6006	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	99.80%	2	2	2	0.02%	8.37%	HMYVFGDFRDVLIPGK	2.42	1,909.96
Control	6006	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	99.80%	2	2	2	0.02%	8.37%	SDPIQELHDLAEITPDR	2.14	2,050.01
Control	6006	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32, gi|59857977	34,155.00	100.00%	3	3	3	0.03%	14.60%	AVVVNAAQLASYSQSK	2.66	1,635.87
Control	6006	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32, gi|59857977	34,155.00	100.00%	3	3	3	0.03%	14.60%	FLFGGLAGMGATVFVQPLDLVK	2.22	2,296.24

Control	6006	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32,gi|59857977	34,155.00	100.00%	3	3	3	0.03%	14.60%	NVFNALFR	2.16	980.5311
Control	6006	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	3	3	3	0.03%	10.70%	ISEIEDAAFLAR	2.81	1,334.70
Control	6006	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	3	3	3	0.03%	10.70%	SVQTTLQTDEVK	3.47	1,348.70
Control	6006	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	3	3	3	0.03%	10.70%	VTKPNIPEAIRR	2.06	1,393.83
Control	6006	GLI pathogenesis-related 2	gi|111307081,gi|115497826	17,191.20	99.80%	2	2	2	0.02%	16.90%	ASASDGSSFVVAR	2.56	1,253.61
Control	6006	GLI pathogenesis-related 2	gi|111307081,gi|115497826	17,191.20	99.80%	2	2	2	0.02%	16.90%	EAQQYSEALASTR	2.68	1,453.69
Control	6006	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	7	8	9	0.10%	16.40%	ITVLEALR	2.61	914.567
Control	6006	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	7	8	9	0.10%	16.40%	LKEYEAAVEQLKGDQIR	3.31	1,990.06
Control	6006	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	7	8	9	0.10%	16.40%	MYFDKYVLKPATEGK	2.5	1,805.91
Control	6006	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	7	8	9	0.10%	16.40%	NVLMYGPPGTGK	2.83	1,249.62
Control	6006	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	7	8	9	0.10%	16.40%	QQQLLNEENLR	2.25	1,384.72
Control	6006	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	7	8	9	0.10%	16.40%	RLLSKPQDALEGVVLSPSLEAR	3.88	2,378.34
Control	6006	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	7	8	9	0.10%	16.40%	TAGTLFGEGFR	3.4	1,155.58

Control	6006	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	7	7	8	0.09%	12.60%	AQAYQTGKDISTNYYASQKK	3.67	2,265.11
Control	6006	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	7	7	8	0.09%	12.60%	ELISNASDALDKIR	3.84	1,544.83
Control	6006	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	7	7	8	0.09%	12.60%	FAFQAEVNR	2.9	1,081.54
Control	6006	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	7	7	8	0.09%	12.60%	FQSSHHPSDMTSLDQYVER	3.79	2,280.00
Control	6006	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	7	7	8	0.09%	12.60%	GLFDEYGSK	2.57	1,015.47
Control	6006	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	7	7	8	0.09%	12.60%	NLLHVTDTGVGMTREELVK	2.67	2,128.11
Control	6006	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	7	7	8	0.09%	12.60%	SILFVPTSAPR	3.26	1,187.68
Control	6006	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	5	6	6	0.07%	6.98%	ALSAIADLLTNEHER	4.54	1,652.86
Control	6006	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	5	6	6	0.07%	6.98%	APSRQDVYGPQPQVR	4.4	1,697.87
Control	6006	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	5	6	6	0.07%	6.98%	FVGDADLER	2.4	1,021.50
Control	6006	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	5	6	6	0.07%	6.98%	KPTEDPTNDTVDFPKR	1.84	1,859.91
Control	6006	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	5	6	6	0.07%	6.98%	SLDNNYSTLNER	2.27	1,425.66

Control	6006	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	6	7	7	0.08%	15.30%	DPLVIELGQK	3.4	1,111.64
Control	6006	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	6	7	7	0.08%	15.30%	IFDTSLTR	2.14	952.5099
Control	6006	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	6	7	7	0.08%	15.30%	IFDTSLTRDPLVIELGQK	5.66	2,045.13
Control	6006	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	6	7	7	0.08%	15.30%	RVIIPSHLAYGK	3.28	1,353.80
Control	6006	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	6	7	7	0.08%	15.30%	VIIPSHLAYGK	2.39	1,197.70
Control	6006	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	6	7	7	0.08%	15.30%	VIIPSHLAYGKR	2.04	1,353.80
Control	6006	endoglin	gi|115497110,gi|92097469	69,885.10	99.80%	2	3	3	0.03%	3.25%	FSFLLR	1.71	782.4559
Control	6006	endoglin	gi|115497110,gi|92097469	69,885.10	99.80%	2	3	3	0.03%	3.25%	LQAPGIPLQLAYDSK	4.05	1,613.89
Control	6006	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	2	3	3	0.03%	7.47%	NIGVVVVGFPATPIIESR	4.17	1,868.06
Control	6006	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	2	3	3	0.03%	7.47%	SSAAAAAAAGQIHHVTENGGLYK	4.18	2,295.15
Control	6006	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	8	0.09%	8.67%	DKLNPQSTYSEA	3.18	1,352.63
Control	6006	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	8	0.09%	8.67%	FVTAVGTQGAISK	3.19	1,278.71
Control	6006	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	8	0.09%	8.67%	IAPSSFVSSGPFLFIK	2.79	1,696.93
Control	6006	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	8	0.09%	8.67%	SFEGNNNYDTPELR	2.69	1,655.73

Control	6006	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	8	0.09%	8.67%	TGPIQDHTGDGNFIYSQADENQK	4.32	2,535.14
Control	6006	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	8	0.09%	8.67%	TGPIQDHTGDGNFIYSQADENQKGK	2.57	2,720.26
Control	6006	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	7	7	8	0.09%	15.40%	GGTGADPVQTVTGGLR	3.94	1,485.77
Control	6006	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	7	7	8	0.09%	15.40%	LFEAEAQDLFR	3.14	1,338.67
Control	6006	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	7	7	8	0.09%	15.40%	LFEAEAQDLFRDIQSLPQK	3.88	2,248.16
Control	6006	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	7	7	8	0.09%	15.40%	LIEAVDNMLTNK	2.7	1,376.71
Control	6006	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	7	7	8	0.09%	15.40%	LPEIYIQLQR	2.79	1,272.73
Control	6006	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	7	7	8	0.09%	15.40%	SISIIDSPGILSGEK	3.85	1,515.83
Control	6006	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	7	7	8	0.09%	15.40%	YLLEQDFPGMR	3.3	1,384.66
Control	6006	RRAS2 protein	gi|148743916,gi|149944707	23,381.60	99.80%	2	3	3	0.03%	13.70%	LDILDTAGQEEFGAMR	3.6	1,781.84
Control	6006	RRAS2 protein	gi|148743916,gi|149944707	23,381.60	99.80%	2	3	3	0.03%	13.70%	MNVDQAFHELVR	2.64	1,474.71
Control	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	32.60%	AAYFGIYDTAK	3.61	1,219.60
Control	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	32.60%	DFLAGGVAAAISK	4.27	1,219.67
Control	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	32.60%	DKYKQIFLGGVDK	3.69	1,510.83

Control	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	32.60%	GLYQGFNVSVQGIIIYR	2.95	1,927.04
Control	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	32.60%	GMGGAFVLVLYDEIKK	3.66	1,755.94
Control	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	32.60%	GMGGAFVLVLYDEIKKFT	2.78	2,004.05
Control	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	32.60%	QIFLGGVDKR	2.39	1,132.65
Control	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	32.60%	VKLLLQVQHASK	4.01	1,363.84
Control	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	32.60%	YFPTQALNFAFK	4.78	1,446.74
Control	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	32.60%	YFPTQALNFAFKDK	3.72	1,689.86
Control	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	32.60%	YFPTQALNFAFKDKYK	3.76	1,981.02
Control	6006	heme oxygenase (decycling) 2	gi|164448721	37,538.70	100.00%	3	3	3	0.03%	9.28%	LPTQDGLPVHDGKGDLRK	3.33	1,946.05
Control	6006	heme oxygenase (decycling) 2	gi|164448721	37,538.70	100.00%	3	3	3	0.03%	9.28%	YMGDLSGGQVLK	3.01	1,283.63
Control	6006	heme oxygenase (decycling) 2	gi|164448721	37,538.70	100.00%	3	3	3	0.03%	9.28%	YMGDLSGGQVLKK	2.4	1,411.73
Control	6006	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	gi|59858119,gi|60650208,gi|60650268,gi|61889066,gi|75070049,gi|88954151	42,933.90	100.00%	3	3	3	0.03%	11.30%	FTRPIIAGMEFSR	5.12	1,540.79

Control	6006	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	gi|59858119,gi|60650208,gi|60650268,gi|61889066,gi|75070049,gi|88954151	42,933.90	100.00%	3	3	3	0.03%	11.30%	SDNSSHPQKDDGDNPETIMSSGNVNSSS	4.65	2,922.19
Control	6006	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	gi|59858119,gi|60650208,gi|60650268,gi|61889066,gi|75070049,gi|88954151	42,933.90	100.00%	3	3	3	0.03%	11.30%	SKSDNSSHPQKDDGDNPETIMSSGNVNSSS	3.84	3,137.32
Control	6006	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	3	3	4	0.04%	4.94%	DAFVYAIK	2.65	926.4982
Control	6006	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	3	3	4	0.04%	4.94%	VNAVPRPIPEK	1.98	1,219.72
Control	6006	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	3	3	4	0.04%	4.94%	YLDPSFFQHR	1.75	1,309.63
Control	6006	hypothetical protein LOC516334	gi|115496252,gi|151556904,gi|95768630	43,057.10	99.80%	2	2	3	0.03%	3.62%	ETAFEEDVQLPR	2.16	1,433.69
Control	6006	hypothetical protein LOC516334	gi|115496252,gi|151556904,gi|95768630	43,057.10	99.80%	2	2	3	0.03%	3.62%	MRETAFEEDVQLPR	2.94	1,736.83
Control	6006	PREDICTED: similar to Transmembrane emp24 domain-containing protein 2 precursor (Membrane protein p24A)	gi|194674620	22,715.40	99.80%	2	3	4	0.04%	12.40%	IVMFTIDIGEAPK	2.37	1,449.77

Control	6006	PREDICTED: similar to Transmembrane emp24 domain-containing protein 2 precursor (Membrane protein p24A)	gi|194674620	22,715.40	99.80%	2	3	4	0.04%	12.40%	YTFAAHMDGTYK	2.11	1,420.62
Control	6006	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	7	11	14	0.15%	8.16%	EATSTFTNITYR	2.57	1,403.68
Control	6006	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	7	11	14	0.15%	8.16%	EATSTFTNITYRGT	2.72	1,561.75
Control	6006	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	7	11	14	0.15%	8.16%	GTGDSSQITQVSPQR	3.36	1,560.76
Control	6006	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	7	11	14	0.15%	8.16%	HVLTLTDQVTR	3.71	1,282.71
Control	6006	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	7	11	14	0.15%	8.16%	ILEARPLSDKGTGDSSQITQVSPQR	6.12	2,683.40

Control	6006	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	7	11	14	0.15%	8.16%	LRPDDSKIFSVQVR	3.2	1,659.92
Control	6006	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	7	11	14	0.15%	8.16%	PLSDKGTGDSSQITQVSPQR	4.84	2,101.05
Control	6006	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	6	7	9	0.10%	12.40%	ADLVNNLGTIAK	3.48	1,228.69
Control	6006	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	6	7	9	0.10%	12.40%	ALLFIPR	1.75	829.5295
Control	6006	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	6	7	9	0.10%	12.40%	ELISNASDALDKIR	3.84	1,544.83
Control	6006	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	6	7	9	0.10%	12.40%	GVVDSEDLPLNISR	3.57	1,513.79
Control	6006	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	6	7	9	0.10%	12.40%	HLEINPDHPIVETLR	3.72	1,782.95
Control	6006	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	6	7	9	0.10%	12.40%	NPDDITQEEYGEFYK	3	1,847.80
Control	6006	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	6	7	9	0.10%	12.40%	TLTLVDTGIGMTK	4.22	1,365.73
Control	6006	Solute carrier family 1 (neutral amino acid transporter), member 5	gi|115305216,gi|15145909,gi|21541958,gi|27807087	56,431.20	99.90%	2	2	2	0.02%	4.45%	EVLDSFLDLVR	2.37	1,305.71

Control	6006	Solute carrier family 1 (neutral amino acid transporter), member 5	gi|115305216,gi|15145909,gi|21541958,gi|27807087	56,431.20	99.90%	2	2	2	0.02%	4.45%	NIFPSNLVSAAFR	2.69	1,435.77
Control	6006	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	5	0.05%	10.50%	GSFSEQGINEFLR	3.07	1,483.72
Control	6006	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	5	0.05%	10.50%	GSTAPVGGGAFPTISTR	2.97	1,575.81
Control	6006	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	5	0.05%	10.50%	IFQKGESPVDYDGGR	4.98	1,667.80
Control	6006	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	5	0.05%	10.50%	LAAVDATVNQVLASR	2.82	1,527.85
Control	6006	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	5	0.05%	10.50%	VKLAAVDATVNQVLASR	3.17	1,755.01
Control	6006	Deoxyribonuclease I-like 1	gi|151553571	35,175.30	100.00%	3	5	5	0.05%	13.30%	IVLHGEHLQSLLR	3.21	1,514.88
Control	6006	Deoxyribonuclease I-like 1	gi|151553571	35,175.30	100.00%	3	5	5	0.05%	13.30%	SKVLPSLVLVPLHTTPK	3.58	1,829.13
Control	6006	Deoxyribonuclease I-like 1	gi|151553571	35,175.30	100.00%	3	5	5	0.05%	13.30%	VAREPVLDTLVK	3.36	1,339.79

Control	6011	TIMM23 protein	gi|134025149,gi|139947578,gi|215274655	21,809.90	100.00%	3	3	4	0.03%	32.50%	NVQILNMVTR	3.29	1,203.65
Control	6011	TIMM23 protein	gi|134025149,gi|139947578,gi|215274655	21,809.90	100.00%	3	3	4	0.03%	32.50%	TTGGLAGFFGAGGAGYSHADLAGVPLTGMNPLSPYLNVDPR	5.64	4,034.97
Control	6011	TIMM23 protein	gi|134025149,gi|139947578,gi|215274655	21,809.90	100.00%	3	3	4	0.03%	32.50%	YLVQDTDEFILPTGANK	3.72	1,923.97
Control	6011	TMEM115 protein	gi|133777923,gi|134085844,gi|146186960,gi|218551717	38,121.60	99.80%	2	3	3	0.02%	6.84%	RYDVGAPSSITISLPGTDPQDAER	3.29	2,545.25
Control	6011	TMEM115 protein	gi|133777923,gi|134085844,gi|146186960,gi|218551717	38,121.60	99.80%	2	3	3	0.02%	6.84%	YDVGAPSSITISLPGTDPQDAER	4.31	2,389.15
Control	6011	Chain B, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591027,gi|110591030,gi|114686,gi|27807305,gi|599873,gi|74356487	18,544.10	100.00%	3	5	8	0.06%	20.60%	IQEYEKELEK	3.6	1,308.67
Control	6011	Chain B, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591027,gi|110591030,gi|114686,gi|27807305,gi|599873,gi|74356487	18,544.10	100.00%	3	5	8	0.06%	20.60%	IQEYEKELEKMR	2.75	1,611.80
Control	6011	Chain B, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591027,gi|110591030,gi|114686,gi|27807305,gi|599873,gi|74356487	18,544.10	100.00%	3	5	8	0.06%	20.60%	NIIPFDQMTIEDLNEVFPETK	3.5	2,509.22
Control	6011	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	9	17	0.13%	12.90%	AQILLDCGEDNICVPDLQLEVFGEQNHVYLGDK	4.7	3,687.77

Control	6011	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	9	17	0.13%	12.90%	DLDGNGYPDLIVGSFGVDK	3.64	1,980.96
Control	6011	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	9	17	0.13%	12.90%	FGSSLTPLGDLDQDGYNDVAIGAAFGGENR	2.76	3,056.42
Control	6011	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	9	17	0.13%	12.90%	LAGMEPTPTLTLTGQDEFGR	5.02	2,150.04
Control	6011	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	9	17	0.13%	12.90%	QATLTQTLLIQNGAR	3.64	1,627.91
Control	6011	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	9	17	0.13%	12.90%	TIQFDFQILSK	2.97	1,339.73
Control	6011	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	9	17	0.13%	12.90%	VTAPPEAEYSGLVR	2.95	1,488.77

Control	6011	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	4	7	15	0.12%	29.20%	AMAEEMNEKQVYDAHTK	3.19	2,010.89
Control	6011	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	4	7	15	0.12%	29.20%	ASFTTFTVTK	2.83	1,102.58
Control	6011	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	4	7	15	0.12%	29.20%	YVDSEGHLYTVPIR	3.09	1,648.83
Control	6011	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	4	7	15	0.12%	29.20%	YVDSEGHLYTVPIREQGNIYKPNNK	5.27	2,934.47
Control	6011	RTN3 protein	gi|115305093,gi|122132179,gi|146231798,gi|151554368,gi|32880223,gi|38327594	25,478.60	100.00%	3	5	5	0.04%	10.50%	LFLVEDLVDSLK	3.53	1,390.78
Control	6011	RTN3 protein	gi|115305093,gi|122132179,gi|146231798,gi|151554368,gi|32880223,gi|38327594	25,478.60	100.00%	3	5	5	0.04%	10.50%	TQIDHYVGIAR	3.19	1,272.67
Control	6011	RTN3 protein	gi|115305093,gi|122132179,gi|146231798,gi|151554368,gi|32880223,gi|38327594	25,478.60	100.00%	3	5	5	0.04%	10.50%	YKTQIDHYVGIAR	3.13	1,563.83
Control	6011	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	5	6	11	0.09%	20.30%	DNFHGLAIFLDTYPNDETTER	4.92	2,468.14
Control	6011	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	5	6	11	0.09%	20.30%	DNVDDPTGNFR	2.96	1,249.54
Control	6011	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	5	6	11	0.09%	20.30%	DRLVPGPVFGSK	2.28	1,271.71
Control	6011	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	5	6	11	0.09%	20.30%	LPTGYYFGASAGTGDLSDNHDIISMK	5.74	2,746.27
Control	6011	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	5	6	11	0.09%	20.30%	SPKDNVDDPTGNFR	3.72	1,561.72

Control	6011	RPS9 protein	gi|151554648,gi|151554779,gi|155372029,gi|189044386,gi|190576593,gi|197215709,gi|217418300	22,574.50	100.00%	2	2	3	0.02%	8.76%	LFEGNALLR	2.76	1,032.58
Control	6011	RPS9 protein	gi|151554648,gi|151554779,gi|155372029,gi|189044386,gi|190576593,gi|197215709,gi|217418300	22,574.50	100.00%	2	2	3	0.02%	8.76%	LIGEYGLR	2.53	920.5201
Control	6011	PREDICTED: similar to Splicing factor, proline- and glutamine-rich (Polypyrimidine tract-binding protein-associated-splicing factor) (PTB-associated-splicing factor) (PSF) (DNA-binding p52/p100 complex,	gi|194665922	76,230.60	100.00%	3	3	3	0.02%	7.21%	FATHAALSVR	3.19	1,143.63

Control	6011	PREDICTED: similar to Splicing factor, proline- and glutamine-rich (Polypyrimidine tract-binding protein-associated-splicing factor) (PTB-associated-splicing factor) (PSF) (DNA-binding p52/p100 complex,	gi|194665922	76,230.60	100.00%	3	3	3	0.02%	7.21%	LFVGNLPADITEDEFKR	2.03	1,964.01
Control	6011	PREDICTED: similar to Splicing factor, proline- and glutamine-rich (Polypyrimidine tract-binding protein-associated-splicing factor) (PTB-associated-splicing factor) (PSF) (DNA-binding p52/p100 complex,	gi|194665922	76,230.60	100.00%	3	3	3	0.02%	7.21%	NLSPYVSNELLEEAFSQFGPIER	2.87	2,639.30
Control	6011	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	4	4	4	0.03%	12.60%	EIILVDDYSNDPEDGALLGK	3.82	2,176.07
Control	6011	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	4	4	4	0.03%	12.60%	NKFNQVESDKLR	2.59	1,477.78

Control	6011	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	4	4	4	0.03%	12.60%	QHPYTFPGGSGTVFAR	4.07	1,721.84
Control	6011	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	4	4	4	0.03%	12.60%	VVSPIIDVINMDNFQYVGASADLK	2.97	2,624.33
Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	ADIGVAMGIAGSDVSK	4.06	1,506.75
Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	AVAGDASESALLK	4.11	1,231.65
Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	AVFQANQDNLPILK	4.02	1,570.86
Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	AVFQANQDNLPILKR	4.06	1,726.96
Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	DMTPEQLDDILK	2.47	1,417.69
Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	EQPLDEELKDAFQNAYLELGGLGER	3.6	2,834.38
Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	GVGIISEGNETVEDIAAR	4.56	1,829.92

Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	IVEIPFNSTNK	2.93	1,261.68
Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	KADIGVAMGIAGSDVSK	5.55	1,634.84
Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	LNIPVSQVNPR	3.98	1,236.71
Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	LSLDELHR	2.43	982.5317
Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	MSINAEEVVVGDLVEVK	4.71	1,846.95
Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	NMVPQQALVIR	3.28	1,284.71
Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	QAADMILLDDNFASIVTGVEEGR	3.44	2,480.20
Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	QGAIVAVTGDGVNDSPALK	4.99	1,811.95
Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	QGAIVAVTGDGVNDSPALKK	3.67	1,940.05
Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	SPDFTNENPLETR	4.46	1,519.70

Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	VDNSSLTGESEPQTR	3.92	1,619.75
Control	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	29	53	0.41%	23.60%	VIMVTGDHPITAK	4.45	1,397.75
Control	6011	PTPLAD1 protein	gi|154425645,gi|157074148,gi|166199295	43,116.60	99.80%	2	3	4	0.03%	8.56%	FSFTLPYPVK	2.21	1,198.65
Control	6011	PTPLAD1 protein	gi|154425645,gi|157074148,gi|166199295	43,116.60	99.80%	2	3	4	0.03%	8.56%	VELSDVQNPAISITENVLHFK	3.73	2,353.24
Control	6011	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	99.80%	2	3	3	0.02%	16.50%	AFDLLVDRPVTLVR	2.32	1,613.94
Control	6011	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	99.80%	2	3	3	0.02%	16.50%	DYKVDQEIVNIIQER	4.21	1,861.97
Control	6011	ribosomal protein L18	gi|59858459,gi|62752012,gi|75060915,gi|75775560,gi|89573893	21,518.10	100.00%	3	3	7	0.05%	18.10%	ILTFDQLALDSPK	4.41	1,460.80
Control	6011	ribosomal protein L18	gi|59858459,gi|62752012,gi|75060915,gi|75775560,gi|89573893	21,518.10	100.00%	3	3	7	0.05%	18.10%	TNRPPLSLSR	3.8	1,140.65
Control	6011	ribosomal protein L18	gi|59858459,gi|62752012,gi|75060915,gi|75775560,gi|89573893	21,518.10	100.00%	3	3	7	0.05%	18.10%	TNSTFNQVVLK	2.6	1,250.67

Control	6011	RecName: Full=Isocitrate dehydrogenase [NADP], mitochondrial; Short=IDH; AltName: Full=Oxalosuccinate decarboxylase; AltName: Full=NADP(+)-specific ICDH; AltName: Full=IDP; AltName:	gi|109891934,gi|28461205,gi|430,gi|73587323	50,807.00	100.00%	5	7	7	0.05%	17.00%	FKDIFQAIFEK	3.53	1,385.75
Control	6011	RecName: Full=Isocitrate dehydrogenase [NADP], mitochondrial; Short=IDH; AltName: Full=Oxalosuccinate decarboxylase; AltName: Full=NADP(+)-specific ICDH; AltName: Full=IDP; AltName:	gi|109891934,gi|28461205,gi|430,gi|73587323	50,807.00	100.00%	5	7	7	0.05%	17.00%	GKLDGNQDLIR	3.32	1,228.66

Control	6011	RecName: Full=Isocitrate dehydrogenase [NADP], mitochondrial; Short=IDH; AltName: Full=Oxalosuccinate decarboxylase; AltName: Full=NADP(+)-specific ICDH; AltName: Full=IDP; AltName:	gi|109891934,gi|28461205,gi|430,gi|73587323	50,807.00	100.00%	5	7	7	0.05%	17.00%	LNEHFLNTSDFLDTIK	3.87	1,906.95
Control	6011	RecName: Full=Isocitrate dehydrogenase [NADP], mitochondrial; Short=IDH; AltName: Full=Oxalosuccinate decarboxylase; AltName: Full=NADP(+)-specific ICDH; AltName: Full=IDP; AltName:	gi|109891934,gi|28461205,gi|430,gi|73587323	50,807.00	100.00%	5	7	7	0.05%	17.00%	TIEAEAAHGTVTR	4.4	1,355.69

Control	6011	RecName: Full=Isocitrate dehydrogenase [NADP], mitochondrial; Short=IDH; AltName: Full=Oxalosuccinate decarboxylase; AltName: Full=NADP(+)-specific ICDH; AltName: Full=IDP; AltName:	gi|109891934,gi|28461205,gi|430,gi|73587323	50,807.00	100.00%	5	7	7	0.05%	17.00%	YFDLGLPNRDQTNDQVTIDSALATQK	4.59	2,923.44
Control	6011	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	9	14	25	0.20%	18.90%	AFEESLSTLK	3.05	1,124.58
Control	6011	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	9	14	25	0.20%	18.90%	EKADAIYNMIGYPNFIMDPK	3.51	2,346.11
Control	6011	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	9	14	25	0.20%	18.90%	ELDKVFNDYTAVPDLYFENAMR	4.44	2,666.24
Control	6011	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	9	14	25	0.20%	18.90%	HTLGENIADNGGLK	4.02	1,438.73

Control	6011	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	9	14	25	0.20%	18.90%	NEIVFPAGILQAPFYTR	5.05	1,936.03
Control	6011	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	9	14	25	0.20%	18.90%	SSPNALNFGGIGVVVGHELTHAFDDQGR	2.61	2,894.42
Control	6011	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	9	14	25	0.20%	18.90%	TPESSHEGLITDPHSPSR	4.95	1,946.92
Control	6011	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	9	14	25	0.20%	18.90%	VFNDYTAVPDLYFENAMR	3.05	2,181.00
Control	6011	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	9	14	25	0.20%	18.90%	VLTGYLNYMVQLGK	3.37	1,614.86
Control	6011	RecName: Full=60S ribosomal protein L5	gi|108862056,gi|119900687,gi|119905361,gi|61552973,gi|75775327,gi|78369655	34,327.50	99.80%	2	3	3	0.02%	8.75%	GAVDGGLSIPHSTK	4.08	1,338.70
Control	6011	RecName: Full=60S ribosomal protein L5	gi|108862056,gi|119900687,gi|119905361,gi|61552973,gi|75775327,gi|78369655	34,327.50	99.80%	2	3	3	0.02%	8.75%	YLIEEDEDAYKK	3.11	1,515.72

Control	6011	hydroxyacyl-Coenzyme A dehydrogenase	gi|114052468,gi|194678883,gi|86821535	34,251.40	99.80%	2	2	2	0.02%	7.67%	FAGLHFFNPVPLMK	3.23	1,633.86
Control	6011	hydroxyacyl-Coenzyme A dehydrogenase	gi|114052468,gi|194678883,gi|86821535	34,251.40	99.80%	2	2	2	0.02%	7.67%	TFESLLDFSR	2.31	1,214.61
Control	6011	secretory carrier membrane protein 3 isoform 1	gi|61553277,gi|71649517,gi|73586519,gi|78369651	38,348.80	100.00%	3	3	3	0.02%	15.00%	AQQEFAAGVFSNPAVR	3.76	1,691.85
Control	6011	secretory carrier membrane protein 3 isoform 1	gi|61553277,gi|71649517,gi|73586519,gi|78369651	38,348.80	100.00%	3	3	3	0.02%	15.00%	NYGSYSTQASTAAATAELLK	4.69	2,047.00
Control	6011	secretory carrier membrane protein 3 isoform 1	gi|61553277,gi|71649517,gi|73586519,gi|78369651	38,348.80	100.00%	3	3	3	0.02%	15.00%	TAAANAAAGAAENAFR	2.69	1,476.72
Control	6011	ANO10 protein	gi|154425799,gi|156120985	76,294.20	100.00%	3	3	3	0.02%	5.61%	ETLENQNLYLVGASK	3.16	1,678.86
Control	6011	ANO10 protein	gi|154425799,gi|156120985	76,294.20	100.00%	3	3	3	0.02%	5.61%	LEFESLEALK	2.26	1,178.63
Control	6011	ANO10 protein	gi|154425799,gi|156120985	76,294.20	100.00%	3	3	3	0.02%	5.61%	LLLGAEAVGLVK	3.25	1,182.75
Control	6011	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	4	4	5	0.04%	18.80%	GHAAPTPTPVKPPR	3.64	1,425.80
Control	6011	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	4	4	5	0.04%	18.80%	LATMLETLR	2.46	1,063.58
Control	6011	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	4	4	5	0.04%	18.80%	LEANHGLLVAR	2.87	1,192.68
Control	6011	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	4	4	5	0.04%	18.80%	SHDTTSNTLAQLLAK	3.26	1,599.83
Control	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	108	0.84%	56.30%	DAVTYTEHAK	2.61	1,134.54

Control	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	108	0.84%	56.30%	DNIQGITKPAIR	4.13	1,325.75
Control	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	108	0.84%	56.30%	ISGLIYEETR	4.17	1,180.62
Control	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	108	0.84%	56.30%	KTVTAMDVVYALK	3.94	1,454.79
Control	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	108	0.84%	56.30%	KTVTAMDVVYALKR	4.98	1,610.89
Control	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	108	0.84%	56.30%	RISGLIYEETR	2.54	1,336.72
Control	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	108	0.84%	56.30%	TVTAMDVVYALK	3.83	1,326.70
Control	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	108	0.84%	56.30%	TVTAMDVVYALKR	3.5	1,482.80

Control	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	108	0.84%	56.30%	VFLENVIR	3.26	989.5778
Control	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	108	0.84%	56.30%	VFLENVIRDAVTYTEHAK	4.74	2,105.10
Control	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	108	0.84%	56.30%	VLRDNIQGITKPAIR	4.19	1,694.01
Control	6011	RecName: Full=Cleft lip and palate transmembrane protein 1 homolog	gi|110278913,gi|114051439,gi|84708720	75,864.60	99.80%	2	3	3	0.02%	4.63%	ALNTFIDDLFAFVIK	3.67	1,726.94
Control	6011	RecName: Full=Cleft lip and palate transmembrane protein 1 homolog	gi|110278913,gi|114051439,gi|84708720	75,864.60	99.80%	2	3	3	0.02%	4.63%	NLLTGETEADPEMIKR	3.63	1,832.91
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	AVDEAADALLK	2.84	1,115.59
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	ELDSITPEVLPGWK	3.95	1,583.83
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	GDTSASTTAGDTLSVPAPVVQHEELIK	4.78	2,723.37
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	KAVDEAADALLK	3.98	1,243.69

Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	KVEEVRDAMENEMR	2.71	1,751.81
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	LAEQELQFR	3.03	1,133.60
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	LAQQEKQEQVKIESLAK	2.3	1,970.09
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	LSADDLNALIAHAHR	2.84	1,616.85
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	LSQEQVDNFTLDINTAYAR	4.01	2,198.07
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	MKTASADLPTVPLGSAVEAIR	3.73	2,143.14
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	QIVEILTAYASAVGIGTTQVQQQEGLGR	3.93	2,930.56
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	QKGDTSASTTAGDTLSVPAPVVQHEELIK	3.06	2,979.53
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	SEIQAEQDRKVEEVR	3.7	1,815.92
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	SVIENAKKEEVAGAK	5.61	1,572.86
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	TASADLPTVPLGSAVEAIR	4.35	1,868.01
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	TDHPETGEGKPKPATSEEASSTSVR	4.31	2,598.23
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	TIPYSDKLFEMVLGSPPYTVPLPK	2.96	2,708.43
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	VQEQELKYEFEQDLSEK	4.51	2,142.02

Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	VQEQELKYEFEQDLSEKLAEQELQFR	4.31	3,256.60
Control	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	20	24	42	0.33%	37.50%	VVSQYHELVVQAR	4.38	1,527.83
Control	6011	SCARB2 protein	gi|151556135,gi|156120953	53,968.70	100.00%	2	2	2	0.02%	6.49%	GQGSTDEGTADERAPLIR	2.16	1,872.90
Control	6011	SCARB2 protein	gi|151556135,gi|156120953	53,968.70	100.00%	2	2	2	0.02%	6.49%	HDVSPYFGLFYGK	3.55	1,529.74
Control	6011	ATAD1 protein	gi|154426126,gi|76671592	41,750.40	99.80%	2	4	6	0.05%	11.40%	EYVNSTSEESHDEDEIRPVQQQDLHR	3.64	3,140.42
Control	6011	ATAD1 protein	gi|154426126,gi|76671592	41,750.40	99.80%	2	4	6	0.05%	11.40%	LQPSIIFIDEIDSFLR	4.31	1,906.03
Control	6011	dolichyl-phosphate beta-glucosyltransferase isoform 2	gi|114052030,gi|215276972,gi|86826341	36,996.60	99.80%	2	2	2	0.02%	7.72%	EALPSIQDSPTK	2.3	1,285.66
Control	6011	dolichyl-phosphate beta-glucosyltransferase isoform 2	gi|114052030,gi|215276972,gi|86826341	36,996.60	99.80%	2	2	2	0.02%	7.72%	QLSVVVPSYNEEK	2.46	1,491.77
Control	6011	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	7	8	12	0.09%	27.70%	EEGILGFFAGLIPR	2.91	1,518.83
Control	6011	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	7	8	12	0.09%	27.70%	GLFTGLTPR	2.45	961.5467
Control	6011	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	7	8	12	0.09%	27.70%	GNSLFFR	2.49	840.4362
Control	6011	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	7	8	12	0.09%	27.70%	QVCQLPGLFCYAQHIASIDGK	3.07	2,291.13
Control	6011	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	7	8	12	0.09%	27.70%	QVCQLPGLFCYAQHIASIDGKR	2.36	2,447.23

Control	6011	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	7	8	12	0.09%	27.70%	SAATLITHPFHVITLR	4.54	1,777.01
Control	6011	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	7	8	12	0.09%	27.70%	VLIQVGYEPLAPTVGR	4.5	1,711.97
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	AAALRPEEDGAFRPSEAFETLQK	3.32	2,533.27
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	AEESAAHLPEEIR	3.13	1,451.71
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	AEESAAHLPEEIRR	2.16	1,607.81
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	ASVGQVESDLK	3.32	1,132.58
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	DFTSLENTVEER	3.41	1,439.66
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	DLSDGIHVVK	1.73	1,082.58
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	EAADSEHHTLQALTEK	3.61	1,779.85

Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	EELGQGLQGVEQK	3.59	1,414.72
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	ELVSLKQEQQR	3.66	1,357.74
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	ERDFTSLENTVEER	4.34	1,724.81
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	EVVKEIQTSVK	3.15	1,259.72
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	FKEAADSEHHTLQALTEK	4.81	2,055.01
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	GLGEAQLSLAGDVDELK	4.88	1,714.89
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	GLGEAQLSLAGDVDELKR	4.46	1,870.99
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	GLLEDLRNDLDR	2.18	1,428.74

Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	IETNENNLESAK	3.29	1,361.65
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	ILRAEESAAHLPEEIR	2.74	1,833.98
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	LEEELGQLK	3.1	1,058.57
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	LQNEILKDLSDGIHVVK	5.68	1,921.08
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	LQSVEDGVQAAR	3.74	1,272.65
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	QREELGQGLQGVEQK	3.26	1,698.88
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	RLEEELGQLK	3.85	1,214.67
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	SINDNIAIFTDVQK	4.72	1,577.82

Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	SINDNIAIFTDVQKR	4.03	1,733.92
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	STIQTMESDVYTEVK	3.06	1,746.81
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	STIQTMESDVYTEVKELVSLKQEQQR	3.41	3,069.54
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	TAVDSLVAYSVK	4.41	1,252.68
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	VQEQVHTLLGR	4.03	1,279.71
Control	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	46	108	0.84%	45.70%	VQSLQATFGTFESLVR	4.4	1,782.94
Control	6011	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	4	5	9	0.07%	18.70%	KQYDSYTFTASK	3.46	1,438.68
Control	6011	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	4	5	9	0.07%	18.70%	QYDSYTFTASK	2.18	1,310.59
Control	6011	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	4	5	9	0.07%	18.70%	SVIDYQTHFR	3.08	1,265.63
Control	6011	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	4	5	9	0.07%	18.70%	TVYFDFQVGEDPPLFPSENR	3.53	2,357.11
Control	6011	similar to peptidylprolyl isomerase A (cyclophilin A)	gi|28189771,gi|58760424,gi|75948300	17,851.80	100.00%	3	4	4	0.03%	24.40%	SIYGEKFDDENFILK	3.33	1,817.90

Control	6011	similar to peptidylprolyl isomerase A (cyclophilin A)	gi|28189771,gi|58760424,gi|75948300	17,851.80	100.00%	3	4	4	0.03%	24.40%	VKEGMNIVEAMER	2.89	1,521.74
Control	6011	similar to peptidylprolyl isomerase A (cyclophilin A)	gi|28189771,gi|58760424,gi|75948300	17,851.80	100.00%	3	4	4	0.03%	24.40%	VSFELFADKVPK	3.07	1,379.76
Control	6011	Clusterin	gi|109939936,gi|116530,gi|146231734,gi|151555910,gi|163115,gi|27806907	51,096.70	99.80%	2	2	2	0.02%	6.38%	LYDQLLQSYQQK	3.82	1,526.79
Control	6011	Clusterin	gi|109939936,gi|116530,gi|146231734,gi|151555910,gi|163115,gi|27806907	51,096.70	99.80%	2	2	2	0.02%	6.38%	RPQDTQYYSPFSSFPR	3.57	1,975.93
Control	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	9	13	35	0.27%	47.80%	AAELIANSLATAGDGLIELR	4.23	1,998.09
Control	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	9	13	35	0.27%	47.80%	DLQNVNITLR	3.82	1,185.66
Control	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	9	13	35	0.27%	47.80%	FDAGELITQR	3.72	1,149.59
Control	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	9	13	35	0.27%	47.80%	FGLALAVAGGVVNSALYNVDAGHR	3.79	2,371.25
Control	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	9	13	35	0.27%	47.80%	IFTSIGEDYDER	3.25	1,444.66
Control	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	9	13	35	0.27%	47.80%	ILFRPVASQLPR	3.11	1,396.84
Control	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	9	13	35	0.27%	47.80%	KLEAAEDIAYQLSR	4.33	1,606.84
Control	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	9	13	35	0.27%	47.80%	NITYLPAGQSVLLQLPQ	3.9	1,855.03
Control	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	9	13	35	0.27%	47.80%	VLPSITTEILK	2.71	1,213.74

Control	6011	Stromal cell derived factor 4	gi|73586919,gi|78369298	41,088.60	99.80%	2	2	2	0.02%	9.58%	QMIAIADENQNHYLEPEEVLK	2.91	2,500.20
Control	6011	Stromal cell derived factor 4	gi|73586919,gi|78369298	41,088.60	99.80%	2	2	2	0.02%	9.58%	TAEHFQEAVAESR	4.02	1,474.69
Control	6011	ras-related C3 botulinum toxin substrate 1	gi|27806443,gi|51702785,gi|6007014,gi|73587375	21,432.60	100.00%	2	3	6	0.05%	7.81%	KLTPITYPQGLAMAK	4.31	1,647.91
Control	6011	ras-related C3 botulinum toxin substrate 1	gi|27806443,gi|51702785,gi|6007014,gi|73587375	21,432.60	100.00%	2	3	6	0.05%	7.81%	LTPITYPQGLAMAK	3.32	1,519.82
Control	6011	Interferon induced transmembrane protein 1 (9-27)	gi|112362418,gi|118151192,gi|118151350,gi|118151354,gi|119919513,gi|14279576,gi|14279578,gi|148744152,gi|32480628,gi|73586549,gi|73587371	13,629.20	99.80%	2	3	4	0.03%	13.70%	KMVGDITGAQSYASTAK	3.3	1,743.86
Control	6011	Interferon induced transmembrane protein 1 (9-27)	gi|112362418,gi|118151192,gi|118151350,gi|118151354,gi|119919513,gi|14279576,gi|14279578,gi|148744152,gi|32480628,gi|73586549,gi|73587371	13,629.20	99.80%	2	3	4	0.03%	13.70%	MVGDITGAQSYASTAK	4.88	1,615.76
Control	6011	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	5	7	7	0.05%	42.30%	ALAAAGYDVEK	3.46	1,107.57
Control	6011	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	5	7	7	0.05%	42.30%	ALAAAGYDVEKNSR	4.85	1,578.79

Control	6011	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	5	7	7	0.05%	42.30%	ASGPPVSELITK	2.35	1,198.67
Control	6011	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	5	7	7	0.05%	42.30%	KASGPPVSELITK	3.97	1,326.76
Control	6011	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	5	7	7	0.05%	42.30%	SETAPAAPAAAPPAEK	3.23	1,478.75
Control	6011	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	4	5	8	0.06%	17.50%	ILHVNGFNGEGGEEDPQAAR	6.17	2,110.00
Control	6011	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	4	5	8	0.06%	17.50%	LLLLGAGESGK	3.47	1,057.63
Control	6011	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	4	5	8	0.06%	17.50%	SKIEDYFPEFAR	3.54	1,501.73
Control	6011	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	4	5	8	0.06%	17.50%	VLTSGIFETK	2.24	1,094.61
Control	6011	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	4	5	8	0.06%	17.50%	YTTPEDATPEPGEDPR	3.35	1,774.78
Control	6011	PREDICTED: similar to Transmembrane 9 superfamily member 2 precursor (p76), partial	gi|194671915	72,962.00	100.00%	3	5	5	0.04%	4.40%	IYYHVVETGSMGAR	4.4	1,598.76
Control	6011	PREDICTED: similar to Transmembrane 9 superfamily member 2 precursor (p76), partial	gi|194671915	72,962.00	100.00%	3	5	5	0.04%	4.40%	PSENLGQVLFGER	3.64	1,445.74

Control	6011	PREDICTED: similar to Transmembrane 9 superfamily member 2 precursor (p76), partial	gi|194671915	72,962.00	100.00%	3	5	5	0.04%	4.40%	RPSENLGQVLFGER	2.81	1,601.84
Control	6011	interferon stimulated gene 17 [Ovis aries]	gi|12082402,gi|57619183	17,482.10	100.00%	4	4	4	0.03%	33.10%	EVLQEGVPLVHQGLK	4.23	1,645.93
Control	6011	interferon stimulated gene 17 [Ovis aries]	gi|12082402,gi|57619183	17,482.10	100.00%	4	4	4	0.03%	33.10%	INVPAFQQR	2.77	1,072.59
Control	6011	interferon stimulated gene 17 [Ovis aries]	gi|12082402,gi|57619183	17,482.10	100.00%	4	4	4	0.03%	33.10%	MLGGEEILVPLR	3.08	1,342.74
Control	6011	interferon stimulated gene 17 [Ovis aries]	gi|12082402,gi|57619183	17,482.10	100.00%	4	4	4	0.03%	33.10%	SSSYEVQLTQTVAVLK	3.92	1,752.94
Control	6011	RecName: Full=60S acidic ribosomal protein P0; AltName: Full=L10E	gi|108935888,gi|2293577,gi|59858525,gi|60592767	34,353.40	99.80%	2	2	2	0.02%	13.20%	AFLADPSAFVAAAPVAAAPAAAPAATTAAPAK	4.23	2,849.52
Control	6011	RecName: Full=60S acidic ribosomal protein P0; AltName: Full=L10E	gi|108935888,gi|2293577,gi|59858525,gi|60592767	34,353.40	99.80%	2	2	2	0.02%	13.20%	IIQLLDDYPK	3.23	1,217.68
Control	6011	PREDICTED: similar to hypoxia up-regulated 1	gi|119907132	111,596.90	99.80%	2	2	2	0.02%	4.60%	VAIVKPGVPMEIVLNK	2.78	1,723.02
Control	6011	PREDICTED: similar to hypoxia up-regulated 1	gi|119907132	111,596.90	99.80%	2	2	2	0.02%	4.60%	VPGPVQQALQSAEMKLDEIEQVILVGGATR	3.71	3,192.69

Control	6011	UPF0404 protein C11orf59 homolog	gi|122140364,gi|74267677,gi|77736483	17,713.10	99.80%	2	2	2	0.02%	26.70%	LPPLPSLTSQPHQVLASEPVPFSDLQQVSR	4.67	3,267.74
Control	6011	UPF0404 protein C11orf59 homolog	gi|122140364,gi|74267677,gi|77736483	17,713.10	99.80%	2	2	2	0.02%	26.70%	TDEQALLSSILAK	3.56	1,388.76
Control	6011	RPL12 protein	gi|148744191,gi|42564206,gi|45430019,gi|47117092,gi|74354972	17,801.10	100.00%	3	3	3	0.02%	40.00%	EILGTAQSVGCNVDGRHPHDIIDDINSGAVECPAS	3.04	3,589.67
Control	6011	RPL12 protein	gi|148744191,gi|42564206,gi|45430019,gi|47117092,gi|74354972	17,801.10	100.00%	3	3	3	0.02%	40.00%	HSGNITFDEIVNIAR	4.12	1,685.86
Control	6011	RPL12 protein	gi|148744191,gi|42564206,gi|45430019,gi|47117092,gi|74354972	17,801.10	100.00%	3	3	3	0.02%	40.00%	QAQIEVVPSASALIIK	3.3	1,666.97
Control	6011	Nucleobindin 2	gi|113912161,gi|115496067	49,171.70	100.00%	3	3	3	0.02%	9.16%	LHDVNSDGFLDEQELEALFTK	3.03	2,420.16
Control	6011	Nucleobindin 2	gi|113912161,gi|115496067	49,171.70	100.00%	3	3	3	0.02%	9.16%	LHDVNSDGFLDEQELEALFTKELEK	2.73	2,919.43
Control	6011	Nucleobindin 2	gi|113912161,gi|115496067	49,171.70	100.00%	3	3	3	0.02%	9.16%	QVIDVLETDSHFR	2.64	1,558.79
Control	6011	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	gi|111304648,gi|115496338,gi|121957506	27,838.90	99.80%	2	4	7	0.05%	11.20%	FKGPFTDVVTTNLK	3.86	1,566.85
Control	6011	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	gi|111304648,gi|115496338,gi|121957506	27,838.90	99.80%	2	4	7	0.05%	11.20%	GPFTDVVTTNLK	3.99	1,291.69

Control	6011	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	gi|111304648,gi|115496338,gi|121957506	27,838.90	99.80%	2	4	7	0.05%	11.20%	HEQILVLDPPTDLK	4.26	1,617.89
Control	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	20	0.16%	21.00%	AEVQNLGGELVVSGVDSAMSLIQAAK	4.55	2,602.34
Control	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	20	0.16%	21.00%	AHVLAASVEQATENFLEK	3.55	1,957.00
Control	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	20	0.16%	21.00%	AHVLAASVEQATENFLEKGDK	2.69	2,257.15
Control	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	20	0.16%	21.00%	AIMAQLPQEQK	3.15	1,256.67
Control	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	20	0.16%	21.00%	HVNPVQALSEFK	3.27	1,368.73
Control	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	20	0.16%	21.00%	IAEQVASFQEEK	4.19	1,378.68
Control	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	20	0.16%	21.00%	LLEPLVTQVTTLVNTNSK	4.41	1,970.12
Control	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	20	0.16%	21.00%	NAGTEQDLGIQYK	2.96	1,436.70
Control	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	20	0.16%	21.00%	NLMNAVVQTVK	3.62	1,232.67
Control	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	20	0.16%	21.00%	TSVQTEDDQLIAGQSAR	3.42	1,818.88
Control	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	20	0.16%	21.00%	VIHVVTSEMDNYEPGVYTEK	3.6	2,310.10

Control	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	20	0.16%	21.00%	VLTDAVDDITSIDDFLAVSENHILEDVNK	4.81	3,200.58
Control	6011	RecName: Full=Transmembrane and coiled-coil domain-containing protein 1	gi|109895213,gi|74354058,gi|77736477	21,158.30	99.80%	2	3	4	0.03%	15.40%	LPFTPLSYIQGLSHR	4.37	1,728.94
Control	6011	RecName: Full=Transmembrane and coiled-coil domain-containing protein 1	gi|109895213,gi|74354058,gi|77736477	21,158.30	99.80%	2	3	4	0.03%	15.40%	QAGGFLGPPPPSGK	3.03	1,309.69
Control	6011	GOSR2 protein	gi|148743889,gi|149642953	24,629.80	99.80%	2	2	2	0.02%	18.90%	LETADKQALHLVENEIQASIDQIFSQLER	3.04	3,338.72
Control	6011	GOSR2 protein	gi|148743889,gi|149642953	24,629.80	99.80%	2	2	2	0.02%	18.90%	YDVQHLQTALR	2.74	1,343.71
Control	6011	mitochondrial trifunctional protein, beta subunit precursor	gi|146231862,gi|27885005,gi|2832715,gi|6015048,gi|74268350	51,329.00	99.80%	2	2	2	0.02%	8.21%	DTVTQDNGIRPSSLDQMAK	2.6	2,092.00
Control	6011	mitochondrial trifunctional protein, beta subunit precursor	gi|146231862,gi|27885005,gi|2832715,gi|6015048,gi|74268350	51,329.00	99.80%	2	2	2	0.02%	8.21%	TPFLLSGTSYKDLMPHDLAR	4.54	2,278.15
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	AKFEELNMDLFR	4.03	1,512.75
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	DAGTIAGLNVMR	3.76	1,233.63

Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	DNHLLGTFDLTGIPPAPR	2.56	1,934.01
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	ELEEIVQPIISK	4.28	1,397.79
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	FEELNMDLFR	2.97	1,329.61
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	IDTRNELESYAYSLK	4.42	1,801.90
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	IEIESFYEGEDFSETLTR	3.05	2,164.99
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	IINEPTAAAIAYGLDK	4.4	1,659.90
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	ITPSYVAFTPEGER	4.17	1,566.78
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	KKELEEIVQPIISK	4.16	1,653.98

Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	KSQIFSTASDNQPTVTIK	4.72	1,965.03
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	MKETAEAYLGKK	3.13	1,384.71
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	MVNDAEKFAEEDK	2.57	1,541.68
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	MVNDAEKFAEEDKK	3.77	1,669.77
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	NELESYAYSLK	3.6	1,316.64
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	NQLTSNPENTVFDAK	3.91	1,677.81
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	NQLTSNPENTVFDAKR	4.02	1,833.91
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	SDIDEIVLVGGSTR	2.83	1,460.76

Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	SQIFSTASDNQPTVTIK	4.13	1,836.93
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	TFAPEEISAMVLTK	4.17	1,552.79
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	TKPYIQVDVGGGQTK	4.6	1,590.85
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	TWNDPSVQQDIK	2.58	1,430.69
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	VLEDSDLKKSDIDEIVLVGGSTR	5.02	2,488.31
Control	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	33	59	0.46%	39.70%	VTHAVVTVPAYFNDAQR	4.25	1,887.97
Control	6011	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	5	6	10	0.08%	12.90%	LLNDEDPVVVTK	3.13	1,341.73
Control	6011	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	5	6	10	0.08%	12.90%	LNTIPLFVQLLYSSVENIQR	3.96	2,347.30

Control	6011	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	5	6	10	0.08%	12.90%	MLSSPVESVLFYAITTLHNLLLYQEGAK	4.42	3,153.65
Control	6011	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	5	6	10	0.08%	12.90%	SAIVHLINYQDDAELATR	3.93	2,029.04
Control	6011	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	5	6	10	0.08%	12.90%	TLVTQNSGVEALIHAILR	2.72	1,935.10
Control	6011	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	29.60%	AALVDLEPGTMDSVR	3.05	1,589.78
Control	6011	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	29.60%	ALTVPELTQQMFDAK	2.54	1,707.86
Control	6011	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	29.60%	FPGQLNADLRK	3.12	1,258.69
Control	6011	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	29.60%	GHYTEGAELVDSVLDVVR	3.66	1,958.98
Control	6011	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	29.60%	GHYTEGAELVDSVLDVVRK	3.32	2,087.08
Control	6011	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	29.60%	LAVNMVPFPR	3.55	1,159.63
Control	6011	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	29.60%	LHFFMPGFAPLTAR	3.73	1,620.84
Control	6011	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	29.60%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	4.94	4,479.06
Control	6011	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	29.60%	YLTVAAVFR	2.56	1,039.59

Control	6011	RecName: Full=Rab GDP dissociation inhibitor beta; Short=Rab GDI beta; AltName: Full=Guanosine diphosphate dissociation inhibitor 2; Short=GDI-2	gi|109939713,gi|146231738,gi|75773612,gi|76253900	50,472.30	100.00%	3	4	4	0.03%	11.20%	FVSISDLLVPK	2.62	1,217.71
Control	6011	RecName: Full=Rab GDP dissociation inhibitor beta; Short=Rab GDI beta; AltName: Full=Guanosine diphosphate dissociation inhibitor 2; Short=GDI-2	gi|109939713,gi|146231738,gi|75773612,gi|76253900	50,472.30	100.00%	3	4	4	0.03%	11.20%	KFDLGQDVIDFTGHALALYR	6.25	2,279.18
Control	6011	RecName: Full=Rab GDP dissociation inhibitor beta; Short=Rab GDI beta; AltName: Full=Guanosine diphosphate dissociation inhibitor 2; Short=GDI-2	gi|109939713,gi|146231738,gi|75773612,gi|76253900	50,472.30	100.00%	3	4	4	0.03%	11.20%	SPYLYPLYGLGELPQGFAR	5.46	2,141.11

Control	6011	RecName: Full=60S ribosomal protein L11	gi|108860925,gi|115497634,gi|74268362	20,235.20	99.80%	2	2	3	0.02%	12.90%	VLEQLTGQTPVFSK	4.38	1,546.85
Control	6011	RecName: Full=60S ribosomal protein L11	gi|108860925,gi|115497634,gi|74268362	20,235.20	99.80%	2	2	3	0.02%	12.90%	YDGIILPGK	2.57	975.5512
Control	6011	syntaxin 7	gi|118150840,gi|122140829,gi|73586654	29,638.60	99.80%	2	2	2	0.02%	10.70%	EFGSLPTTPSDQR	2.83	1,434.69
Control	6011	syntaxin 7	gi|118150840,gi|122140829,gi|73586654	29,638.60	99.80%	2	2	2	0.02%	10.70%	TLNQLGTPQDSPELR	4.59	1,668.86
Control	6011	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	4	5	7	0.05%	19.60%	GDLLFLTNR	2.59	1,048.58
Control	6011	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	4	5	7	0.05%	19.60%	GDLLFLTNRVEDPIR	3.93	1,757.95
Control	6011	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	4	5	7	0.05%	19.60%	MLSLDFLDDVRR	2.08	1,495.76
Control	6011	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	4	5	7	0.05%	19.60%	VGEIVVFR	2.92	918.5407
Control	6011	CAND1 protein	gi|154426008,gi|155372073,gi|182627583	136,363.10	99.80%	2	2	2	0.02%	2.36%	ISGSILNELIGLVR	4.61	1,483.88
Control	6011	CAND1 protein	gi|154426008,gi|155372073,gi|182627583	136,363.10	99.80%	2	2	2	0.02%	2.36%	SVILEAFSSPSEEVK	3.06	1,621.83
Control	6011	RecName: Full=Acyl-protein thioesterase 1; AltName: Full=Lysophospholipase 1; AltName: Full=Lysophospholipase I	gi|115311636,gi|75948308,gi|77736321	24,578.40	99.80%	2	2	2	0.02%	10.40%	ASFPQGPIGGVNR	2.43	1,299.68

Control	6011	RecName: Full=Acyl-protein thioesterase 1; AltName: Full=Lysophospholipase 1; AltName: Full=Lysophospholipase I	gi|115311636,gi|75948308,gi|77736321	24,578.40	99.80%	2	2	2	0.02%	10.40%	TLVNPANVTFR	2.62	1,231.68
Control	6011	PREDICTED: brain protein 44	gi|119889010,gi|194665199	14,264.40	99.80%	2	3	4	0.03%	18.90%	LRPLYNHPAGPR	3.5	1,390.77
Control	6011	PREDICTED: brain protein 44	gi|119889010,gi|194665199	14,264.40	99.80%	2	3	4	0.03%	18.90%	VLDKVELLLPEK	3.8	1,395.85
Control	6011	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	12	18	0.14%	21.30%	FLVVLNFGDVGQLAR	4.7	1,647.92
Control	6011	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	12	18	0.14%	21.30%	FTGLSKEELLK	3.63	1,264.71
Control	6011	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	12	18	0.14%	21.30%	LLIAGTDSSDLQQILR	5.73	1,742.97
Control	6011	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	12	18	0.14%	21.30%	NQEDDLTETNLEQIDPIFGSK	4.55	2,406.13
Control	6011	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	12	18	0.14%	21.30%	NQEDDLTETNLEQIDPIFGSKEDFESLLHSAK	4.7	3,662.73
Control	6011	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	12	18	0.14%	21.30%	SLLHGDFYDLSSGPDLFSYIR	2.95	2,402.17
Control	6011	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	12	18	0.14%	21.30%	SVSEDRLLIAGTDSSDLQQILR	2.98	2,416.27
Control	6011	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	12	18	0.14%	21.30%	VDLLLSTQPGR	3.32	1,198.68

Control	6011	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	12	18	0.14%	21.30%	VILDLTPNYK	3.32	1,175.67
Control	6011	MHC class I antigen	gi|84095083	40,657.50	100.00%	9	11	67	0.52%	28.20%	DYIALNEDLR	3.86	1,221.61
Control	6011	MHC class I antigen	gi|84095083	40,657.50	100.00%	9	11	67	0.52%	28.20%	EGEDQTQDMELVETRPSGDGTFQK	2.99	2,713.19
Control	6011	MHC class I antigen	gi|84095083	40,657.50	100.00%	9	11	67	0.52%	28.20%	FIAVGYVDDTQFVR	5.22	1,629.83
Control	6011	MHC class I antigen	gi|84095083	40,657.50	100.00%	9	11	67	0.52%	28.20%	QDAYDGRDYIALNEDLR	3.51	2,026.95
Control	6011	MHC class I antigen	gi|84095083	40,657.50	100.00%	9	11	67	0.52%	28.20%	RYLENGKDTLLR	3.56	1,477.81
Control	6011	MHC class I antigen	gi|84095083	40,657.50	100.00%	9	11	67	0.52%	28.20%	VQHEGLQEPLTLR	4.25	1,519.82
Control	6011	MHC class I antigen	gi|84095083	40,657.50	100.00%	9	11	67	0.52%	28.20%	WAALVVPSGEEQR	3.44	1,441.74
Control	6011	MHC class I antigen	gi|84095083	40,657.50	100.00%	9	11	67	0.52%	28.20%	YFYTAVSR	2.61	1,006.50
Control	6011	MHC class I antigen	gi|84095083	40,657.50	100.00%	9	11	67	0.52%	28.20%	YLENGKDTLLR	2.24	1,321.71
Control	6011	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	6	8	10	0.08%	11.10%	ALLELQLEPEELYQTFQR	4.96	2,220.15
Control	6011	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	6	8	10	0.08%	11.10%	ARPFPDGLAEDIDKGEVSAR	4.81	2,143.08
Control	6011	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	6	8	10	0.08%	11.10%	EGIPALDNFLDKL	2.44	1,444.77
Control	6011	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	6	8	10	0.08%	11.10%	STAISLFYELSENDLNFIK	3.99	2,204.11
Control	6011	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	6	8	10	0.08%	11.10%	TGTITTFEHAHNMR	2.67	1,631.76

Control	6011	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	6	8	10	0.08%	11.10%	VFSGLVSTGLK	2.98	1,107.64
Control	6011	RecName: Full=Serine palmitoyltransferase 1; AltName: Full=Serine-palmitoyl-CoA transferase 1; Short=SPT 1; Short=SPT1; AltName: Full=Long chain base biosynthesis protein 1; Short=L	gi|122139929,gi|75948211,gi|77736443	52,771.80	100.00%	3	4	5	0.04%	8.88%	LLKEQEIEDQKNPR	4.91	1,739.93
Control	6011	RecName: Full=Serine palmitoyltransferase 1; AltName: Full=Serine-palmitoyl-CoA transferase 1; Short=SPT 1; Short=SPT1; AltName: Full=Long chain base biosynthesis protein 1; Short=L	gi|122139929,gi|75948211,gi|77736443	52,771.80	100.00%	3	4	5	0.04%	8.88%	VVVTVEQTEEDLEK	3.52	1,617.82

Control	6011	RecName: Full=Serine palmitoyltransferase 1; AltName: Full=Serine-palmitoyl-CoA transferase 1; Short=SPT 1; Short=SPT1; AltName: Full=Long chain base biosynthesis protein 1; Short=L	gi|122139929,gi|75948211,gi|77736443	52,771.80	100.00%	3	4	5	0.04%	8.88%	VVVTVEQTEEDLEKAASTISEVAQTVLL	3.08	3,001.58
Control	6011	RecName: Full=Calcium/calmodulin-dependent protein kinase type II beta chain; Short=CaM-kinase II beta chain; Short=CaM kinase II subunit beta; Short=CaMK-II subunit beta	gi|118572489,gi|75773666,gi|78369262	60,464.50	100.00%	3	3	3	0.02%	13.10%	DLKPENLLLASK	3.45	1,340.78

Control	6011	RecName: Full=Calcium/calmodulin-dependent protein kinase type II beta chain; Short=CaM-kinase II beta chain; Short=CaM kinase II subunit beta; Short=CaMK-II subunit beta	gi|118572489,gi|75773666,gi|78369262	60,464.50	100.00%	3	3	3	0.02%	13.10%	LHDSISEEGFHYLVFDLVTGGELFEDIVAR	2.9	3,407.68
Control	6011	RecName: Full=Calcium/calmodulin-dependent protein kinase type II beta chain; Short=CaM-kinase II beta chain; Short=CaM kinase II subunit beta; Short=CaMK-II subunit beta	gi|118572489,gi|75773666,gi|78369262	60,464.50	100.00%	3	3	3	0.02%	13.10%	QTTAPATMSTAASGATMGLVEQAKSLLNK	2.6	2,894.46

Control	6011	RecName: Full=Polypeptide N-acetylgalactosaminyltransferase 1; AltName: Full=Protein-UDP acetylgalactosaminyltransferase 1; AltName: Full=UDP-GalNAc: polypeptide N-acetylgalactosaminyltransferase 1; AltName:	gi|1171989,gi|289412,gi|29135331,gi|304259	64,174.80	100.00%	2	3	3	0.02%	7.51%	GLPAGDVLEPVQKPHEGPGEMGKPVVIPK	3.37	2,991.60
Control	6011	RecName: Full=Polypeptide N-acetylgalactosaminyltransferase 1; AltName: Full=Protein-UDP acetylgalactosaminyltransferase 1; AltName: Full=UDP-GalNAc: polypeptide N-acetylgalactosaminyltransferase 1; AltName:	gi|1171989,gi|289412,gi|29135331,gi|304259	64,174.80	100.00%	2	3	3	0.02%	7.51%	TPTMAGGLFSIDR	3.19	1,381.68
Control	6011	RecName: Full=Galectin-9	gi|122145068,gi|59858325,gi|62751460,gi|75775171,gi|87044899	39,329.70	99.80%	2	2	2	0.02%	9.30%	NLPAINNLEVGGDIQLTHVQT	4.43	2,246.18
Control	6011	RecName: Full=Galectin-9	gi|122145068,gi|59858325,gi|62751460,gi|75775171,gi|87044899	39,329.70	99.80%	2	2	2	0.02%	9.30%	SGSDIAFHLNPR	2.68	1,313.66

Control	6011	negative response regulator [Escherichia coli]	gi|57996866	20,725.50	99.80%	2	2	2	0.02%	13.90%	AGGGSATLSMGQAAAR	3.8	1,421.68
Control	6011	negative response regulator [Escherichia coli]	gi|57996866	20,725.50	99.80%	2	2	2	0.02%	13.90%	IQNAGTEVVEAK	3.15	1,258.66
Control	6011	PREDICTED: similar to Calpain-5 (nCL-3) (htra-3) isoform 1	gi|76636134	72,988.00	100.00%	4	5	5	0.04%	10.20%	ANADDLQALHTLHLR	3.09	1,687.89
Control	6011	PREDICTED: similar to Calpain-5 (nCL-3) (htra-3) isoform 1	gi|76636134	72,988.00	100.00%	4	5	5	0.04%	10.20%	DSPTGANSYVIIK	3.72	1,364.71
Control	6011	PREDICTED: similar to Calpain-5 (nCL-3) (htra-3) isoform 1	gi|76636134	72,988.00	100.00%	4	5	5	0.04%	10.20%	VLFEDPNFPATDDSLYYK	2.99	2,134.00
Control	6011	PREDICTED: similar to Calpain-5 (nCL-3) (htra-3) isoform 1	gi|76636134	72,988.00	100.00%	4	5	5	0.04%	10.20%	YVIIPTTFEPGHTGEFLLR	3.85	2,190.16
Control	6011	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	4	5	7	0.05%	25.90%	GAQAAIVVYDITNTDTFAR	2.94	2,026.02
Control	6011	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	4	5	7	0.05%	25.90%	GVDLQENNPASR	2.8	1,299.63
Control	6011	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	4	5	7	0.05%	25.90%	LVLLGESAVGK	3.1	1,085.66
Control	6011	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	4	5	7	0.05%	25.90%	QASPNIVIALAGNK	2.85	1,395.80

Control	6011	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	5	6	12	0.09%	27.40%	ELNVMFIETSAK	3.51	1,397.70
Control	6011	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	5	6	12	0.09%	27.40%	GSDVIIMLVGNK	3.13	1,261.68
Control	6011	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	5	6	12	0.09%	27.40%	GSDVIIMLVGNKTDLADKR	3.24	2,061.10
Control	6011	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	5	6	12	0.09%	27.40%	LQLWDTAGQER	2.59	1,316.66
Control	6011	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	5	6	12	0.09%	27.40%	RVAAALPGMESTQDR	3.18	1,617.80
Control	6011	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	5	6	12	0.09%	27.40%	VAAALPGMESTQDR	2.7	1,461.70
Control	6011	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	4	0.03%	27.40%	DLTDYLMK	1.87	1,014.48
Control	6011	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	4	0.03%	27.40%	GYSFTTTAER	3.43	1,132.53

Control	6011	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	4	0.03%	27.40%	HQGVMVGMGQKDCYVGDEAQSK	3.83	2,383.05
Control	6011	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	4	0.03%	27.40%	HQGVMVGMGQKDCYVGDEAQSKR	3.32	2,539.15
Control	6011	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	4	0.03%	27.40%	IKIIAPPERK	2.5	1,164.75
Control	6011	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	4	0.03%	27.40%	LDLAGRDLTDYLMK	2.75	1,639.84
Control	6011	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	4	0.03%	27.40%	SYELPDGQVITIGNER	4.51	1,790.89
Control	6011	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	4	0.03%	27.40%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	6.32	3,183.61
Control	6011	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	gi|27806197,gi|3676399,gi|71153779,gi|73586683	29,157.00	99.80%	2	3	5	0.04%	15.70%	AAFDDAIAELDTLSEESYKDSTLIMQLLR	4.33	3,274.60

Control	6011	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	gi|27806197,gi|3676399,gi|71153779,gi|73586683	29,157.00	99.80%	2	3	5	0.04%	15.70%	EAAENSLVAYK	2.19	1,194.60
Control	6011	Transducin (beta)-like 2	gi|112362303,gi|115495815	49,894.00	100.00%	3	3	4	0.03%	7.85%	APIVNIGIADTGK	3.49	1,268.72
Control	6011	Transducin (beta)-like 2	gi|112362303,gi|115495815	49,894.00	100.00%	3	3	4	0.03%	7.85%	LFHNTPGYR	2.1	1,104.56
Control	6011	Transducin (beta)-like 2	gi|112362303,gi|115495815	49,894.00	100.00%	3	3	4	0.03%	7.85%	LQQQLTQAQEALK	5.08	1,498.82
Control	6011	proteasome activator 28 alpha subunit	gi|63139650,gi|73921836,gi|86821522,gi|91680535	28,675.80	100.00%	3	3	3	0.02%	15.30%	APLDIPVPDPVKEK	2.84	1,517.86
Control	6011	proteasome activator 28 alpha subunit	gi|63139650,gi|73921836,gi|86821522,gi|91680535	28,675.80	100.00%	3	3	3	0.02%	15.30%	NAYAVLYDIILK	3.18	1,395.79
Control	6011	proteasome activator 28 alpha subunit	gi|63139650,gi|73921836,gi|86821522,gi|91680535	28,675.80	100.00%	3	3	3	0.02%	15.30%	QLVHELDEAEYR	2.53	1,501.73
Control	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	15	20	31	0.24%	17.90%	FKASGVEGTDVVK	3.41	1,336.71
Control	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	15	20	31	0.24%	17.90%	GAALITAVGVR	3.69	1,027.63
Control	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	15	20	31	0.24%	17.90%	GAAMVTAVAYR	3.4	1,125.57
Control	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	15	20	31	0.24%	17.90%	GDFIALDLGGSSFR	2.91	1,454.73
Control	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	15	20	31	0.24%	17.90%	GKFNTSDVSAIEK	4.07	1,395.71
Control	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	15	20	31	0.24%	17.90%	HIDLVEGDEGR	4.09	1,239.60
Control	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	15	20	31	0.24%	17.90%	LSDETLLDIMNR	4.26	1,435.71
Control	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	15	20	31	0.24%	17.90%	LVDEFSLNSGK	3.36	1,208.62

Control	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	15	20	31	0.24%	17.90%	QIEETLAHFSLTK	3.58	1,516.80
Control	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	15	20	31	0.24%	17.90%	SANLVAATLGAILSR	4.53	1,456.85
Control	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	15	20	31	0.24%	17.90%	SIPDGSEKGDFIALDLGGSSFR	4.16	2,268.11
Control	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	15	20	31	0.24%	17.90%	TIYDKLVDEFSLNSGK	3.78	1,828.93
Control	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	15	20	31	0.24%	17.90%	TTVGVDGSLYK	2.65	1,139.59
Control	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	15	20	31	0.24%	17.90%	YLSQIESDR	2.84	1,110.54
Control	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	15	20	31	0.24%	17.90%	YLSQIESDRLALLQVR	3.3	1,904.06
Control	6011	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	4	5	6	0.05%	8.42%	DIQGSLQDIFK	3.07	1,263.66
Control	6011	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	4	5	6	0.05%	8.42%	INENTGSVSVTR	3.99	1,276.65
Control	6011	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	4	5	6	0.05%	8.42%	SIVVSPILIPENQR	3.21	1,564.91
Control	6011	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	4	5	6	0.05%	8.42%	TLEGPVPLEVIVIDQNDNRPIFR	2.86	2,634.43
Control	6011	alpha-actinin 1	gi|145286437,gi|77567675,gi|78369242	102,966.00	100.00%	3	3	3	0.02%	5.27%	IDQLEGDHQLIQEALIFDNK	4.26	2,339.19
Control	6011	alpha-actinin 1	gi|145286437,gi|77567675,gi|78369242	102,966.00	100.00%	3	3	3	0.02%	5.27%	LLETIDQLYLEYAK	3.42	1,711.92
Control	6011	alpha-actinin 1	gi|145286437,gi|77567675,gi|78369242	102,966.00	100.00%	3	3	3	0.02%	5.27%	LSNRPAFMPSEGR	2.8	1,477.72

Control	6011	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein H (hnRNP H) isoform 26	gi|194668611	49,211.80	99.80%	2	2	2	0.02%	7.35%	ATENDIYNFFSPLNPVR	2.75	1,996.98
Control	6011	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein H (hnRNP H) isoform 26	gi|194668611	49,211.80	99.80%	2	2	2	0.02%	7.35%	HTGPNSPDTANDGFVR	5.29	1,684.77
Control	6011	PREDICTED: similar to programmed cell death 8 isoform 2	gi|76658657	66,854.50	99.90%	2	2	2	0.02%	5.22%	ISGLGLTPEEK	3.6	1,143.63
Control	6011	PREDICTED: similar to programmed cell death 8 isoform 2	gi|76658657	66,854.50	99.90%	2	2	2	0.02%	5.22%	KVETDHIVAAVGLEPNVELAK	3.52	2,232.22
Control	6011	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	8	11	17	0.13%	19.40%	FAIQTDPNSNDGLVTVVKPIDFETNR	4.15	2,890.46

Control	6011	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	8	11	17	0.13%	19.40%	FLEAGIYEVPIIITDSGNPPK	3.41	2,273.21
Control	6011	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	8	11	17	0.13%	19.40%	MYVLTVAAENQVPLAK	2.95	1,762.94
Control	6011	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	8	11	17	0.13%	19.40%	QLLIDPEDDVRDNILK	2.16	1,896.01

Control	6011	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	8	11	17	0.13%	19.40%	SAAPHPGDIGDFINEGLK	4.62	1,837.91
Control	6011	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	8	11	17	0.13%	19.40%	YDEEGGGEEDQDYDLSQLQQPDTVEPDAIKPVGIR	5.34	3,905.78
Control	6011	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	8	11	17	0.13%	19.40%	YSVTGPGADQPPTGIFIINPISGQLSVTKPLDR	3.4	3,438.83

Control	6011	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	8	11	17	0.13%	19.40%	YSVTGPGADQPPTGIFIINPISGQLSVTKPLDRELIAR	4.51	4,021.18
Control	6011	RecName: Full=Cytochrome c1, heme protein, mitochondrial; AltName: Full=Ubiquinol-cytochrome-c reductase complex cytochrome c1 subunit; Short=Cytochrome c-1; AltName: Full=Cytochrome b-c1 complex	gi|109940069,gi|114793904,gi|71042588,gi|75765182,gi|75765193,gi|82407279,gi|82407290,gi|83638779,gi|84000289	27,269.70	100.00%	5	6	8	0.06%	36.50%	AANNGALPPDLSYIVR	3.02	1,670.89

Control	6011	RecName: Full=Cytochrome c1, heme protein, mitochondrial; AltName: Full=Ubiquinol-cytochrome-c reductase complex cytochrome c1 subunit; Short=Cytochrome c-1; AltName: Full=Cytochrome b-c1 complex	gi|109940069,gi|114793904,gi|71042588,gi|75765182,gi|75765193,gi|82407279,gi|82407290,gi|83638779,gi|84000289	27,269.70	100.00%	5	6	8	0.06%	36.50%	ALAEEVEVQDGPNEDGEMFMRPGK	3.19	2,664.19
Control	6011	RecName: Full=Cytochrome c1, heme protein, mitochondrial; AltName: Full=Ubiquinol-cytochrome-c reductase complex cytochrome c1 subunit; Short=Cytochrome c-1; AltName: Full=Cytochrome b-c1 complex	gi|109940069,gi|114793904,gi|71042588,gi|75765182,gi|75765193,gi|82407279,gi|82407290,gi|83638779,gi|84000289	27,269.70	100.00%	5	6	8	0.06%	36.50%	GLLSSLDHTSIR	3.25	1,298.71

Control	6011	RecName: Full=Cytochrome c1, heme protein, mitochondrial; AltName: Full=Ubiquinol-cytochrome-c reductase complex cytochrome c1 subunit; Short=Cytochrome c-1; AltName: Full=Cytochrome b-c1 complex	gi|109940069,gi|114793904,gi|71042588,gi|75765182,gi|75765193,gi|82407279,gi|82407290,gi|83638779,gi|84000289	27,269.70	100.00%	5	6	8	0.06%	36.50%	LSDYFPKPYPNPEAAR	3.97	1,864.92
Control	6011	RecName: Full=Cytochrome c1, heme protein, mitochondrial; AltName: Full=Ubiquinol-cytochrome-c reductase complex cytochrome c1 subunit; Short=Cytochrome c-1; AltName: Full=Cytochrome b-c1 complex	gi|109940069,gi|114793904,gi|71042588,gi|75765182,gi|75765193,gi|82407279,gi|82407290,gi|83638779,gi|84000289	27,269.70	100.00%	5	6	8	0.06%	36.50%	MGLKMLLMMGLLLPLVYAMK	3.42	2,266.26
Control	6011	mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor	gi|61553497,gi|70778822,gi|73919274,gi|83638650	31,226.90	100.00%	3	3	3	0.02%	16.20%	AQFGQPEILIGTIPGAGGTQR	4.69	2,111.12

Control	6011	mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor	gi|61553497,gi|70778822,gi|73919274,gi|83638650	31,226.90	100.00%	3	3	3	0.02%	16.20%	KLFYSTFATEDRK	3.49	1,605.83
Control	6011	mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor	gi|61553497,gi|70778822,gi|73919274,gi|83638650	31,226.90	100.00%	3	3	3	0.02%	16.20%	NSNVGLIQLNRPK	4.11	1,452.83
Control	6011	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	99.80%	2	2	6	0.05%	35.20%	ELAEAQEDTILK	3.52	1,359.70
Control	6011	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	99.80%	2	2	6	0.05%	35.20%	YSALFLGMAYGAK	3.13	1,407.70
Control	6011	PREDICTED: similar to ATP-binding cassette, sub-family B, member 7	gi|194680502	83,040.70	100.00%	5	6	8	0.06%	12.20%	ADNDAGNAAIDSLLNYETVK	4.24	2,094.00
Control	6011	PREDICTED: similar to ATP-binding cassette, sub-family B, member 7	gi|194680502	83,040.70	100.00%	5	6	8	0.06%	12.20%	AVGVVPQDAVLFHNTIYYNLLYGNISASPEEVYAVAK	4.83	4,025.07
Control	6011	PREDICTED: similar to ATP-binding cassette, sub-family B, member 7	gi|194680502	83,040.70	100.00%	5	6	8	0.06%	12.20%	LAGLHDAILR	2.09	1,078.64

Control	6011	PREDICTED: similar to ATP-binding cassette, sub-family B, member 7	gi|194680502	83,040.70	100.00%	5	6	8	0.06%	12.20%	QALIDMNTLFTLLK	3.31	1,636.90
Control	6011	PREDICTED: similar to ATP-binding cassette, sub-family B, member 7	gi|194680502	83,040.70	100.00%	5	6	8	0.06%	12.20%	YFNNENYEAQR	2.98	1,447.62
Control	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	14	0.11%	34.30%	FDEGRNNFEGEVTK	3.18	1,641.75
Control	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	14	0.11%	34.30%	FLESGGQDGAGDDDDLEDLEEAEEPDLEEDDDQKAVKDEL	4.5	4,394.84
Control	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	14	0.11%	34.30%	GNFDEALAAHK	2.8	1,172.57
Control	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	14	0.11%	34.30%	HNQLPLVIEFTEQTAPK	3.14	1,965.04
Control	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	14	0.11%	34.30%	ILEFFGLK	2.01	966.566
Control	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	14	0.11%	34.30%	NFEEVAFDEKK	3.5	1,355.65
Control	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	14	0.11%	34.30%	QFLLAAEAIDDIPFGITSNSDVFSK	4.77	2,698.36
Control	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	14	0.11%	34.30%	THILLFLPK	2.35	1,081.68
Control	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	14	0.11%	34.30%	VDATEESDLAQQYGVR	3.54	1,780.83
Control	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	14	0.11%	34.30%	YKPESDELTAEK	4	1,409.68
Control	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	14	0.11%	34.30%	YQLDKDGVVLFK	2.55	1,424.78
Control	6011	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	6	9	0.07%	29.40%	GAVGALLVYDIAK	3.8	1,289.75
Control	6011	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	6	9	0.07%	29.40%	HLTYENVER	2.26	1,160.57

Control	6011	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	6	9	0.07%	29.40%	NNLSFIETSALDSTNVEEAFK	4.65	2,329.12
Control	6011	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	6	9	0.07%	29.40%	STIGVEFATR	2.78	1,080.57
Control	6011	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	6	9	0.07%	29.40%	VVLIGDSGVGK	2.38	1,043.61
Control	6011	SEPT11 protein	gi|126010811,gi|126723403,gi|162416046	48,974.60	99.80%	2	2	2	0.02%	5.41%	FESDPATHNEPGVR	1.69	1,555.71
Control	6011	SEPT11 protein	gi|126010811,gi|126723403,gi|162416046	48,974.60	99.80%	2	2	2	0.02%	5.41%	VNIIPIIAK	2.12	980.6504
Control	6011	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	6	9	10	0.08%	18.60%	IPDEFDNDPILVQQLR	4.65	1,911.98
Control	6011	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	6	9	10	0.08%	18.60%	QNLFFSSLTSR	2.63	1,299.67
Control	6011	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	6	9	10	0.08%	18.60%	TIALNGVEDVR	3.22	1,186.64
Control	6011	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	6	9	10	0.08%	18.60%	TVLEHYALEEDPLEAFK	3.34	2,004.00
Control	6011	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	6	9	10	0.08%	18.60%	TVLEHYALEEDPLEAFKQR	5.16	2,288.16

Control	6011	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	6	9	10	0.08%	18.60%	VLLDLSAFLK	3.04	1,118.68
Control	6011	PREDICTED: ATP-binding cassette, sub-family B (MDR/TAP), member 1	gi|194685301	144,522.00	100.00%	4	4	4	0.03%	5.40%	GNELELENTPGESLSK	5.37	1,716.83
Control	6011	PREDICTED: ATP-binding cassette, sub-family B (MDR/TAP), member 1	gi|194685301	144,522.00	100.00%	4	4	4	0.03%	5.40%	ILLLDEATSALDTESEAVVQAALDK	4.96	2,615.37
Control	6011	PREDICTED: ATP-binding cassette, sub-family B (MDR/TAP), member 1	gi|194685301	144,522.00	100.00%	4	4	4	0.03%	5.40%	LYDPTEGMVSIDGQDIR	3.63	1,924.90
Control	6011	PREDICTED: ATP-binding cassette, sub-family B (MDR/TAP), member 1	gi|194685301	144,522.00	100.00%	4	4	4	0.03%	5.40%	YGREDVTMDEIQK	3.76	1,599.73
Control	6011	CSE1L protein	gi|146186877,gi|164448620,gi|193806599	110,362.80	99.80%	2	2	3	0.02%	4.84%	FLESVEGNQNYPLLLLTLLEK	4.58	2,433.33
Control	6011	CSE1L protein	gi|146186877,gi|164448620,gi|193806599	110,362.80	99.80%	2	2	3	0.02%	4.84%	GPNSATLFTAAEIAPFVEILLTNLFK	2.71	2,777.51
Control	6011	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	9	12	12	0.09%	14.50%	EVLDKNDMVELLGPRPFAEK	3.66	2,316.19
Control	6011	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	9	12	12	0.09%	14.50%	GLGYAQYLPR	2.77	1,137.61

Control	6011	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	9	12	12	0.09%	14.50%	GMGGLFSVGETTAK	3.37	1,370.66
Control	6011	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	9	12	12	0.09%	14.50%	GVVDRLEVVNKR	3.09	1,383.81
Control	6011	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	9	12	12	0.09%	14.50%	ILINDAYKR	1.96	1,105.64
Control	6011	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	9	12	12	0.09%	14.50%	NLETLQQELGIEGENR	3.65	1,842.92
Control	6011	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	9	12	12	0.09%	14.50%	VGQISFDLPR	3.38	1,131.62
Control	6011	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	9	12	12	0.09%	14.50%	VSEEIFFGR	2.76	1,083.55
Control	6011	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	9	12	12	0.09%	14.50%	VTQSAYAQIVQFGMNEK	2.98	1,929.94
Control	6011	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	8	12	36	0.28%	49.30%	HLIIGVSSDR	2.77	1,096.61
Control	6011	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	8	12	36	0.28%	49.30%	IIGVGDKIR	2.91	970.6046

Control	6011	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	8	12	36	0.28%	49.30%	NASEMIDKLTLTFNR	3.67	1,768.89
Control	6011	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	8	12	36	0.28%	49.30%	NYQEYSLANIIYYSLK	3.89	1,981.99
Control	6011	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	8	12	36	0.28%	49.30%	RPPTFGDASVIALELLNSGYEFDEGSIIFNR	4.82	3,427.72
Control	6011	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	8	12	36	0.28%	49.30%	TEEKPIFSLDTISSAESMSIYDDIDADVLR	6.13	3,376.60
Control	6011	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	8	12	36	0.28%	49.30%	THSDQFLVTFK	3.19	1,322.67

Control	6011	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	8	12	36	0.28%	49.30%	VYGVGSLALYEK	4.38	1,298.70
Control	6011	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	3	3	3	0.02%	18.60%	QMEQISQFLQAAER	3.37	1,694.82
Control	6011	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	3	3	3	0.02%	18.60%	TLMNLGGLAVAR	3.43	1,231.68
Control	6011	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	3	3	3	0.02%	18.60%	YFSDNQLQEGK	2.58	1,328.61
Control	6011	PREDICTED: similar to Heparan sulfate 2-O-sulfotransferase 1 (2-O-sulfotransferase) (2OST), partial	gi|119889909	37,063.70	99.80%	2	2	4	0.03%	9.24%	EKDGDLYILAQNFFYEK	3.75	2,093.02
Control	6011	PREDICTED: similar to Heparan sulfate 2-O-sulfotransferase 1 (2-O-sulfotransferase) (2OST), partial	gi|119889909	37,063.70	99.80%	2	2	4	0.03%	9.24%	NNPVMSLQDQVR	3.73	1,416.69
Control	6011	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	7	11	0.09%	10.50%	FVKEMNLFR	2.04	1,199.62
Control	6011	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	7	11	0.09%	10.50%	IMKVEYHLLSPYVSPR	2.35	1,948.04
Control	6011	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	7	11	0.09%	10.50%	LAADEEENVDSNMR	3.38	1,608.68

Control	6011	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	7	11	0.09%	10.50%	SAFSNLFGGEPLSYTR	4.32	1,745.85
Control	6011	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	7	11	0.09%	10.50%	SSVGTSLLLTLAR	2.47	1,317.77
Control	6011	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	7	11	0.09%	10.50%	VEYHLLSPYVSPR	3.09	1,559.82
Control	6011	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	7	11	0.09%	10.50%	VSASPLLYSLIEK	4.03	1,419.81
Control	6011	Unknown (protein for IMAGE: 8481405)	gi|151554181	51,930.50	99.80%	2	2	2	0.02%	6.00%	FQLSNSGPNSSLK	3.63	1,378.70
Control	6011	Unknown (protein for IMAGE: 8481405)	gi|151554181	51,930.50	99.80%	2	2	2	0.02%	6.00%	NLIAFSEDGSDPYVR	2.61	1,682.80
Control	6011	Leucine rich repeat containing 8 family, member A	gi|115304767,gi|116003833	93,997.70	100.00%	4	4	4	0.03%	8.64%	ALSETVVEESDPKPAFSK	3.55	1,933.98
Control	6011	Leucine rich repeat containing 8 family, member A	gi|115304767,gi|116003833	93,997.70	100.00%	4	4	4	0.03%	8.64%	IEAPALAFLR	3.01	1,100.65
Control	6011	Leucine rich repeat containing 8 family, member A	gi|115304767,gi|116003833	93,997.70	100.00%	4	4	4	0.03%	8.64%	MANLTELELIR	2.84	1,318.70
Control	6011	Leucine rich repeat containing 8 family, member A	gi|115304767,gi|116003833	93,997.70	100.00%	4	4	4	0.03%	8.64%	YLDLSHNNLTFLPADIGLLQSLQNLAVTANR	3.88	3,424.82

Control	6011	Caveolin 2	gi|157279219,gi|38322700,gi|51512145,gi|56119130,gi|66774044	18,142.30	99.80%	2	2	6	0.05%	16.00%	ADVQLFMDDDSYSR	2.8	1,677.71
Control	6011	Caveolin 2	gi|157279219,gi|38322700,gi|51512145,gi|56119130,gi|66774044	18,142.30	99.80%	2	2	6	0.05%	16.00%	SFSSVSLQLSHD	3.42	1,306.63
Control	6011	solute carrier family 29 (nucleoside transporters), member 1	gi|110331885,gi|73587285,gi|77735743	49,866.60	100.00%	3	3	3	0.02%	10.10%	DIQASASPLAPSPER	3.54	1,538.78
Control	6011	solute carrier family 29 (nucleoside transporters), member 1	gi|110331885,gi|73587285,gi|77735743	49,866.60	100.00%	3	3	3	0.02%	10.10%	LAFVPLLLLCNVQPR	3.51	1,696.00
Control	6011	solute carrier family 29 (nucleoside transporters), member 1	gi|110331885,gi|73587285,gi|77735743	49,866.60	100.00%	3	3	3	0.02%	10.10%	LEGPGEQETKLDLISK	3.62	1,756.93
Control	6011	PREDICTED: similar to trinucleotide repeat containing 6B isoform 3	gi|119893244	182,751.00	99.70%	2	2	2	0.02%	4.06%	KTGSVGSWGAARGPSGTDTASGQSNSGNNGNNGK	3.44	3,178.45
Control	6011	PREDICTED: similar to trinucleotide repeat containing 6B isoform 3	gi|119893244	182,751.00	99.70%	2	2	2	0.02%	4.06%	YSTKQEAAKAQTALHMCVLGNTTILAEFATDDEVSR	2.41	3,912.91
Control	6011	ACTN4 protein	gi|146186472,gi|148238040,gi|162416099	104,913.30	100.00%	3	3	3	0.02%	5.16%	KDDPVTNLNNAFEVAEK	2.62	1,903.94
Control	6011	ACTN4 protein	gi|146186472,gi|148238040,gi|162416099	104,913.30	100.00%	3	3	3	0.02%	5.16%	LSNRPAFMPSEGK	3.45	1,449.72

Control	6011	ACTN4 protein	gi|146186472,gi|148238040,gi|162416099	104,913.30	100.00%	3	3	3	0.02%	5.16%	MAPYQGPDAVPGALDYK	3.06	1,808.85
Control	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	gi|146231724,gi|77736299	40,519.40	99.80%	2	2	3	0.02%	16.90%	ISQTNYIPTQQDVLR	4.02	1,775.93
Control	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	gi|146231724,gi|77736299	40,519.40	99.80%	2	2	3	0.02%	16.90%	LLLLGAGESGK	3.47	1,057.63
Control	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	gi|146231724,gi|77736299	40,519.40	99.80%	2	2	3	0.02%	16.90%	NVQFVFDAVTDVIIK	2.94	1,707.93
Control	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	gi|146231724,gi|77736299	40,519.40	99.80%	2	2	3	0.02%	16.90%	SREYQLNDSASYYLNDLDR	4.4	2,322.06
Control	6011	Chromosome 9 open reading frame 46 ortholog	gi|74354529,gi|77735799	17,091.30	99.80%	2	2	4	0.03%	15.60%	GMITFESLEK	2.97	1,170.57
Control	6011	Chromosome 9 open reading frame 46 ortholog	gi|74354529,gi|77735799	17,091.30	99.80%	2	2	4	0.03%	15.60%	MKGEAENILETEK	3.88	1,507.73
Control	6011	STAT1 protein	gi|154426144	86,914.50	100.00%	4	4	4	0.03%	6.96%	ELSAVTFPDIIR	2.95	1,360.75
Control	6011	STAT1 protein	gi|154426144	86,914.50	100.00%	4	4	4	0.03%	6.96%	FHDLLSQLDDQYSR	3.62	1,736.82
Control	6011	STAT1 protein	gi|154426144	86,914.50	100.00%	4	4	4	0.03%	6.96%	GLNVDQLNMLGEK	3.5	1,446.73

Control	6011	STAT1 protein	gi|154426144	86,914.50	100.00%	4	4	4	0.03%	6.96%	VMAAENIPENPLK	4.07	1,441.74
Control	6011	Amyloid beta (A4) precursor protein	gi|115305312,gi|116003813	78,577.00	99.80%	2	2	2	0.02%	5.32%	LALENYITALQAVPPRPRHVFNMLK	3.11	2,907.60
Control	6011	Amyloid beta (A4) precursor protein	gi|115305312,gi|116003813	78,577.00	99.80%	2	2	2	0.02%	5.32%	VESLEQEAANER	3.05	1,374.65
Control	6011	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	100.00%	3	4	19	0.15%	15.20%	DYLALNEDLR	3.86	1,221.61
Control	6011	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	100.00%	3	4	19	0.15%	15.20%	FITVGYVDDTQFVR	3.48	1,659.84
Control	6011	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	100.00%	3	4	19	0.15%	15.20%	VQHEGLQEPLTLR	4.25	1,519.82
Control	6011	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	100.00%	3	4	19	0.15%	15.20%	YFLTAVSR	2.71	956.5199
Control	6011	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	100.00%	3	4	19	0.15%	15.20%	YFLTAVSRPGLGEPR	3.14	1,662.90
Control	6011	claudin 1	gi|47827197,gi|49258204,gi|61555400,gi|68052146,gi|73587015	22,847.70	99.80%	2	2	3	0.02%	14.70%	IVQEFYDPMTPVNAR	2.82	1,795.87
Control	6011	claudin 1	gi|47827197,gi|49258204,gi|61555400,gi|68052146,gi|73587015	22,847.70	99.80%	2	2	3	0.02%	14.70%	VFDSLLNLNSTLQATR	2.75	1,791.96
Control	6011	v-ral simian leukemia viral oncogene homolog B	gi|146231722,gi|147900776,gi|148878477	23,421.00	99.80%	2	3	3	0.02%	13.60%	AEEDKIPLLVVGNK	3.71	1,524.86
Control	6011	v-ral simian leukemia viral oncogene homolog B	gi|146231722,gi|147900776,gi|148878477	23,421.00	99.80%	2	3	3	0.02%	13.60%	ANVDKVFFDLMR	3.98	1,470.74

Control	6011	v-ral simian leukemia viral oncogene homolog B	gi|146231722,gi|147900776,gi|148878477	23,421.00	99.80%	2	3	3	0.02%	13.60%	VFFDLMR	2.39	943.4707
Control	6011	v-ral simian leukemia viral oncogene homolog B	gi|146231722,gi|147900776,gi|148878477	23,421.00	99.80%	2	3	3	0.02%	13.60%	VKAEEDKIPLLVVGNK	4.25	1,752.03
Control	6011	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	4	4	4	0.03%	15.30%	IATSGYLPTQQDVLR	4.13	1,661.89
Control	6011	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	4	4	4	0.03%	15.30%	ILHSHLVDYFPEFDGPQR	3.96	2,170.07

Control	6011	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	4	4	4	0.03%	15.30%	VPTTGIIEYPFDLENIIFR	2.99	2,237.19
Control	6011	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	4	4	4	0.03%	15.30%	VRVPTTGIIEYPFDLENIIFR	5.79	2,492.36
Control	6011	family with sequence similarity 82, member C	gi|115496878,gi|122143776,gi|94574211	51,888.40	99.80%	2	3	3	0.02%	8.07%	SSLQGLAGQIVGEVR	4.42	1,513.83
Control	6011	family with sequence similarity 82, member C	gi|115496878,gi|122143776,gi|94574211	51,888.40	99.80%	2	3	3	0.02%	8.07%	TATALSESPLGATVQDALSSFLK	3.99	2,307.21

Control	6011	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	4	4	7	0.05%	26.40%	IALMPLLQAEK	3.62	1,242.71
Control	6011	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	4	4	7	0.05%	26.40%	LQIEDFEAR	2.91	1,120.56
Control	6011	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	4	4	7	0.05%	26.40%	VKQDMPPVGGYGPIDYK	3.27	1,879.93
Control	6011	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	4	4	7	0.05%	26.40%	VKQDMPPVGGYGPIDYKR	5.96	2,036.03
Control	6011	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	4	5	6	0.05%	17.70%	FFVVSSESR	3.05	1,057.53
Control	6011	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	4	5	6	0.05%	17.70%	RKPDEVLDDEDIGSAPLK	5.18	1,997.02
Control	6011	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	4	5	6	0.05%	17.70%	VLKEDALPDLK	2.68	1,240.72
Control	6011	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	4	5	6	0.05%	17.70%	VLKEDALPDLKTEYEVDSEDR	4.15	2,464.21
Control	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	14	25	0.20%	41.80%	ALTVPELTQQMFDAK	2.54	1,707.86
Control	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	14	25	0.20%	41.80%	AVLVDLEPGTMDSVR	3.58	1,617.82

Control	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	14	25	0.20%	41.80%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	3.41	3,213.49
Control	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	14	25	0.20%	41.80%	FPGQLNADLRK	3.12	1,258.69
Control	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	14	25	0.20%	41.80%	GHYTEGAELVDSVLDVVR	3.66	1,958.98
Control	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	14	25	0.20%	41.80%	GHYTEGAELVDSVLDVVRK	3.32	2,087.08
Control	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	14	25	0.20%	41.80%	IMNTFSVVPSPK	4.39	1,335.70
Control	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	14	25	0.20%	41.80%	ISEQFTAMFR	2.98	1,245.59
Control	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	14	25	0.20%	41.80%	LAVNMVPFPR	3.55	1,159.63
Control	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	14	25	0.20%	41.80%	LHFFMPGFAPLTSR	3.66	1,620.84
Control	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	14	25	0.20%	41.80%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	4.94	4,479.06
Control	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	14	25	0.20%	41.80%	YLTVAAVFR	2.56	1,039.59
Control	6011	RAN binding protein 6	gi|78174362,gi|83715972	47,285.80	100.00%	3	3	3	0.02%	8.29%	ITFLLQAIR	3.07	1,074.67
Control	6011	RAN binding protein 6	gi|78174362,gi|83715972	47,285.80	100.00%	3	3	3	0.02%	8.29%	KQAEETYENIPGQSK	2.99	1,721.83
Control	6011	RAN binding protein 6	gi|78174362,gi|83715972	47,285.80	100.00%	3	3	3	0.02%	8.29%	SLVEIADTVPK	3.07	1,171.66
Control	6011	chromatin modifying protein 4C	gi|114051754,gi|87578327	26,417.80	99.80%	2	2	2	0.02%	12.30%	EALENSYTNTEVLK	3.68	1,610.79
Control	6011	chromatin modifying protein 4C	gi|114051754,gi|87578327	26,417.80	99.80%	2	2	2	0.02%	12.30%	LPNAPSSSLPAQPDR	3.53	1,549.80
Control	6011	RecName: Full=LAG1 longevity assurance homolog 2	gi|109892506,gi|73587265,gi|77736279	44,887.70	99.80%	2	2	3	0.02%	10.00%	AGTLIMALHDSSDYLLESAK	3.12	2,151.06

Control	6011	RecName: Full=LAG1 longevity assurance homolog 2	gi|109892506,gi|73587265,gi|77736279	44,887.70	99.80%	2	2	3	0.02%	10.00%	LRAPPNPTLEHFYMTSGK	3.19	2,075.04
Control	6011	RecName: Full=Peptidyl-prolyl cis-trans isomerase B; Short=PPIase; Short=Rotamase; AltName: Full=Cyclophilin B; AltName: Full=S-cyclophilin; Short=SCYLP; Flags: Precursor	gi|215274238,gi|27806469,gi|529242,gi|59858297,gi|74268324	23,726.00	99.80%	2	2	3	0.02%	12.50%	TVDNFVALATGEK	4.5	1,364.71
Control	6011	RecName: Full=Peptidyl-prolyl cis-trans isomerase B; Short=PPIase; Short=Rotamase; AltName: Full=Cyclophilin B; AltName: Full=S-cyclophilin; Short=SCYLP; Flags: Precursor	gi|215274238,gi|27806469,gi|529242,gi|59858297,gi|74268324	23,726.00	99.80%	2	2	3	0.02%	12.50%	VIKDFMIQGGDFTR	3.58	1,642.83
Control	6011	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	7	8	9	0.07%	23.10%	DVYDKVDYLSSLGK	3.05	1,601.81
Control	6011	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	7	8	9	0.07%	23.10%	KIGEAEAAVIEAR	3.63	1,356.75

Control	6011	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	7	8	9	0.07%	23.10%	LLAELPASVHALTGVDLSK	4.42	1,934.10
Control	6011	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	7	8	9	0.07%	23.10%	MALVLDALPR	3.86	1,114.63
Control	6011	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	7	8	9	0.07%	23.10%	NVVLQTLEGHLR	2.14	1,378.78
Control	6011	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	7	8	9	0.07%	23.10%	QVLLAQAEAEK	3.16	1,199.66
Control	6011	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	7	8	9	0.07%	23.10%	SILGTLTVEQIYQDRDQFAK	2.33	2,325.21
Control	6011	RecName: Full=GPI transamidase component PIG-S; AltName: Full=Phosphatidylinositol-glycan biosynthesis class S protein	gi|116248578,gi|74268100,gi|77735383	61,769.20	100.00%	4	7	8	0.06%	16.40%	APLPYSQISGLNSLK	3.79	1,587.87
Control	6011	RecName: Full=GPI transamidase component PIG-S; AltName: Full=Phosphatidylinositol-glycan biosynthesis class S protein	gi|116248578,gi|74268100,gi|77735383	61,769.20	100.00%	4	7	8	0.06%	16.40%	FDSASSSYYLAAHSLPHVINPVESR	4.44	2,747.34
Control	6011	RecName: Full=GPI transamidase component PIG-S; AltName: Full=Phosphatidylinositol-glycan biosynthesis class S protein	gi|116248578,gi|74268100,gi|77735383	61,769.20	100.00%	4	7	8	0.06%	16.40%	LMVPVTVVFTQESVPLDDQEKLPFTVVHER	4.48	3,468.81

Control	6011	RecName: Full=GPI transamidase component PIG-S; AltName: Full=Phosphatidylinositol-glycan biosynthesis class S protein	gi|116248578,gi|74268100,gi|77735383	61,769.20	100.00%	4	7	8	0.06%	16.40%	SVENLATATTTLTSLAQLLGK	4.51	2,132.18
Control	6011	PREDICTED: phosphoenolpyruvate carboxykinase 2 (mitochondrial) isoform 1	gi|194670361	70,632.70	100.00%	3	3	3	0.02%	6.56%	EIISFGSGYGGNSLLGK	3.37	1,698.87
Control	6011	PREDICTED: phosphoenolpyruvate carboxykinase 2 (mitochondrial) isoform 1	gi|194670361	70,632.70	100.00%	3	3	3	0.02%	6.56%	EVLAELEALEGR	2.3	1,328.71
Control	6011	PREDICTED: phosphoenolpyruvate carboxykinase 2 (mitochondrial) isoform 1	gi|194670361	70,632.70	100.00%	3	3	3	0.02%	6.56%	SYLTEQVNQDLPK	3.79	1,534.77

Control	6011	PREDICTED: similar to 1-acylglycerophosphocholine O-acyltransferase 1 (Lung-type acyl-CoA:lysophosphatidylcholine acyltransferase 1) (Lysophosphatidylcholine acyltransferase 1) (Acyltransferase-like 2)	gi|194676422	54,069.40	100.00%	3	3	3	0.02%	7.84%	MFGSQDGSVEEHALSSILK	2.49	2,050.98
Control	6011	PREDICTED: similar to 1-acylglycerophosphocholine O-acyltransferase 1 (Lung-type acyl-CoA:lysophosphatidylcholine acyltransferase 1) (Lysophosphatidylcholine acyltransferase 1) (Acyltransferase-like 2)	gi|194676422	54,069.40	100.00%	3	3	3	0.02%	7.84%	TLDTIQLAFK	2.99	1,149.65

Control	6011	PREDICTED: similar to 1-acylglycerophosphocholine O-acyltransferase 1 (Lung-type acyl-CoA:lysophosphatidylcholine acyltransferase 1) (Lysophosphatidylcholine acyltransferase 1) (Acyltransferase-like 2)	gi|194676422	54,069.40	100.00%	3	3	3	0.02%	7.84%	YIRPVFVSR	2.63	1,136.66
Control	6011	YWHAG protein	gi|157279400,gi|157744500,gi|2852385,gi|71153781	28,235.10	99.80%	2	2	4	0.03%	17.40%	NVTELNEPLSNEER	4.14	1,643.79
Control	6011	YWHAG protein	gi|157279400,gi|157744500,gi|2852385,gi|71153781	28,235.10	99.80%	2	2	4	0.03%	17.40%	TAFDDAIAELDTLNEDSYKDSTLIMQLLR	4.34	3,317.61
Control	6011	Chain C, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591028,gi|110591031,gi|114687,gi|163036,gi|27807291,gi|55670489,gi|73586602	12,514.70	99.80%	2	2	2	0.02%	43.50%	ADMNTFPNFTFEDPKFEVVEKPQS	3.24	2,833.30
Control	6011	Chain C, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591028,gi|110591031,gi|114687,gi|163036,gi|27807291,gi|55670489,gi|73586602	12,514.70	99.80%	2	2	2	0.02%	43.50%	QTSGGPVDAGPEYQQDLDRELFK	3.86	2,550.21
Control	6011	heterogeneous nuclear ribonucleoprotein A2/B1	gi|114051756,gi|122145945,gi|87578315	35,988.50	99.80%	2	3	3	0.02%	13.20%	GFGFVTFDDHDPVDKIVLQK	2.96	2,277.16
Control	6011	heterogeneous nuclear ribonucleoprotein A2/B1	gi|114051756,gi|122145945,gi|87578315	35,988.50	99.80%	2	3	3	0.02%	13.20%	NMGGPYGGGNYGPGGSGGSGGYGGR	5.88	2,205.90

Control	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	10	13	15	0.12%	10.10%	AFMTADLPNELIELLEK	4.72	1,963.01
Control	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	10	13	15	0.12%	10.10%	GYFEELITMLEAALGLER	3.01	2,071.04
Control	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	10	13	15	0.12%	10.10%	ISGETIFVTAPHEATAGIIGVNR	4.52	2,353.25
Control	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	10	13	15	0.12%	10.10%	KFDVNTSAVQVLIEHIGNLDR	4.96	2,368.26
Control	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	10	13	15	0.12%	10.10%	LASTLVHLGEYQAAVDGAR	3.17	1,971.03

Control	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	10	13	15	0.12%	10.10%	LLYNNVSNFGR	3.92	1,296.67
Control	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	10	13	15	0.12%	10.10%	NLQNLLILTAIK	4.06	1,353.85
Control	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	10	13	15	0.12%	10.10%	NNLAGAEELFAR	3.18	1,304.66
Control	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	10	13	15	0.12%	10.10%	RPISADSAIMNPASK	3.12	1,573.80
Control	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	10	13	15	0.12%	10.10%	TSIDAYDNFDNISLAQR	3.41	1,942.91

Control	6011	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	5	7	11	0.09%	22.50%	FDAVIGYK	2.92	912.4826
Control	6011	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	5	7	11	0.09%	22.50%	KSVTGEIVLITGAGHGIGR	4.45	1,865.06
Control	6011	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	5	7	11	0.09%	22.50%	LIDGILTEQKMIFVPSSLNFLSLMEK	2.96	2,982.59
Control	6011	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	5	7	11	0.09%	22.50%	NPSTSLGPTLEPEEVVNK	4.66	1,910.97
Control	6011	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	5	7	11	0.09%	22.50%	SVTGEIVLITGAGHGIGR	5.19	1,736.97
Control	6011	pre-B-cell leukemia transcription factor interacting protein 1	gi|110331795,gi|115497324,gi|151554897,gi|158706093	80,239.50	100.00%	3	3	3	0.02%	6.19%	ALESELQQLR	3.44	1,186.64
Control	6011	pre-B-cell leukemia transcription factor interacting protein 1	gi|110331795,gi|115497324,gi|151554897,gi|158706093	80,239.50	100.00%	3	3	3	0.02%	6.19%	EQGPTGQEPSPGFLEQK	3.53	1,828.87
Control	6011	pre-B-cell leukemia transcription factor interacting protein 1	gi|110331795,gi|115497324,gi|151554897,gi|158706093	80,239.50	100.00%	3	3	3	0.02%	6.19%	LLQAQLQAQKEELQSLMR	4.58	2,143.15
Control	6011	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	3	3	3	0.02%	19.30%	AELNEFLTR	2.89	1,092.57
Control	6011	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	3	3	3	0.02%	19.30%	FVDGLMIHSGDPVNYYVDTAVR	5.88	2,484.19
Control	6011	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	3	3	3	0.02%	19.30%	GGKPEPPAMPQPVPTA	3.52	1,589.80

Control	6011	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	10	14	20	0.16%	19.80%	ADDKLIAEEGVDSLNVK	4.97	1,815.93
Control	6011	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	10	14	20	0.16%	19.80%	AMYLPETLSPADQLK	3.67	1,692.85
Control	6011	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	10	14	20	0.16%	19.80%	FLQDTIEEMALK	3.89	1,453.72
Control	6011	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	10	14	20	0.16%	19.80%	IRETGERPSNEEIMR	1.72	1,832.89
Control	6011	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	10	14	20	0.16%	19.80%	KLEEGGPVYSPPAQAAVR	3.03	1,868.99
Control	6011	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	10	14	20	0.16%	19.80%	LEEGGPVYSPPAQAAVR	3.93	1,740.89
Control	6011	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	10	14	20	0.16%	19.80%	LFPNMLPSTFETQSSKEER	1.92	2,257.08
Control	6011	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	10	14	20	0.16%	19.80%	LLELQSIGTNNFLR	4.17	1,617.90

Control	6011	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	10	14	20	0.16%	19.80%	LLSLASALDDNKDGKVDIDDLVK	2.2	2,457.31
Control	6011	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	10	14	20	0.16%	19.80%	STLQTLPEIVAK	2.77	1,299.75
Control	6011	unnamed protein product	gi|117576085,gi|117576087,gi|119935998,gi|1902982,gi|27806503,gi|73621334	30,875.20	99.80%	2	2	4	0.03%	8.52%	EMIETLAHKLDEK	3.02	1,572.79
Control	6011	unnamed protein product	gi|117576085,gi|117576087,gi|119935998,gi|1902982,gi|27806503,gi|73621334	30,875.20	99.80%	2	2	4	0.03%	8.52%	QNLNLQEVLK	2.9	1,198.68
Control	6011	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	40	0.31%	35.70%	LTFDSSFSPNTGK	4.4	1,400.67
Control	6011	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	40	0.31%	35.70%	LTFDSSFSPNTGKK	1.93	1,528.76
Control	6011	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	40	0.31%	35.70%	LTLSALLDGK	3.74	1,030.61
Control	6011	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	40	0.31%	35.70%	SENGLEFTSSGSANTETTK	4.53	1,959.88
Control	6011	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	40	0.31%	35.70%	SRVTQSNFAVGYK	4.11	1,456.75
Control	6011	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	40	0.31%	35.70%	TDEFQLHTNVNDGTEFGGSIYQK	6.18	2,600.19
Control	6011	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	40	0.31%	35.70%	TKSENGLEFTSSGSANTETTK	5.66	2,189.02
Control	6011	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	40	0.31%	35.70%	VNNSSLIGLGYTQTLKPGIK	4.71	2,103.18
Control	6011	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	40	0.31%	35.70%	VTQSNFAVGYK	3.9	1,213.62

Control	6011	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	8	9	31	0.24%	32.30%	GFGFGLVK	1.96	824.4666
Control	6011	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	8	9	31	0.24%	32.30%	LTFDTTFSPNTGK	3.02	1,428.70
Control	6011	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	8	9	31	0.24%	32.30%	LTFDTTFSPNTGKK	3.89	1,556.80
Control	6011	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	8	9	31	0.24%	32.30%	LTLSALVDGK	3.26	1,016.60
Control	6011	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	8	9	31	0.24%	32.30%	NNFAVGYR	2.17	940.4634
Control	6011	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	8	9	31	0.24%	32.30%	TGDFQLHTNVNDGTEFGGSIYQK	5.81	2,528.17
Control	6011	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	8	9	31	0.24%	32.30%	VNNSSLIGVGYTQTLRPGVK	4.88	2,103.16
Control	6011	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	8	9	31	0.24%	32.30%	YQLDPTASISAK	3.16	1,293.67
Control	6011	Trx-like protein	gi|109726696,gi|115494922,gi|122145628,gi|126920889,gi|146231808	31,563.90	100.00%	4	4	4	0.03%	8.63%	KLLPESSQPLK	2.89	1,239.73
Control	6011	Trx-like protein	gi|109726696,gi|115494922,gi|122145628,gi|126920889,gi|146231808	31,563.90	100.00%	4	4	4	0.03%	8.63%	KLLPESSQPLKK	3.86	1,367.83

Control	6011	Trx-like protein	gi|109726696,gi|115494922,gi|122145628,gi|126920889,gi|146231808	31,563.90	100.00%	4	4	4	0.03%	8.63%	LLPESSQPLKK	2.33	1,239.73
Control	6011	Trx-like protein	gi|109726696,gi|115494922,gi|122145628,gi|126920889,gi|146231808	31,563.90	100.00%	4	4	4	0.03%	8.63%	VDVTEQPGLSGR	4.54	1,257.64
Control	6011	PREDICTED: similar to Vezatin isoform 2	gi|119891996	88,604.30	99.80%	2	2	2	0.02%	4.10%	NDTEEENNKTSTADNEISSR	3.42	2,253.97
Control	6011	PREDICTED: similar to Vezatin isoform 2	gi|119891996	88,604.30	99.80%	2	2	2	0.02%	4.10%	YFETQHQSVPQR	2.14	1,519.73
Control	6011	Ribosomal protein L26	gi|148744293,gi|28189348,gi|28189641,gi|62751887,gi|74268218,gi|76613859	12,702.40	99.70%	2	2	3	0.02%	23.10%	MKFNPFVTSDR	2.45	1,357.66
Control	6011	Ribosomal protein L26	gi|148744293,gi|28189348,gi|28189641,gi|62751887,gi|74268218,gi|76613859	12,702.40	99.70%	2	2	3	0.02%	23.10%	SMPIRKDDEVQVVR	2.97	1,687.88
Control	6011	endothelial cell-specific molecule 2	gi|114053335,gi|86438024	20,621.00	99.80%	2	3	7	0.05%	13.20%	ESEDPQKPGSSGLSESGSTANGEK	5.05	2,378.06
Control	6011	endothelial cell-specific molecule 2	gi|114053335,gi|86438024	20,621.00	99.80%	2	3	7	0.05%	13.20%	NKESEDPQKPGSSGLSESGSTANGEK	3.34	2,620.20
Control	6011	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	4	6	9	0.07%	6.11%	ANLINNIFELAGLGK	3.64	1,586.89
Control	6011	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	4	6	9	0.07%	6.11%	GLGEHELDEDEEDYESSAK	4.95	2,151.88

Control	6011	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	4	6	9	0.07%	6.11%	IFGELSSYEDFLDAR	4.04	1,761.83
Control	6011	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	4	6	9	0.07%	6.11%	IKRDEQYTALSNMPK	4.57	1,809.92
Control	6011	PREDICTED: similar to Zinc finger protein basonuclin-1	gi|76647059	111,795.20	99.80%	2	3	3	0.02%	2.48%	IEKETMETADEKR	3.86	1,595.76
Control	6011	PREDICTED: similar to Zinc finger protein basonuclin-1	gi|76647059	111,795.20	99.80%	2	3	3	0.02%	2.48%	VEPCVPFPDYIK	2.29	1,406.70
Control	6011	CYB5B protein	gi|158455068,gi|76640228	26,782.70	99.80%	2	4	5	0.04%	22.40%	FLDEHPGGEEVLMEQAGGDATESFEDVGHSSDAR	4.36	3,634.55
Control	6011	CYB5B protein	gi|158455068,gi|76640228	26,782.70	99.80%	2	4	5	0.04%	22.40%	QYYIGDVHPNDLKPGGGSK	2.72	2,045.01
Control	6011	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	6	8	9	0.07%	25.70%	EQNGDSLVHAALVAESAAIGSAEANAFSVLQHVLGAGPHVK	3.4	4,065.08
Control	6011	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	6	8	9	0.07%	25.70%	GSNATSSLYQAVAK	3.48	1,396.71

Control	6011	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	6	8	9	0.07%	25.70%	LPNGLVIASLENYAPASR	3.53	1,885.02
Control	6011	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	6	8	9	0.07%	25.70%	MALIGLGVSHPVLK	3.86	1,450.85
Control	6011	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	6	8	9	0.07%	25.70%	QVAEQFLNIR	3.18	1,217.66
Control	6011	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	6	8	9	0.07%	25.70%	TIAQGNLSNPDVQAAK	4.02	1,626.84
Control	6011	Chain A, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793901,gi|71042575,gi|71042585,gi|75765179,gi|75765190,gi|82407287	49,194.40	100.00%	4	7	7	0.05%	13.50%	ADLTEYLSR	2.69	1,067.54

Control	6011	Chain A, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793901,gi|71042575,gi|71042585,gi|75765179,gi|75765190,gi|82407287	49,194.40	100.00%	4	7	7	0.05%	13.50%	EVESMGAHLNAYSTR	3.36	1,680.76
Control	6011	Chain A, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793901,gi|71042575,gi|71042585,gi|75765179,gi|75765190,gi|82407287	49,194.40	100.00%	4	7	7	0.05%	13.50%	MVLAAAGGLEHR	2.75	1,240.65
Control	6011	Chain A, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793901,gi|71042575,gi|71042585,gi|75765179,gi|75765190,gi|82407287	49,194.40	100.00%	4	7	7	0.05%	13.50%	TATYAQALQSVPETQVSQLDNGLR	3.78	2,590.31
Control	6011	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	gi|111308529,gi|128825,gi|163414,gi|27807355	79,425.10	100.00%	5	5	5	0.04%	11.10%	ALSEIAGMTLPYDTLDQVR	3.24	2,109.05
Control	6011	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	gi|111308529,gi|128825,gi|163414,gi|27807355	79,425.10	100.00%	5	5	5	0.04%	11.10%	AVEDKNIGPLVK	3.37	1,282.74

Control	6011	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	gi|111308529,gi|128825,gi|163414,gi|27807355	79,425.10	100.00%	5	5	5	0.04%	11.10%	ILQDIASGSHPFSQVLQEAK	3.62	2,168.13
Control	6011	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	gi|111308529,gi|128825,gi|163414,gi|27807355	79,425.10	100.00%	5	5	5	0.04%	11.10%	NRLEEVSPNLVR	2.78	1,425.78
Control	6011	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	gi|111308529,gi|128825,gi|163414,gi|27807355	79,425.10	100.00%	5	5	5	0.04%	11.10%	YDDVEGANYFQQASELSK	2.68	2,063.92
Control	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	13	17	21	0.16%	41.90%	AQQVAVQEQEIAR	4.53	1,469.77
Control	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	13	17	21	0.16%	41.90%	DIHDDQDYLHSLGK	3.41	1,655.77
Control	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	13	17	21	0.16%	41.90%	ISLNTLTLNVK	3.2	1,215.73
Control	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	13	17	21	0.16%	41.90%	ITLVSSGSGAMGAAK	4.34	1,365.70
Control	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	13	17	21	0.16%	41.90%	KAEAFQLYQEAAQLDMLLEK	3.92	2,355.19

Control	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	13	17	21	0.16%	41.90%	KAEAFQLYQEAAQLDMLLEKLPQVAEEISGPLTSANK	4.21	4,090.11
Control	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	13	17	21	0.16%	41.90%	LPQVAEEISGPLTSANK	5.12	1,753.93
Control	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	13	17	21	0.16%	41.90%	MRGEAEAFAIGAR	2.97	1,394.68
Control	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	13	17	21	0.16%	41.90%	SQLIMQAEAEAEAVR	4.66	1,661.82
Control	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	13	17	21	0.16%	41.90%	TEAEIAHIALETLEGHQR	3.43	2,018.03
Control	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	13	17	21	0.16%	41.90%	VASSDLVNMGISVVSYTLK	3.11	1,999.04
Control	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	13	17	21	0.16%	41.90%	VSAQYLSEIEMAK	3.12	1,484.73
Control	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	13	17	21	0.16%	41.90%	VTGEVLDILSR	3.03	1,201.68
Control	6011	similar to 40S ribosomal protein S18	gi|28189422,gi|28189549,gi|28189799,gi|74268023,gi|75812924,gi|91207636	15,380.70	99.80%	2	2	2	0.02%	16.00%	IAFAITAIK	2.64	947.5925
Control	6011	similar to 40S ribosomal protein S18	gi|28189422,gi|28189549,gi|28189799,gi|74268023,gi|75812924,gi|91207636	15,380.70	99.80%	2	2	2	0.02%	16.00%	RAGELTEDEVER	3.74	1,403.68
Control	6011	glutathione peroxidase 8	gi|114052907,gi|122143886,gi|84708688	23,965.80	100.00%	3	3	3	0.02%	15.80%	ILGSEAEPAFR	3.79	1,189.62

Control	6011	glutathione peroxidase 8	gi|114052907,gi|122143886,gi|84708688	23,965.80	100.00%	3	3	3	0.02%	15.80%	INSFYTFEVK	2.18	1,247.63
Control	6011	glutathione peroxidase 8	gi|114052907,gi|122143886,gi|84708688	23,965.80	100.00%	3	3	3	0.02%	15.80%	NNFGVTFPIFHK	3.47	1,420.74
Control	6011	ANXA6 protein	gi|154426044,gi|157151716,gi|160332337	75,893.80	99.80%	2	2	2	0.02%	4.75%	GLGTDEDTIIDIIAHR	2.1	1,738.90
Control	6011	ANXA6 protein	gi|154426044,gi|157151716,gi|160332337	75,893.80	99.80%	2	2	2	0.02%	4.75%	GTVRPAGDFNPDADAK	3.31	1,630.78
Control	6011	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	8	10	25	0.20%	30.50%	GFVLTFK	2.11	811.4713
Control	6011	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	8	10	25	0.20%	30.50%	GVGMVADPDNPLVLDILTGSSTSYSFFPDKPITQYPHAVGK	5.6	4,350.16
Control	6011	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	8	10	25	0.20%	30.50%	LPDVYGVFQFK	3.49	1,312.69
Control	6011	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	8	10	25	0.20%	30.50%	SSLNPILFR	2.72	1,046.60
Control	6011	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	8	10	25	0.20%	30.50%	TADDPSLSLIK	3.14	1,159.62
Control	6011	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	8	10	25	0.20%	30.50%	TAVIDHHNYDVSDLGQHTLIVADTENLLK	6.6	3,231.63
Control	6011	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	8	10	25	0.20%	30.50%	TLVLLDNLNLR	4.3	1,283.77

Control	6011	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|15155878,gi|155371877,gi|215275740	48,774.90	100.00%	8	10	25	0.20%	30.50%	YSQTGNYELAVALSR	4.25	1,671.83
Control	6011	reticulon 4 isoform 2	gi|164259354,gi|92096636	40,940.20	100.00%	3	5	8	0.06%	10.30%	GPLPAAPLAAPER	3.46	1,259.71
Control	6011	reticulon 4 isoform 2	gi|164259354,gi|92096636	40,940.20	100.00%	3	5	8	0.06%	10.30%	HQAQIDHYLGLANK	4.77	1,607.83
Control	6011	reticulon 4 isoform 2	gi|164259354,gi|92096636	40,940.20	100.00%	3	5	8	0.06%	10.30%	LFLVDDLVDSLK	4.03	1,376.77
Control	6011	ADP-ribosylation factor-like 8B	gi|114051548,gi|86438183,gi|93204537	21,493.90	99.80%	2	3	4	0.03%	21.50%	GVNAIVYMIDAADREK	3.92	1,780.89
Control	6011	ADP-ribosylation factor-like 8B	gi|114051548,gi|86438183,gi|93204537	21,493.90	99.80%	2	3	4	0.03%	21.50%	NELHNLLDKPQLQGIPVLVLGNKR	4.45	2,708.56
Control	6011	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	8	13	19	0.15%	20.10%	ALASILLQDHIR	2.18	1,349.79
Control	6011	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	8	13	19	0.15%	20.10%	DIASEFKEQLQTLILHVLNPANLMEK	4.06	3,010.59
Control	6011	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	8	13	19	0.15%	20.10%	IYQGEDLPHPK	3.15	1,296.66
Control	6011	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	8	13	19	0.15%	20.10%	KVAVVLMDTQGAFDSQSTVK	4.75	2,140.10
Control	6011	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	8	13	19	0.15%	20.10%	LAMDEIFQKPFQTLMFLVR	3.96	2,343.22
Control	6011	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	8	13	19	0.15%	20.10%	LKDIASEFKEQLQTLILHVLNPANLMEK	5.77	3,251.77
Control	6011	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	8	13	19	0.15%	20.10%	SMLQATAEANLAAAASAK	5.63	1,848.91
Control	6011	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	8	13	19	0.15%	20.10%	VAVVLMDTQGAFDSQSTVK	3.94	2,012.00
Control	6011	RecName: Full=Glutathione S-transferase P; AltName: Full=GST class-pi	gi|121744,gi|29135329,gi|404,gi|74268086	23,595.90	99.70%	2	2	2	0.02%	15.70%	ALPQHLKPFETLLSQNK	2.44	1,964.10

Control	6011	RecName: Full=Glutathione S-transferase P; AltName: Full=GST class-pi	gi|121744,gi|29135329,gi|404,gi|74268086	23,595.90	99.70%	2	2	2	0.02%	15.70%	FQDGDLTLYQSNAILR	2.73	1,853.94
Control	6011	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	7	7	7	0.05%	15.90%	EAALSTALSEKR	2.79	1,275.69
Control	6011	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	7	7	7	0.05%	15.90%	IRIDSLSAQLSQLQK	3.91	1,699.97
Control	6011	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	7	7	7	0.05%	15.90%	LKDLEALLNSK	3.62	1,243.73
Control	6011	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	7	7	7	0.05%	15.90%	LQEKEDLQELNDR	4.2	1,629.81
Control	6011	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	7	7	7	0.05%	15.90%	MQQQLDEYQELLDIK	3.45	1,909.92
Control	6011	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	7	7	7	0.05%	15.90%	NIYSEELRETK	2.94	1,381.70
Control	6011	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	7	7	7	0.05%	15.90%	TALINSTGEEVAMR	3.31	1,507.74
Control	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	16	37	0.29%	36.80%	AVAISLPK	2.37	798.5084
Control	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	16	37	0.29%	36.80%	AVLSAEQLRDDEVHAGLGELLR	6.3	2,391.26

Control	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	16	37	0.29%	36.80%	DQAVENILLSPVVVASSLGLVSLGGK	6.35	2,565.45
Control	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	16	37	0.29%	36.80%	DTQSGSLLFIGR	2.81	1,293.68
Control	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	16	37	0.29%	36.80%	GVVEVTHDLQK	3.86	1,224.66
Control	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	16	37	0.29%	36.80%	HLAGLGLTEAIDK	2.92	1,337.74

Control	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	16	37	0.29%	36.80%	HLAGLGLTEAIDKNK	4.88	1,579.88
Control	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	16	37	0.29%	36.80%	KAVAISLPK	2.62	926.6034
Control	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	16	37	0.29%	36.80%	LFYADHPFIFLVR	3.66	1,637.88
Control	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	16	37	0.29%	36.80%	LSSLIIIMPHHVEPLER	3.24	2,000.10

Control	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	16	37	0.29%	36.80%	LYGPSSVSFAEDFVR	4.83	1,673.82
Control	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	16	37	0.29%	36.80%	SAGLAFSLYQAMAK	3.73	1,473.74
Control	6011	PREDICTED: similar to Leucine-rich PPR motif-containing protein, mitochondrial precursor (130 kDa leucine-rich protein) (LRP 130) (GP130)	gi|194671407	153,330.30	100.00%	3	3	3	0.02%	2.59%	LIEKGETELIQK	2.65	1,400.80
Control	6011	PREDICTED: similar to Leucine-rich PPR motif-containing protein, mitochondrial precursor (130 kDa leucine-rich protein) (LRP 130) (GP130)	gi|194671407	153,330.30	100.00%	3	3	3	0.02%	2.59%	TALDLDQIPSR	2.71	1,228.65

Control	6011	PREDICTED: similar to Leucine-rich PPR motif-containing protein, mitochondrial precursor (130 kDa leucine-rich protein) (LRP 130) (GP130)	gi|194671407	153,330.30	100.00%	3	3	3	0.02%	2.59%	VIEGQLEPALEK	3.85	1,325.73
Control	6011	PREDICTED: hypothetical protein	gi|194667311	68,113.30	100.00%	4	7	8	0.06%	9.11%	ELESQISELQEDLESER	3.59	2,033.95
Control	6011	PREDICTED: hypothetical protein	gi|194667311	68,113.30	100.00%	4	7	8	0.06%	9.11%	IRELESQISELQEDLESER	5.82	2,303.14
Control	6011	PREDICTED: hypothetical protein	gi|194667311	68,113.30	100.00%	4	7	8	0.06%	9.11%	RKLEGDSTDLNDQIAELQAQIAELK	2.85	2,798.45
Control	6011	PREDICTED: hypothetical protein	gi|194667311	68,113.30	100.00%	4	7	8	0.06%	9.11%	XXXXXXXXXXX	3.78	1,240.02
Control	6011	PREDICTED: transmembrane emp24 protein transport domain containing 4	gi|194666384	37,465.50	100.00%	4	6	7	0.05%	14.90%	DKLTELQLR	3.25	1,115.64
Control	6011	PREDICTED: transmembrane emp24 protein transport domain containing 4	gi|194666384	37,465.50	100.00%	4	6	7	0.05%	14.90%	QKEVFLPSTPGLGMHVEVKDPEGK	3.04	2,638.36
Control	6011	PREDICTED: transmembrane emp24 protein transport domain containing 4	gi|194666384	37,465.50	100.00%	4	6	7	0.05%	14.90%	QLLDQVEQIQK	3.7	1,341.74

Control	6011	PREDICTED: transmembrane emp24 protein transport domain containing 4	gi|194666384	37,465.50	100.00%	4	6	7	0.05%	14.90%	QLLDQVEQIQKEQDYQR	3.39	2,161.09
Control	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	14	19	34	0.27%	17.60%	AVVLAANHFGR	2.03	1,154.64
Control	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	14	19	34	0.27%	17.60%	FFTGQITAAGK	2.64	1,140.60
Control	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	14	19	34	0.27%	17.60%	GITHIGYTDLPSR	4.46	1,429.74
Control	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	14	19	34	0.27%	17.60%	GTVVMKDGQVIFPAPTPK	3.47	1,901.02
Control	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	14	19	34	0.27%	17.60%	ILIVGGGVAGLASAGAAK	5.04	1,524.91
Control	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	14	19	34	0.27%	17.60%	MATQASTLYSNNITK	5.01	1,658.81
Control	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	14	19	34	0.27%	17.60%	QKTVAELEAEK	3.47	1,245.67
Control	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	14	19	34	0.27%	17.60%	RVALSPAGVQALVK	2.67	1,408.86
Control	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	14	19	34	0.27%	17.60%	SLGAEPLEVDLK	3.08	1,270.69
Control	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	14	19	34	0.27%	17.60%	SLGVGYAAVDNPIFYKPNTAMLLGDAK	3.89	2,841.45

Control	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	14	19	34	0.27%	17.60%	SLGVGYAAVDNPIFYKPNTAMLLGDAKK	2.65	2,969.54
Control	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	14	19	34	0.27%	17.60%	TSGTLISFIYPAQNPDLLNK	3.72	2,192.16
Control	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	14	19	34	0.27%	17.60%	VALSPAGVQALVK	4.91	1,252.76
Control	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	14	19	34	0.27%	17.60%	VTIAQGYDALSSMANIAGYK	3.47	2,089.03
Control	6011	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	15	29	0.23%	32.40%	IPDQLVILDMK	4.09	1,300.72
Control	6011	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	15	29	0.23%	32.40%	IPDQLVILDMKHGVEAK	2.12	1,922.04
Control	6011	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	15	29	0.23%	32.40%	ITDSAGHILYSK	1.94	1,304.68
Control	6011	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	15	29	0.23%	32.40%	ITDSAGHILYSKEDATK	4.83	1,848.93
Control	6011	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	15	29	0.23%	32.40%	LEDLSESIVNDFAYMK	4.14	1,889.88

Control	6011	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	15	29	0.23%	32.40%	LKPLEVELR	3.89	1,096.67
Control	6011	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	15	29	0.23%	32.40%	NYEEIAKVEK	2.76	1,222.63
Control	6011	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	15	29	0.23%	32.40%	RLEDLSESIVNDFAYMK	5.77	2,045.99
Control	6011	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	15	29	0.23%	32.40%	RLEDLSESIVNDFAYMKK	5.16	2,174.08
Control	6011	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	100.00%	6	6	7	0.05%	14.60%	DAAGIAMEAIAFAR	3.4	1,422.70
Control	6011	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	100.00%	6	6	7	0.05%	14.60%	LIDGIVLTK	2.93	971.6138
Control	6011	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	100.00%	6	6	7	0.05%	14.60%	LITVNTPDLVLFVGEALVGNEAVDQLVK	5.06	2,966.65
Control	6011	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	100.00%	6	6	7	0.05%	14.60%	NQGFDVVLVDTAGR	3.67	1,490.76
Control	6011	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	100.00%	6	6	7	0.05%	14.60%	QALQESLVQILQPQR	4.2	1,750.98
Control	6011	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	100.00%	6	6	7	0.05%	14.60%	VMGTFSTVTSTVK	3.15	1,373.70
Control	6011	CAPZA1 protein	gi|133777466,gi|134085807,gi|152941212,gi|218563517	32,913.90	99.80%	2	2	2	0.02%	9.79%	FITHAPPGEFNEVFNDVR	3.98	2,089.01

Control	6011	CAPZA1 protein	gi|133777466,gi|134085807,gi|152941212,gi|218563517	32,913.90	99.80%	2	2	2	0.02%	9.79%	LLLNNDNLLR	3.01	1,197.70
Control	6011	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	5	5	5	0.04%	7.64%	FLFLLLGPAGK	3.27	1,175.72
Control	6011	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	5	5	5	0.04%	7.64%	GPDEEAVVDLGK	3.09	1,228.61
Control	6011	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	5	5	5	0.04%	7.64%	KIPSGAEASNVLVGEVDFLERPIIAFVR	3.11	3,026.67
Control	6011	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	5	5	5	0.04%	7.64%	LAPAVLLSGLTEVPVPTR	3.96	1,833.08
Control	6011	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	5	5	5	0.04%	7.64%	MLQAGEDTVHLPFEGGSLLQIPVK	4.3	2,595.35
Control	6011	phosphatidylinositol glycan anchor biosynthesis, class K	gi|118151384,gi|119889964,gi|75775270,gi|91206763	45,155.70	99.90%	2	2	2	0.02%	7.09%	NMELNVYGDDVEVDYR	2.74	1,946.84
Control	6011	phosphatidylinositol glycan anchor biosynthesis, class K	gi|118151384,gi|119889964,gi|75775270,gi|91206763	45,155.70	99.90%	2	2	2	0.02%	7.09%	NVLITDFFGSVR	2.89	1,367.73

Control	6011	Stromal interaction molecule 1	gi|154426132,gi|61555683,gi|75057528,gi|78369570	77,134.40	100.00%	6	6	7	0.05%	13.00%	AAAEEDNGSIGEETDSSPGR	3.76	1,991.84
Control	6011	Stromal interaction molecule 1	gi|154426132,gi|61555683,gi|75057528,gi|78369570	77,134.40	100.00%	6	6	7	0.05%	13.00%	DLTHSDSESSLHMSDR	3.84	1,832.77
Control	6011	Stromal interaction molecule 1	gi|154426132,gi|61555683,gi|75057528,gi|78369570	77,134.40	100.00%	6	6	7	0.05%	13.00%	KAAAEEDNGSIGEETDSSPGR	4.19	2,119.94
Control	6011	Stromal interaction molecule 1	gi|154426132,gi|61555683,gi|75057528,gi|78369570	77,134.40	100.00%	6	6	7	0.05%	13.00%	LMDDDANGDVDVEESDEFLREDLNYHDPTVK	3.33	3,611.56
Control	6011	Stromal interaction molecule 1	gi|154426132,gi|61555683,gi|75057528,gi|78369570	77,134.40	100.00%	6	6	7	0.05%	13.00%	QALSEVTAALR	2.83	1,158.65
Control	6011	Stromal interaction molecule 1	gi|154426132,gi|61555683,gi|75057528,gi|78369570	77,134.40	100.00%	6	6	7	0.05%	13.00%	YAEEELEQVR	3.14	1,265.60
Control	6011	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	6	6	0.05%	23.00%	FSDLDSASVDSDMYDLPK	2.9	2,020.87
Control	6011	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	6	6	0.05%	23.00%	FSDLDSASVDSDMYDLPKKEDALLYQSK	4	3,196.49
Control	6011	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	6	6	0.05%	23.00%	GFRQPSASLSDADPFHR	3.56	1,887.91
Control	6011	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	6	6	0.05%	23.00%	LSPPSSSASSFSYR	1.99	1,472.70
Control	6011	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	6	6	0.05%	23.00%	RLSPPSSSASSFSYR	3.25	1,628.80
Control	6011	NADH dehydrogenase (ubiquinone) 42 kDa subunit	gi|228,gi|45430053,gi|464255,gi|74268236,gi|95768472	41,642.50	99.80%	2	2	2	0.02%	5.15%	FLNYFANIR	3.05	1,157.61
Control	6011	NADH dehydrogenase (ubiquinone) 42 kDa subunit	gi|228,gi|45430053,gi|464255,gi|74268236,gi|95768472	41,642.50	99.80%	2	2	2	0.02%	5.15%	IPQAIAQVSK	2.33	1,054.63

Control	6011	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	6	6	11	0.09%	39.60%	ATIGADFLTK	2.63	1,036.57
Control	6011	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	6	6	11	0.09%	39.60%	DPENFPFVVLGNK	3.86	1,475.75
Control	6011	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	6	6	11	0.09%	39.60%	FQSLGVAFYR	3.03	1,187.62
Control	6011	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	6	6	11	0.09%	39.60%	GADCCVLVFDVTAPNTFK	2.96	1,899.90
Control	6011	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	6	6	11	0.09%	39.60%	NALKQETEVELYNEFPEPIK	4.21	2,391.21
Control	6011	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	6	6	11	0.09%	39.60%	VIILGDSGVGK	2.66	1,057.63
Control	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	14	17	21	0.16%	28.80%	ARFEELNADLFR	3.95	1,480.75
Control	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	14	17	21	0.16%	28.80%	DAGTIAGLNVLR	3.63	1,199.67
Control	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	14	17	21	0.16%	28.80%	FEELNADLFR	2.36	1,253.62
Control	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	14	17	21	0.16%	28.80%	IINEPTAAAIAYGLDK	4.4	1,659.90
Control	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	14	17	21	0.16%	28.80%	IINEPTAAAIAYGLDKK	2.86	1,787.99
Control	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	14	17	21	0.16%	28.80%	LDKSQIHDIVLVGGSTR	4.06	1,838.01
Control	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	14	17	21	0.16%	28.80%	LLQDFFNGK	2.35	1,081.57
Control	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	14	17	21	0.16%	28.80%	MVNHFIAEFK	2.26	1,251.62

Control	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	14	17	21	0.16%	28.80%	NQVAMNPTNTVFDAK	3.98	1,665.79
Control	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	14	17	21	0.16%	28.80%	NSLESYAFNMK	2.98	1,319.59
Control	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	14	17	21	0.16%	28.80%	SFYPEEVSSMVLTK	2.93	1,632.78
Control	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	14	17	21	0.16%	28.80%	SINPDEAVAYGAAVQAAILSGDK	3.29	2,260.15
Control	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	14	17	21	0.16%	28.80%	STAGDTHLGGEDFDNR	3.25	1,691.73
Control	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	14	17	21	0.16%	28.80%	TTPSYVAFTDTER	3.3	1,487.70
Control	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	14	17	21	0.16%	28.80%	TVTNAVVTVPAYFNDSQR	3.34	1,982.00
Control	6011	Solute carrier family 25 (mitochondrial carrier: glutamate), member 22	gi|115305383,gi|115495639,gi|122132287	34,514.50	100.00%	5	5	5	0.04%	26.10%	DVPFSIVYFPLFANLNELGR	3.39	2,311.21
Control	6011	Solute carrier family 25 (mitochondrial carrier: glutamate), member 22	gi|115305383,gi|115495639,gi|122132287	34,514.50	100.00%	5	5	5	0.04%	26.10%	GAAVNLTLVTPEK	3.42	1,312.75
Control	6011	Solute carrier family 25 (mitochondrial carrier: glutamate), member 22	gi|115305383,gi|115495639,gi|122132287	34,514.50	100.00%	5	5	5	0.04%	26.10%	KILSAQAQLSGQGSAQPSVEAPATPRPTATQLTR	5.24	3,460.85
Control	6011	Solute carrier family 25 (mitochondrial carrier: glutamate), member 22	gi|115305383,gi|115495639,gi|122132287	34,514.50	100.00%	5	5	5	0.04%	26.10%	LAANDFFR	2.51	953.4839

Control	6011	Solute carrier family 25 (mitochondrial carrier: glutamate), member 22	gi|115305383,gi|115495639,gi|122132287	34,514.50	100.00%	5	5	5	0.04%	26.10%	SEGYFGMYR	2.66	1,125.47
Control	6011	chaperonin containing TCP1, subunit 7	gi|114051425,gi|115305840,gi|84708838	59,426.00	99.80%	2	2	2	0.02%	5.89%	SLHDAIMIVR	2.35	1,170.63
Control	6011	chaperonin containing TCP1, subunit 7	gi|114051425,gi|115305840,gi|84708838	59,426.00	99.80%	2	2	2	0.02%	5.89%	SQDAEVGDGTTSVTLLAAEFLK	4.17	2,252.13
Control	6011	ras homolog gene family, member G	gi|122692461,gi|92096969	21,261.90	100.00%	3	4	4	0.03%	19.90%	EQGQAPITPQQGQALAK	3.98	1,764.92
Control	6011	ras homolog gene family, member G	gi|122692461,gi|92096969	21,261.90	100.00%	3	4	4	0.03%	19.90%	EYIPTVFDNYSAQSAVDGR	2.99	2,131.99
Control	6011	ras homolog gene family, member G	gi|122692461,gi|92096969	21,261.90	100.00%	3	4	4	0.03%	19.90%	LKEQGQAPITPQQGQALAK	4.64	2,006.10
Control	6011	Cofilin 2 (muscle)	gi|109939921,gi|115495595,gi|118572238,gi|164623755	18,719.30	99.80%	2	2	2	0.02%	18.70%	QILVGDIGDTVEDPYTSFVK	2.99	2,196.11
Control	6011	Cofilin 2 (muscle)	gi|109939921,gi|115495595,gi|118572238,gi|164623755	18,719.30	99.80%	2	2	2	0.02%	18.70%	YALYDATYETK	2.53	1,337.63
Control	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	14	125	0.98%	33.60%	AAYFGIYDTAK	4.01	1,219.60
Control	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	14	125	0.98%	33.60%	DFLAGGIAAAISK	5.37	1,233.68
Control	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	14	125	0.98%	33.60%	EQGVLSFWR	2.58	1,121.57

Control	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	14	125	0.98%	33.60%	GLYQGFNVSVQGIIIYR	2.63	1,927.04
Control	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	14	125	0.98%	33.60%	GMGGAFVLVLYDELK	4.27	1,627.84
Control	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	14	125	0.98%	33.60%	GMGGAFVLVLYDELKK	3.05	1,755.94
Control	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	14	125	0.98%	33.60%	LLLQVQHASK	2.8	1,136.68
Control	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	14	125	0.98%	33.60%	QIFLGGVDKR	1.84	1,132.65
Control	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	14	125	0.98%	33.60%	YFPTQALNFAFK	3.99	1,446.74
Control	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	14	125	0.98%	33.60%	YFPTQALNFAFKDK	3.69	1,689.86
Control	6011	PREDICTED: insulin-like growth factor 1 receptor	gi|119913553	135,693.80	100.00%	3	3	3	0.02%	5.23%	ELGQGSFGMVYEGVAK	2.66	1,687.80
Control	6011	PREDICTED: insulin-like growth factor 1 receptor	gi|119913553	135,693.80	100.00%	3	3	3	0.02%	5.23%	TEAEKQAEKEEAEYR	2.73	1,810.85
Control	6011	PREDICTED: insulin-like growth factor 1 receptor	gi|119913553	135,693.80	100.00%	3	3	3	0.02%	5.23%	VAGGLGVPGGGPSAQRPHTLPVPTVCPSACGK	2.91	2,967.53

Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	APLNVQFSSPGPGDAVK	4.23	1,683.87
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	FADEHVPGSPFTVK	3.49	1,530.76
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	FNDEHIPESPYVVPVIAPSDDAR	3.1	2,567.24
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	GAGIGGLGITVEGPSESK	4.48	1,628.85
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	GFQDGVYAFEYYPSTQGK	3.17	2,056.93
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	GLVEPVNVVDNGDGTHTVTYTPSQEGPYMVSVK	7.1	3,505.68
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	IVGPGLGSGVR	2.99	1,011.59

Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	LDVTILSPSR	3.21	1,100.63
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	LIALLEVLSQK	2.5	1,226.77
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	SPFEVQVGPEAGMQK	4.91	1,619.77
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	SPFTVGVAAPLDLSR	4.13	1,529.83
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	VLFASQEIPTSPFR	3.9	1,591.85
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	VNQPASFAIR	3.11	1,102.60
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	VSFAGDTIPK	2.54	1,034.55

Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	VSYFPTVPGVYIVSTK	3	1,756.95
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	VTASGPGLSTYGVPASLPVEFAIDAR	3.56	2,575.34
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	VTVLFAGQHISK	3.33	1,299.74
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	YGGELVPHFPTR	2.81	1,372.70
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	YMGSHIPESPLQFYVNYPNSGSVSAYGPGLVYGVANK	5.59	3,978.90
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	YMIGVTYGGDDIPLSPYR	3.64	2,032.97
Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	YNDKHIPGSPFTAK	2.96	1,574.80

Control	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	22	24	26	0.20%	14.50%	YTPTQQGNMQVLVTYGGDPIPK	3.52	2,423.19
Control	6011	septin 2	gi|114052905,gi|122069932,gi|84708845	41,554.10	99.80%	2	2	2	0.02%	8.86%	KVENEDMNKDQILLEK	3.41	1,961.99
Control	6011	septin 2	gi|114052905,gi|122069932,gi|84708845	41,554.10	99.80%	2	2	2	0.02%	8.86%	STLINSLFLTDLYPER	3.2	1,882.00
Control	6011	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	2	2	2	0.02%	9.84%	ADVGFAMGIAGTDVAK	4.08	1,538.75
Control	6011	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	2	2	2	0.02%	9.84%	EANHDGDFGITLAELR	3.55	1,757.85
Control	6011	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	2	2	2	0.02%	9.84%	EASDIILTDDNFTSIVK	2.96	1,880.95
Control	6011	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	2	2	2	0.02%	9.84%	IDESSLTGESDHVKK	3.29	1,644.81
Control	6011	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	2	2	2	0.02%	9.84%	KADVGFAMGIAGTDVAK	4.38	1,666.85
Control	6011	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	2	2	2	0.02%	9.84%	QVVAVTGDGTNDGPALKK	4.19	1,769.94
Control	6011	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	2	2	2	0.02%	9.84%	SLDKDPLLLSGTHVMEGSGR	4.23	2,128.07
Control	6011	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	2	2	2	0.02%	9.84%	YGDLLPADGILIQGNDLK	3.62	1,915.02

Control	6011	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	100.00%	7	7	7	0.05%	6.00%	IIGNLLYYR	3.28	1,124.65
Control	6011	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	100.00%	7	7	7	0.05%	6.00%	ILAIGLINEALDEGDAQK	2.84	1,883.01
Control	6011	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	100.00%	7	7	7	0.05%	6.00%	ILQSPALGLR	2.57	1,067.66
Control	6011	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	100.00%	7	7	7	0.05%	6.00%	TLINAEDPPMIVVR	3.91	1,583.85
Control	6011	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	100.00%	7	7	7	0.05%	6.00%	TLQALQIPAAK	3.02	1,153.69
Control	6011	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	100.00%	7	7	7	0.05%	6.00%	VNLLAALTNIDLALEQGSAPALFK	4.6	2,482.39
Control	6011	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	100.00%	7	7	7	0.05%	6.00%	YQELINDIAR	3.15	1,234.64

Control	6011	RecName: Full=Vesicle transport protein GOT1B; AltName: Full=Golgi transport 1 homolog B	gi|109939723,gi|114053223,gi|82571709	15,408.60	100.00%	3	3	5	0.04%	20.30%	RVPVLGSLLNLPGIR	3.59	1,604.00
Control	6011	RecName: Full=Vesicle transport protein GOT1B; AltName: Full=Golgi transport 1 homolog B	gi|109939723,gi|114053223,gi|82571709	15,408.60	100.00%	3	3	5	0.04%	20.30%	SFVDKVGESNNMV	4.31	1,441.66
Control	6011	RecName: Full=Vesicle transport protein GOT1B; AltName: Full=Golgi transport 1 homolog B	gi|109939723,gi|114053223,gi|82571709	15,408.60	100.00%	3	3	5	0.04%	20.30%	VPVLGSLLNLPGIR	4.07	1,447.90
Control	6011	UNC84B protein	gi|151553917,gi|156121283	81,429.80	100.00%	5	6	7	0.05%	7.42%	IRPTAVTLEHVPK	3.94	1,460.86
Control	6011	UNC84B protein	gi|151553917,gi|156121283	81,429.80	100.00%	5	6	7	0.05%	7.42%	LEGQLAGLR	2.79	956.5525
Control	6011	UNC84B protein	gi|151553917,gi|156121283	81,429.80	100.00%	5	6	7	0.05%	7.42%	LEGQLAGLRQELAALTLK	3.87	1,924.12
Control	6011	UNC84B protein	gi|151553917,gi|156121283	81,429.80	100.00%	5	6	7	0.05%	7.42%	MATYQVVELR	3.27	1,225.62
Control	6011	UNC84B protein	gi|151553917,gi|156121283	81,429.80	100.00%	5	6	7	0.05%	7.42%	SEHQQDSEDLFKK	2.33	1,590.74
Control	6011	heat shock protein beta-1	gi|71037405,gi|74354863,gi|85542053	22,375.10	100.00%	3	3	3	0.02%	20.40%	LFDQAFGLPR	3.51	1,163.62
Control	6011	heat shock protein beta-1	gi|71037405,gi|74354863,gi|85542053	22,375.10	100.00%	3	3	3	0.02%	20.40%	QLSSGVSEIQQTADR	4.48	1,618.80

Control	6011	heat shock protein beta-1	gi|71037405,gi|74354863,gi|85542053	22,375.10	100.00%	3	3	3	0.02%	20.40%	VSLDVNHFAPEELTVK	2.95	1,797.94
Control	6011	ribosomal protein L4	gi|61553010,gi|62460480,gi|73917531,gi|74267758	47,395.70	100.00%	4	5	6	0.05%	10.40%	APIRPDIVNFVHTNLR	2.52	1,862.04
Control	6011	ribosomal protein L4	gi|61553010,gi|62460480,gi|73917531,gi|74267758	47,395.70	100.00%	4	5	6	0.05%	10.40%	APIRPDIVNFVHTNLRK	2	1,990.13
Control	6011	ribosomal protein L4	gi|61553010,gi|62460480,gi|73917531,gi|74267758	47,395.70	100.00%	4	5	6	0.05%	10.40%	NIPGITLLNVSK	2.53	1,268.76
Control	6011	ribosomal protein L4	gi|61553010,gi|62460480,gi|73917531,gi|74267758	47,395.70	100.00%	4	5	6	0.05%	10.40%	PLISVYSEKGESSGK	2.33	1,580.82
Control	6011	PREDICTED: similar to carnitine palmitoyltransferase 1C	gi|194679924	80,680.30	100.00%	2	2	2	0.02%	3.81%	LPVPAVQDTVNR	2.84	1,308.73
Control	6011	PREDICTED: similar to carnitine palmitoyltransferase 1C	gi|194679924	80,680.30	100.00%	2	2	2	0.02%	3.81%	MTALAQDFAVNLGPR	4.38	1,619.82
Control	6011	PREDICTED: similar to ATP-dependent RNA helicase DDX3X (DEAD box protein 3, X-chromosomal) (Helicase-like protein 2) (HLP2) (DEAD box, X isoform) isoform 2	gi|119922075	73,112.60	100.00%	3	3	3	0.02%	7.72%	HVINFDLPSDIEEYVHR	4.52	2,083.02

Control	6011	PREDICTED: similar to ATP-dependent RNA helicase DDX3X (DEAD box protein 3, X-chromosomal) (Helicase-like protein 2) (HLP2) (DEAD box, X isoform) isoform 2	gi|119922075	73,112.60	100.00%	3	3	3	0.02%	7.72%	SFLLDLLNATGK	4.18	1,291.73
Control	6011	PREDICTED: similar to ATP-dependent RNA helicase DDX3X (DEAD box protein 3, X-chromosomal) (Helicase-like protein 2) (HLP2) (DEAD box, X isoform) isoform 2	gi|119922075	73,112.60	100.00%	3	3	3	0.02%	7.72%	TAAFLLPILSQIYSDGPGEALR	4.89	2,332.26
Control	6011	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	8	9	9	0.07%	12.50%	DGIIDFTPGSELLITK	3.33	1,718.92
Control	6011	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	8	9	9	0.07%	12.50%	FRENLIYTYIGPVLVSVNPYR	3.57	2,513.36
Control	6011	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	8	9	9	0.07%	12.50%	GAPVGGHILSYLLEK	3.7	1,553.87
Control	6011	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	8	9	9	0.07%	12.50%	GEELLSPLNLEQAAYAR	4.55	1,873.97

Control	6011	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	8	9	9	0.07%	12.50%	LLQSNPVLEAFGNAK	3.06	1,600.87
Control	6011	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	8	9	9	0.07%	12.50%	MSLLELVEILK	3.06	1,303.75
Control	6011	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	8	9	9	0.07%	12.50%	QLLLTPNAVVIVEDAK	3.81	1,723.00
Control	6011	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	8	9	9	0.07%	12.50%	VLQALGSEPIQYAVPVVK	3.54	1,911.10
Control	6011	PREDICTED: similar to Ras-interacting protein 1 isoform 2	gi|76642189	103,383.20	99.80%	2	2	2	0.02%	4.15%	DAVDTGDIFESFSSHPPLILPLGSSR	2.69	2,757.37
Control	6011	PREDICTED: similar to Ras-interacting protein 1 isoform 2	gi|76642189	103,383.20	99.80%	2	2	2	0.02%	4.15%	LSLTGPVTDDALHR	2.57	1,494.79
Control	6011	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	9	11	12	0.09%	11.80%	EDGSFSFYSLPSGGYTVIPFYR	3.37	2,489.17
Control	6011	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	9	11	12	0.09%	11.80%	FEQAFYTYDTSSPSILTLTAIR	3.29	2,524.26
Control	6011	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	9	11	12	0.09%	11.80%	FLLFSSLVTK	2.65	1,154.68
Control	6011	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	9	11	12	0.09%	11.80%	GQPLGPAGVQVSLR	3.53	1,378.78
Control	6011	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	9	11	12	0.09%	11.80%	ITFDVAPSR	3.08	1,005.54

Control	6011	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	9	11	12	0.09%	11.80%	SQYDFVLPQVSFTAAGYHK	2.41	2,158.06
Control	6011	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	9	11	12	0.09%	11.80%	SSIDSEPALVLGPLK	3.86	1,525.85
Control	6011	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	9	11	12	0.09%	11.80%	VLNGPEGEGVPDAVVTLNSQIK	3.96	2,236.18
Control	6011	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	9	11	12	0.09%	11.80%	VQVMVPEAETR	3.13	1,274.64
Control	6011	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	4	7	14	0.11%	39.40%	ADALQAGASQFETSAAK	4.21	1,665.81
Control	6011	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	4	7	14	0.11%	39.40%	LQQTQNQVDEVVDIMR	4.38	1,931.95
Control	6011	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	4	7	14	0.11%	39.40%	LSELDDRADALQAGASQFETSAAK	5.24	2,494.21
Control	6011	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	4	7	14	0.11%	39.40%	RLQQTQNQVDEVVDIMR	4.13	2,072.06
Control	6011	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	8	13	0.10%	25.50%	DKLSELQLR	2.59	1,101.63
Control	6011	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	8	13	0.10%	25.50%	EEYQPATPGLGMFVEVKDPEDK	2.27	2,495.17

Control	6011	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	8	13	0.10%	25.50%	FSLFAGGMLR	2.95	1,114.57
Control	6011	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	8	13	0.10%	25.50%	QLVEQVEQIQK	4.19	1,341.74
Control	6011	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	8	13	0.10%	25.50%	QLVEQVEQIQKEQNYQR	3.64	2,160.10
Control	6011	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	8	13	0.10%	25.50%	QREEYQPATPGLGMFVEVKDPEDK	4.41	2,779.32
Control	6011	PCDH1 protein	gi|134025143,gi|139947544	114,931.40	100.00%	3	3	3	0.02%	6.13%	NTGLITVQGPVDREDLSTLR	3.11	2,184.16
Control	6011	PCDH1 protein	gi|134025143,gi|139947544	114,931.40	100.00%	3	3	3	0.02%	6.13%	SPKPVKPVEDEDETGLQK	4.45	1,996.02
Control	6011	PCDH1 protein	gi|134025143,gi|139947544	114,931.40	100.00%	3	3	3	0.02%	6.13%	TLLETLLGHSLDTPLDIDIAGDPEYER	2.41	2,996.51
Control	6011	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	7	16	0.13%	31.20%	EFADSLGIPFLETSAK	4.09	1,724.87
Control	6011	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	7	16	0.13%	31.20%	KVVDYTTAKEFADSLGIPFLETSAK	3.09	2,730.42
Control	6011	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	7	16	0.13%	31.20%	LLLIGDSGVGK	3.38	1,071.64
Control	6011	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	7	16	0.13%	31.20%	LQIWDTAGQER	2.59	1,316.66
Control	6011	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	7	16	0.13%	31.20%	NATNVEQSFMTMAAEIK	3.01	1,900.88

Control	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	23	36	0.28%	33.80%	ALYETELADAR	2.92	1,251.62
Control	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	23	36	0.28%	33.80%	DQMQQQLNDYEQLLDVK	3.36	2,123.99
Control	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	23	36	0.28%	33.80%	FKAEHDQLLLNYAK	4.7	1,689.90
Control	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	23	36	0.28%	33.80%	IESLSSQLSNLQK	4.87	1,446.78
Control	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	23	36	0.28%	33.80%	IQELEDLLAK	3.1	1,171.66
Control	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	23	36	0.28%	33.80%	KLLEGEEERLK	2.99	1,343.75
Control	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	23	36	0.28%	33.80%	KNMYEEEINETR	2.18	1,571.70
Control	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	23	36	0.28%	33.80%	LAQALHEMREQHDAQVK	2.3	2,020.00
Control	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	23	36	0.28%	33.80%	LQEKEELRELNDR	2.84	1,671.87
Control	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	23	36	0.28%	33.80%	LREYEAALNSK	3.38	1,293.68
Control	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	23	36	0.28%	33.80%	LYKEELEQTYHAK	3.56	1,651.83
Control	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	23	36	0.28%	33.80%	MRIESLSSQLSNLQK	4.92	1,749.92
Control	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	23	36	0.28%	33.80%	NMYEEEINETR	3.57	1,443.61
Control	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	23	36	0.28%	33.80%	SLESDLEDLKDQIAQLEASLAAAK	5.66	2,558.32
Control	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	23	36	0.28%	33.80%	TTIPEEEEEEEAAEVAVEEELFHQQGAPR	4.19	3,425.55
Control	6011	RecName: Full=40S ribosomal protein S20	gi|108860955,gi|61822677,gi|73587131,gi|77735823	13,355.00	100.00%	2	3	3	0.02%	12.60%	DTGKTPVEPEVAIHR	4.89	1,648.87
Control	6011	RecName: Full=40S ribosomal protein S20	gi|108860955,gi|61822677,gi|73587131,gi|77735823	13,355.00	100.00%	2	3	3	0.02%	12.60%	TPVEPEVAIHR	4.45	1,247.67
Control	6011	RAB8A protein	gi|133778133,gi|157428086	23,667.60	99.80%	2	2	2	0.02%	17.90%	ANINVENAFYTLAR	3.53	1,595.82
Control	6011	RAB8A protein	gi|133778133,gi|157428086	23,667.60	99.80%	2	2	2	0.02%	17.90%	LLLIGDSGVGK	3.38	1,071.64

Control	6011	RAB8A protein	gi|133778133,gi|157428086	23,667.60	99.80%	2	2	2	0.02%	17.90%	NIEEHASADVEK	3.33	1,341.63
Control	6011	Syntaxin 5	gi|115304999,gi|115495735,gi|122132206	39,529.40	99.80%	2	2	2	0.02%	9.86%	APVSALPLAPNHLGGGAVVLGAESR	3.7	2,353.30
Control	6011	Syntaxin 5	gi|115304999,gi|115495735,gi|122132206	39,529.40	99.80%	2	2	2	0.02%	9.86%	QIAQLQDFVR	3.12	1,217.66
Control	6011	Interleukin enhancer binding factor 2, 45kDa	gi|83405442,gi|84000347	43,068.60	100.00%	5	5	5	0.04%	21.50%	ILPTLEAVAALGNK	3.4	1,409.84
Control	6011	Interleukin enhancer binding factor 2, 45kDa	gi|83405442,gi|84000347	43,068.60	100.00%	5	5	5	0.04%	21.50%	INNVIDNLIVAPGTFEVQIEEVR	3.91	2,582.38
Control	6011	Interleukin enhancer binding factor 2, 45kDa	gi|83405442,gi|84000347	43,068.60	100.00%	5	5	5	0.04%	21.50%	NQDLAPNSAEQASILSLVTK	5.34	2,099.10
Control	6011	Interleukin enhancer binding factor 2, 45kDa	gi|83405442,gi|84000347	43,068.60	100.00%	5	5	5	0.04%	21.50%	VKPAPDETSFSEALLKR	3.17	1,888.02
Control	6011	Interleukin enhancer binding factor 2, 45kDa	gi|83405442,gi|84000347	43,068.60	100.00%	5	5	5	0.04%	21.50%	VLQSALAAIR	2.97	1,041.64
Control	6011	RecName: Full=Cytochrome c oxidase polypeptide 7A2, mitochondrial; AltName: Full=Cytochrome c oxidase polypeptide VIIa-liver/heart; Short=Cytochrome c oxidase subunit VIIa-L; Short=VIIC; Flags: Precursor	gi|117120,gi|28461241,gi|488158,gi|74354141	9,305.40	99.80%	2	3	4	0.03%	27.70%	GGIADALLYR	3.14	1,048.58

Control	6011	RecName: Full=Cytochrome c oxidase polypeptide 7A2, mitochondrial; AltName: Full=Cytochrome c oxidase polypeptide VIIa-liver/heart; Short=Cytochrome c oxidase subunit VIIa-L; Short=VIIC; Flags: Precursor	gi|117120,gi|28461241,gi|488158,gi|74354141	9,305.40	99.80%	2	3	4	0.03%	27.70%	LFQEDNGIPVHLK	2.43	1,509.81
Control	6011	SLC25A24 protein	gi|148745486,gi|149642721,gi|167016553	53,268.40	100.00%	5	7	9	0.07%	22.60%	DSVNPGVMVLLGCGALSSTCGQLASYPLALVR	3	3,207.62
Control	6011	SLC25A24 protein	gi|148745486,gi|149642721,gi|167016553	53,268.40	100.00%	5	7	9	0.07%	22.60%	GYVPNLLGIIPYAGIDLAVYELLK	5.45	2,604.47
Control	6011	SLC25A24 protein	gi|148745486,gi|149642721,gi|167016553	53,268.40	100.00%	5	7	9	0.07%	22.60%	HSTGIDIGDSLTIPDEFTEDEKK	4.03	2,547.21
Control	6011	SLC25A24 protein	gi|148745486,gi|149642721,gi|167016553	53,268.40	100.00%	5	7	9	0.07%	22.60%	QLLAGGVAGAVSR	3.73	1,198.69
Control	6011	SLC25A24 protein	gi|148745486,gi|149642721,gi|167016553	53,268.40	100.00%	5	7	9	0.07%	22.60%	VLPAVGISYVVYENMK	2.46	1,797.95
Control	6011	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	5	7	12	0.09%	11.90%	ATTPVIMVGPGTGVAPFIGFIQER	4.54	2,474.31

Control	6011	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	5	7	12	0.09%	11.90%	GMAADPEEYDLADLSSLPEIEK	3.57	2,409.10
Control	6011	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	5	7	12	0.09%	11.90%	SYENQKPPFDAK	4	1,423.69
Control	6011	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	5	7	12	0.09%	11.90%	TALTYYLDITNPPR	3.09	1,637.85
Control	6011	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	5	7	12	0.09%	11.90%	YAVFALGNK	2.95	982.5356
Control	6011	TXNDC10 protein	gi|151554048,gi|156121223	51,713.50	99.80%	2	4	5	0.04%	6.83%	FQNYLTMDGFLLYELGDTGK	3.29	2,341.11
Control	6011	TXNDC10 protein	gi|151554048,gi|156121223	51,713.50	99.80%	2	4	5	0.04%	6.83%	TKDDIIEFAHR	4.37	1,344.69
Control	6011	MTCH1 protein	gi|154426180,gi|157074126	41,499.70	100.00%	6	6	7	0.05%	24.40%	KVLYLPSFFTYAK	3.59	1,576.88
Control	6011	MTCH1 protein	gi|154426180,gi|157074126	41,499.70	100.00%	6	6	7	0.05%	24.40%	LLIQVGHEPMPPTIGTNVLGR	2.65	2,258.23
Control	6011	MTCH1 protein	gi|154426180,gi|157074126	41,499.70	100.00%	6	6	7	0.05%	24.40%	LMSNALSTVTR	3.9	1,208.63

Control	6011	MTCH1 protein	gi|154426180,gi|157074126	41,499.70	100.00%	6	6	7	0.05%	24.40%	RMDGASGGLGSGDNAPTTEALFVALGAGVTALSHPLLYVK	3.43	3,930.01
Control	6011	MTCH1 protein	gi|154426180,gi|157074126	41,499.70	100.00%	6	6	7	0.05%	24.40%	VLYLPSFFTYAK	2.67	1,448.78
Control	6011	MTCH1 protein	gi|154426180,gi|157074126	41,499.70	100.00%	6	6	7	0.05%	24.40%	YSGVLSSIGK	2.53	1,010.55
Control	6011	RecName: Full=Histone H2A.V; AltName: Full=H2A.F/Z	gi|109940032,gi|163150,gi|27807373,gi|410,gi|81674301,gi|81674755,gi|83288407,gi|84000371	13,535.20	99.90%	2	6	6	0.05%	33.60%	ATIAGGGVIPHIHK	4.02	1,370.79
Control	6011	RecName: Full=Histone H2A.V; AltName: Full=H2A.F/Z	gi|109940032,gi|163150,gi|27807373,gi|410,gi|81674301,gi|81674755,gi|83288407,gi|84000371	13,535.20	99.90%	2	6	6	0.05%	33.60%	VGATAAVYSAAILEYLTAEVLELAGNASK	5.34	2,895.54
Control	6011	PREDICTED: vinculin isoform 1	gi|194679457,gi|194679459	123,848.10	99.80%	2	2	2	0.02%	3.79%	AIPDLTAPVAAVQAAVSNLVR	2.56	2,076.18
Control	6011	PREDICTED: vinculin isoform 1	gi|194679457,gi|194679459	123,848.10	99.80%	2	2	2	0.02%	3.79%	LLAVAATAPPDAPNREEVFDER	2.61	2,381.21
Control	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	14	17	0.13%	23.50%	ALEEAMEQKAELER	3.25	1,662.80
Control	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	14	17	0.13%	23.50%	ALEQQVEEMKTQLEELEDELQATEDAK	4.44	3,163.48
Control	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	14	17	0.13%	23.50%	ANLQIDQLNTDLNLER	4.29	1,869.97
Control	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	14	17	0.13%	23.50%	IAQLEEELEEEQGNTELVNDR	3.74	2,458.16
Control	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	14	17	0.13%	23.50%	IAQLEEQLDNETKER	4.52	1,815.91
Control	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	14	17	0.13%	23.50%	KFDQLLAEEK	3.08	1,220.65

Control	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	14	17	0.13%	23.50%	LKDVLLQVDDERR	2.53	1,598.89
Control	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	14	17	0.13%	23.50%	QAQQERDELADEIANSSGK	3.71	2,088.98
Control	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	14	17	0.13%	23.50%	RQLEEAEEEAQR	3.28	1,487.71
Control	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	14	17	0.13%	23.50%	TQLEELEDELQATEDAK	3.8	1,961.92
Control	6011	RecName: Full=T-complex protein 1 subunit delta; Short=TCP-1-delta; AltName: Full=CCT-delta	gi|115305839,gi|83406133,gi|84000361	58,190.00	100.00%	3	3	3	0.02%	10.70%	AFADAMEVIPSTLAENAGLNPISTVTELR	3.72	3,046.54
Control	6011	RecName: Full=T-complex protein 1 subunit delta; Short=TCP-1-delta; AltName: Full=CCT-delta	gi|115305839,gi|83406133,gi|84000361	58,190.00	100.00%	3	3	3	0.02%	10.70%	ALIAGGGAPEIELALR	3.77	1,550.89
Control	6011	RecName: Full=T-complex protein 1 subunit delta; Short=TCP-1-delta; AltName: Full=CCT-delta	gi|115305839,gi|83406133,gi|84000361	58,190.00	100.00%	3	3	3	0.02%	10.70%	VIDPATATSVDLR	2.91	1,357.73
Control	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	22	39	0.30%	36.50%	AASFLLALEPELEAR	4.33	1,629.88
Control	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	22	39	0.30%	36.50%	DTYIENEKLISGK	3.53	1,509.78
Control	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	22	39	0.30%	36.50%	ENLVEQHIQDIVVHYTFNK	4.73	2,326.18

Control	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	22	39	0.30%	36.50%	IDHILDAL	2.38	909.5042
Control	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	22	39	0.30%	36.50%	ISVIVEAVYTHVLQPYPTQITQSEK	3.6	2,843.52
Control	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	22	39	0.30%	36.50%	LPVALDPGAK	2.04	980.5777
Control	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	22	39	0.30%	36.50%	LVDHVFDEQVIDSLTVK	4.82	1,957.03
Control	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	22	39	0.30%	36.50%	NIQVDSPYEISR	3.46	1,420.71
Control	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	22	39	0.30%	36.50%	QFVVFEGNHYFYSPYPTK	3.21	2,223.05
Control	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	22	39	0.30%	36.50%	SEDLLDYGPFR	4.33	1,311.62
Control	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	22	39	0.30%	36.50%	THYIVGYNLPSYEYLYNLGDQYALK	4.4	2,997.47
Control	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	22	39	0.30%	36.50%	VHSENNSPFLTITSMTR	5	1,933.94
Control	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	22	39	0.30%	36.50%	VTAEVVLAHAGSGSSPR	4.01	1,637.86
Control	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	22	39	0.30%	36.50%	YDYQRQPDSGVSSVR	4.04	1,756.82
Control	6011	acyl-Coenzyme A dehydrogenase, very long chain isoform 1 precursor	gi|146231822,gi|160332360,gi|27806205,gi|74267810,gi|930358	70,632.20	100.00%	4	4	4	0.03%	9.92%	DIINEQFLLQR	3	1,388.75
Control	6011	acyl-Coenzyme A dehydrogenase, very long chain isoform 1 precursor	gi|146231822,gi|160332360,gi|27806205,gi|74267810,gi|930358	70,632.20	100.00%	4	4	4	0.03%	9.92%	GQLTTDQVFPYPSVLNEDQTQFLK	4.6	2,768.38
Control	6011	acyl-Coenzyme A dehydrogenase, very long chain isoform 1 precursor	gi|146231822,gi|160332360,gi|27806205,gi|74267810,gi|930358	70,632.20	100.00%	4	4	4	0.03%	9.92%	NPFGNAGLLLGEAGK	4.26	1,457.77

Control	6011	acyl-Coenzyme A dehydrogenase, very long chain isoform 1 precursor	gi|146231822,gi|160332360,gi|27806205,gi|74267810,gi|930358	70,632.20	100.00%	4	4	4	0.03%	9.92%	VPAENVLGEVGGGFK	4.81	1,472.77
Control	6011	PREDICTED: similar to ubiquitin-conjugating enzyme E2, J1 isoform 2	gi|194669972	35,073.60	99.80%	2	2	2	0.02%	10.10%	GPPDSDFDGGVYHGR	2.55	1,575.68
Control	6011	PREDICTED: similar to ubiquitin-conjugating enzyme E2, J1 isoform 2	gi|194669972	35,073.60	99.80%	2	2	2	0.02%	10.10%	SGSDSSQADQEAKELAR	2.99	1,778.82
Control	6011	RecName: Full=60S ribosomal protein L8	gi|108860941,gi|154426156,gi|74267654,gi|77736197	28,006.80	100.00%	4	4	5	0.04%	21.40%	AQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	3.27	3,169.57
Control	6011	RecName: Full=60S ribosomal protein L8	gi|108860941,gi|154426156,gi|74267654,gi|77736197	28,006.80	100.00%	4	4	5	0.04%	21.40%	ASGNYATVISHNPETK	4.32	1,688.82
Control	6011	RecName: Full=60S ribosomal protein L8	gi|108860941,gi|154426156,gi|74267654,gi|77736197	28,006.80	100.00%	4	4	5	0.04%	21.40%	ASGNYATVISHNPETKK	3.22	1,816.92
Control	6011	RecName: Full=60S ribosomal protein L8	gi|108860941,gi|154426156,gi|74267654,gi|77736197	28,006.80	100.00%	4	4	5	0.04%	21.40%	VVFRDPYR	1.32	1,051.57

Control	6011	PREDICTED: similar to Golgi integral membrane protein 4 (Golgi phosphoprotein 4) (Golgi integral membrane protein, cis) (GIMPc) (Golgi-localized phosphoprotein of 130 kDa) (Golgi phosphoprotein of 130 kDa) isoform 2	gi|76607797	81,272.00	100.00%	3	5	6	0.05%	5.48%	LREEQEALHQQR	3.05	1,536.79
Control	6011	PREDICTED: similar to Golgi integral membrane protein 4 (Golgi phosphoprotein 4) (Golgi integral membrane protein, cis) (GIMPc) (Golgi-localized phosphoprotein of 130 kDa) (Golgi phosphoprotein of 130 kDa) isoform 2	gi|76607797	81,272.00	100.00%	3	5	6	0.05%	5.48%	SALAAAQTQVAEYK	4.05	1,450.75

Control	6011	PREDICTED: similar to Golgi integral membrane protein 4 (Golgi phosphoprotein 4) (Golgi integral membrane protein, cis) (GIMPc) (Golgi-localized phosphoprotein of 130 kDa) (Golgi phosphoprotein of 130 kDa) isoform 2	gi|76607797	81,272.00	100.00%	3	5	6	0.05%	5.48%	YSALNVQHQMLK	3.64	1,447.74
Control	6011	Karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	gi|74354742,gi|77735853	57,908.80	100.00%	3	3	3	0.02%	9.83%	LLGATELPIVTPALR	3.09	1,563.95
Control	6011	Karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	gi|74354742,gi|77735853	57,908.80	100.00%	3	3	3	0.02%	9.83%	NKNPAPPLEAIEQILPTLVR	4	2,213.27
Control	6011	Karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	gi|74354742,gi|77735853	57,908.80	100.00%	3	3	3	0.02%	9.83%	NVSSFPDDATSPLQENR	3.58	1,876.87
Control	6011	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	6	8	9	0.07%	9.31%	ALTLGALTLPLAR	2.63	1,309.82
Control	6011	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	6	8	9	0.07%	9.31%	GEGSGTLGSLSLPLSELLVADR	4.89	2,171.16

Control	6011	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	6	8	9	0.07%	9.31%	LHVLEAQDLIAK	3.5	1,349.78
Control	6011	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	6	8	9	0.07%	9.31%	LLAETVAPAVR	3.01	1,139.68
Control	6011	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	6	8	9	0.07%	9.31%	LLVPLVPDLQDVAQLR	3.13	1,789.06
Control	6011	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	6	8	9	0.07%	9.31%	VQLDLAEIDLSQGAAQWYDLMDDKDKGSS	2.88	3,211.51
Control	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	11	14	14	0.11%	17.00%	ALLDSLQLGPDALTVHLINEVTK	2.26	2,460.37
Control	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	11	14	14	0.11%	17.00%	GLLNLEHQR	2.88	1,079.60
Control	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	11	14	14	0.11%	17.00%	KLVAIVDPHIK	3.6	1,232.77
Control	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	11	14	14	0.11%	17.00%	LKVTEGGEPYR	2.88	1,248.66
Control	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	11	14	14	0.11%	17.00%	LSFQHDPETSVLILR	4.28	1,754.94
Control	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	11	14	14	0.11%	17.00%	LVAIVDPHIK	2.04	1,104.68
Control	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	11	14	14	0.11%	17.00%	MALYGSVPVLLAHSPLR	3.47	1,840.02
Control	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	11	14	14	0.11%	17.00%	MLDYLQGSGETPQTDVR	4.22	1,925.89
Control	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	11	14	14	0.11%	17.00%	QYASLTGTQALPPLFSLGYHQSR	3.83	2,535.30

Control	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	11	14	14	0.11%	17.00%	VVIIGAGKPATVVLQTK	4.56	1,694.06
Control	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	11	14	14	0.11%	17.00%	YHGPQTLYLPVTLSSIPVFQR	2.62	2,416.30
Control	6011	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	4	4	4	0.03%	5.57%	DVIDKQHTEQEASYGR	3.62	1,875.88
Control	6011	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	4	4	4	0.03%	5.57%	LNQPQPDFTK	2.71	1,187.61
Control	6011	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	4	4	4	0.03%	5.57%	LVSIIAELLSTK	2.69	1,286.79
Control	6011	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	4	4	4	0.03%	5.57%	SFHSFYQLLQGGSDQMLR	4.21	2,130.01
Control	6011	Chromosome 20 open reading frame 3 ortholog	gi|74268319,gi|78369434	46,074.40	100.00%	3	4	6	0.05%	13.80%	GGADVFVENLPGFPDNIR	4.08	1,916.95
Control	6011	Chromosome 20 open reading frame 3 ortholog	gi|74268319,gi|78369434	46,074.40	100.00%	3	4	6	0.05%	13.80%	LFENQLVGPESIANIGDVMFTGTADGR	4.45	2,867.39
Control	6011	Chromosome 20 open reading frame 3 ortholog	gi|74268319,gi|78369434	46,074.40	100.00%	3	4	6	0.05%	13.80%	LLLSSETPIEGR	4.68	1,314.73
Control	6011	RecName: Full=Pyruvate dehydrogenase E1 component subunit beta, mitochondrial; Short=PDHE1-B; Flags: Precursor	gi|116242689,gi|151556071,gi|164420789	39,108.20	100.00%	3	3	4	0.03%	12.00%	EAINQGMDEELERDEK	2.18	1,921.84

Control	6011	RecName: Full=Pyruvate dehydrogenase E1 component subunit beta, mitochondrial; Short=PDHE1-B; Flags: Precursor	gi|116242689,gi|151556071,gi|164420789	39,108.20	100.00%	3	3	4	0.03%	12.00%	ILEDNSVPQVK	2.59	1,241.67
Control	6011	RecName: Full=Pyruvate dehydrogenase E1 component subunit beta, mitochondrial; Short=PDHE1-B; Flags: Precursor	gi|116242689,gi|151556071,gi|164420789	39,108.20	100.00%	3	3	4	0.03%	12.00%	IMEGPAFNFLDAPAVR	3.62	1,763.88
Control	6011	PREDICTED: similar to Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A	gi|119896006	130,855.40	100.00%	5	6	6	0.05%	5.94%	AEMLLDQYR	2.68	1,154.55

Control	6011	PREDICTED: similar to Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A	gi|119896006	130,855.40	100.00%	5	6	6	0.05%	5.94%	IQFGTLSDYFDALEK	2.87	1,746.86
Control	6011	PREDICTED: similar to Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A	gi|119896006	130,855.40	100.00%	5	6	6	0.05%	5.94%	TQYIFNNMVVK	3.37	1,372.69

Control	6011	PREDICTED: similar to Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A	gi|119896006	130,855.40	100.00%	5	6	6	0.05%	5.94%	TTVVLAPLGDDFR	3.41	1,403.75
Control	6011	PREDICTED: similar to Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A	gi|119896006	130,855.40	100.00%	5	6	6	0.05%	5.94%	YDLYNGNIANEGIFNMNNIK	3.72	2,333.09
Control	6011	RecName: Full=Mitochondrial fission factor	gi|122140919,gi|148744119,gi|73586594,gi|77735489	29,683.40	100.00%	4	5	6	0.05%	37.50%	IVVAGNNEDIPFSRPADLDLIQSTPFKPLALK	2.92	3,478.89
Control	6011	RecName: Full=Mitochondrial fission factor	gi|122140919,gi|148744119,gi|73586594,gi|77735489	29,683.40	100.00%	4	5	6	0.05%	37.50%	RLQLLEEENKER	4.26	1,556.84
Control	6011	RecName: Full=Mitochondrial fission factor	gi|122140919,gi|148744119,gi|73586594,gi|77735489	29,683.40	100.00%	4	5	6	0.05%	37.50%	VAPPNADLEQGFQEGVSNASVIMQVPER	2.94	2,998.46

Control	6011	RecName: Full=Mitochondrial fission factor	gi|122140919,gi|148744119,gi|73586594,gi|77735489	29,683.40	100.00%	4	5	6	0.05%	37.50%	VLTLSERPLDFLDLERPAPTPQNEEIR	5.08	3,148.66
Control	6011	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	5	16	0.13%	20.10%	DYPLPDVAHVK	2.62	1,253.65
Control	6011	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	5	16	0.13%	20.10%	FKESFAEMNR	3.92	1,274.58

Control	6011	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	5	16	0.13%	20.10%	SEDYALPSYVDR	3.66	1,414.65
Control	6011	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	5	16	0.13%	20.10%	SEDYALPSYVDRR	2.06	1,570.75
Control	6011	ERAP1 protein	gi|154425637,gi|156120653	107,090.40	99.80%	2	2	2	0.02%	2.55%	ASLINNAFQLVSIGK	3.46	1,574.89
Control	6011	ERAP1 protein	gi|154425637,gi|156120653	107,090.40	99.80%	2	2	2	0.02%	2.55%	TQEFPDILR	2.4	1,118.58
Control	6011	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	8	12	27	0.21%	15.00%	APVPTGEVYFADSFDR	4.34	1,770.83
Control	6011	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	8	12	27	0.21%	15.00%	IPNPDFFEDLEPFK	3.98	1,707.83
Control	6011	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	8	12	27	0.21%	15.00%	KIPNPDFFEDLEPFK	5.42	1,835.92
Control	6011	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	8	12	27	0.21%	15.00%	LPGDKGLVLMSR	2.97	1,301.72

Control	6011	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	8	12	27	0.21%	15.00%	TDAPQPDVKEDEEEKEEEK	3.39	2,245.00
Control	6011	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	8	12	27	0.21%	15.00%	TPELNLDQFHDK	4.06	1,456.71
Control	6011	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	8	12	27	0.21%	15.00%	TPELNLDQFHDKTPYTIMFGPDK	5.11	2,723.30
Control	6011	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	8	12	27	0.21%	15.00%	VTYKAPVPTGEVYFADSFDR	3.64	2,262.11
Control	6011	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	7	9	12	0.09%	23.60%	ELQQAVLQMEQR	3.64	1,488.75
Control	6011	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	7	9	12	0.09%	23.60%	KQQQQSHNNPAPGPEGQLK	3.16	2,086.04
Control	6011	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	7	9	12	0.09%	23.60%	LVTLEEFLASTQR	3.5	1,506.82
Control	6011	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	7	9	12	0.09%	23.60%	QFEHLDPQNQHTFEAR	2.87	1,996.93
Control	6011	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	7	9	12	0.09%	23.60%	TFFILHDINSDGVLDEQELEALFTK	3.53	2,894.45
Control	6011	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	7	9	12	0.09%	23.60%	YLESLGEEQRK	3.29	1,351.69
Control	6011	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	7	9	12	0.09%	23.60%	YLQEVINVLETDGHFR	4.06	1,932.98
Control	6011	nicalin	gi|115494944,gi|94534903	63,091.10	100.00%	3	3	3	0.02%	8.72%	AAQLVDKDGTFLSTLEHYLSR	6.57	2,364.22
Control	6011	nicalin	gi|115494944,gi|94534903	63,091.10	100.00%	3	3	3	0.02%	8.72%	ELETVAAHQFPEVR	4.36	1,625.83
Control	6011	nicalin	gi|115494944,gi|94534903	63,091.10	100.00%	3	3	3	0.02%	8.72%	MQQYDLQGQPYGTR	3.55	1,700.77
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	DDKESVPISDTIIPAVPPPTDLR	3.53	2,475.30
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	DLQFVEVTDVK	2.68	1,292.67

Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	GATYNIIVEAVK	2.99	1,277.71
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	GDSPASSKPVSINYR	4.25	1,577.79
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	GFNCESKPEPEETCFDKYTGNTYR	3.31	2,815.20
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	GLAFTDVDVDSIK	3.47	1,379.71
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	GLRPGVVYEGQLISVQHYGQR	5.08	2,356.25
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	KKTDELPQLVTLPHPNLHGPEILDVPSTVQK	2.77	3,443.89
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	NLQPGSEYAVSLVAVK	3.8	1,674.91
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	NSITLTNLNPGTEYVVSIVALNSK	4.16	2,547.37
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	NTFAEVTGLSPGVTYHFK	5.44	1,967.99
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	QYNVGPAASQYPLR	4.15	1,563.79
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	RPGAEPGNEGSTAHSYNQYSQR	4.9	2,406.08

Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	SSPVVIDASTAIDAPSNLR	2.87	1,913.00
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	SYTITGLQPGTDYK	3.69	1,543.76
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	TEIDKPSQMQVTDVQDNSISVR	4.71	2,506.21
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	TKTETITGFQVDAIPANGQTPIQR	3.42	2,586.35
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	TPFITNPGYDTGNGIQLPGTSGQQPSLGQQMIFEEHGFRR	2.93	4,392.11
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	VDVIPVNLPGEHGQR	3.97	1,629.87
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	VEYELSEEGDEPQYLDLPSTATSVNIPDLLPGRK	5.29	3,774.86
Control	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	27	37	0.29%	17.90%	VPGTSASATLTGLTR	4.23	1,431.78
Control	6011	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	6	7	15	0.12%	29.60%	KLPPLPLTLALGAFLNHR	2.02	1,971.19
Control	6011	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	6	7	15	0.12%	29.60%	KLPPLPLTLALGAFLNHRK	2.9	2,099.29
Control	6011	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	6	7	15	0.12%	29.60%	MQDTSVSFGYQLDLPK	3.82	1,844.87

Control	6011	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	6	7	15	0.12%	29.60%	QLSPTEAFPVLVGDMDNSGSLNAQVIHQLGPGLR	3.37	3,576.81
Control	6011	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	6	7	15	0.12%	29.60%	RPGEEGAVMSLAGK	3.51	1,417.71
Control	6011	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	6	7	15	0.12%	29.60%	YTLNNWLATVTLGQAGMHATYYHK	4.03	2,769.35
Control	6011	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	11	13	14	0.11%	12.70%	ADVGFAMGIAGTDVAK	4.08	1,538.75
Control	6011	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	11	13	14	0.11%	12.70%	EASDIILTDDNFTSIVK	2.96	1,880.95
Control	6011	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	11	13	14	0.11%	12.70%	GIIDSTVGDQR	3.24	1,160.59
Control	6011	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	11	13	14	0.11%	12.70%	IDESSLTGESDHVKK	3.29	1,644.81

Control	6011	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	11	13	14	0.11%	12.70%	KADVGFAMGIAGTDVAK	4.38	1,666.85
Control	6011	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	11	13	14	0.11%	12.70%	LKTNPVEGLSGNPADLEK	4.95	1,881.99
Control	6011	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	11	13	14	0.11%	12.70%	QVVAVTGDGTNDGPALKK	4.19	1,769.94
Control	6011	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	11	13	14	0.11%	12.70%	TNPVEGLSGNPADLEK	4.43	1,640.81
Control	6011	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	11	13	14	0.11%	12.70%	TPLLDEQEEEIFEK	3.24	1,719.83
Control	6011	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	11	13	14	0.11%	12.70%	TQDGVALEIQPLNSQEGIDSEEKEKK	4.03	2,885.44
Control	6011	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	11	13	14	0.11%	12.70%	YGDLLPADGILIQGNDLK	3.62	1,915.02

Control	6011	Calcium binding atopy-related autoantigen 1	gi|113912006,gi|115496574,gi|122142150	54,406.00	99.80%	2	2	2	0.02%	7.11%	GLTFQEVENFFTFLK	2.1	1,819.93
Control	6011	Calcium binding atopy-related autoantigen 1	gi|113912006,gi|115496574,gi|122142150	54,406.00	99.80%	2	2	2	0.02%	7.11%	VISEHGESEVFMTPQDFVR	3.34	2,223.04
Control	6011	PREDICTED: BCL2/adenovirus E1B 19kDa interacting protein 1 isoform 1	gi|194676367,gi|194676369	22,279.70	99.80%	2	2	2	0.02%	18.60%	ESLAQTSSAITESLMGISR	3.81	1,996.99
Control	6011	PREDICTED: BCL2/adenovirus E1B 19kDa interacting protein 1 isoform 1	gi|194676367,gi|194676369	22,279.70	99.80%	2	2	2	0.02%	18.60%	IQELEQSAKEQDKESEK	3.05	2,018.99
Control	6011	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	6	8	27	0.21%	57.70%	AGLQFPVGR	3	944.5313
Control	6011	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	6	8	27	0.21%	57.70%	HLQLAIR	2.19	850.5258
Control	6011	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	6	8	27	0.21%	57.70%	HLQLAIRNDEELNK	3.13	1,692.90
Control	6011	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	6	8	27	0.21%	57.70%	NDEELNKLLGK	3.51	1,272.68

Control	6011	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	6	8	27	0.21%	57.70%	VGAGAPVYLAAVLEYLTAEILELAGNAAR	6.5	2,915.59
Control	6011	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	6	8	27	0.21%	57.70%	VTIAQGGVLPNIQAVLLPK	5.62	1,931.17
Control	6011	RecName: Full=Proteasome subunit alpha type-1	gi|122140416,gi|74354782,gi|78369458	29,568.00	99.90%	2	3	4	0.03%	12.20%	FVFDRPLPVSR	2.78	1,332.74
Control	6011	RecName: Full=Proteasome subunit alpha type-1	gi|122140416,gi|74354782,gi|78369458	29,568.00	99.90%	2	3	4	0.03%	12.20%	KAQPTQPADEPAEKADEPMEH	4.04	2,335.05
Control	6011	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	100.00%	4	4	4	0.03%	12.40%	EIPVLVTQISSTNHPVK	5.09	1,862.04
Control	6011	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	100.00%	4	4	4	0.03%	12.40%	GSGHPAYAEVEPVGEK	3.3	1,626.78
Control	6011	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	100.00%	4	4	4	0.03%	12.40%	MLTATQYIAPLMANFDPSVSR	4.82	2,342.15
Control	6011	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	100.00%	4	4	4	0.03%	12.40%	VGLSDAFVVVHR	4.15	1,298.72
Control	6011	RecName: Full=OCIA domain-containing protein 2	gi|122140146,gi|74353966,gi|77735471	16,827.50	99.80%	2	2	3	0.02%	14.30%	FHSFEGQLR	2.89	1,120.55
Control	6011	RecName: Full=OCIA domain-containing protein 2	gi|122140146,gi|74353966,gi|77735471	16,827.50	99.80%	2	2	3	0.02%	14.30%	VALAGILGFGLGK	3.79	1,215.75

Control	6011	RecName: Full=Cathepsin D; Flags: Precursor	gi|13637914,gi|194679949,gi|299522	37,693.30	99.80%	2	2	2	0.02%	9.54%	AQPGGELMLGGTDSK	3.3	1,476.70
Control	6011	RecName: Full=Cathepsin D; Flags: Precursor	gi|13637914,gi|194679949,gi|299522	37,693.30	99.80%	2	2	2	0.02%	9.54%	QTFGEAIKQPGVVFIAAK	3.02	1,904.06
Control	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	16	23	43	0.34%	39.00%	ASLDRPFTSLESAFYSIVGLSSLGAQVPDVK	3.8	3,254.69
Control	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	16	23	43	0.34%	39.00%	EETVLATVQALQTASYLSQQADLR	4.38	2,635.36

Control	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	16	23	43	0.34%	39.00%	FELDTSER	2.4	996.4633
Control	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	16	23	43	0.34%	39.00%	FPEDDVPSTVLSK	3.01	1,433.72

Control	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	16	23	43	0.34%	39.00%	FSSGYYDFSVK	2.78	1,299.59
Control	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	16	23	43	0.34%	39.00%	ISTEVGITNVDLSTVDKDQSIAPK	4.6	2,530.33

Control	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	16	23	43	0.34%	39.00%	LDELGGVYLQFEEGLETTALFVAATYK	4.46	2,977.51
Control	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	16	23	43	0.34%	39.00%	LMDHVGTEPSIK	2.96	1,342.67

Control	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	16	23	43	0.34%	39.00%	LMDHVGTEPSIKEDQVIQLMNAIFSK	5.27	2,959.49
Control	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	16	23	43	0.34%	39.00%	LQVTNVLSQPLTQATVK	5.48	1,840.05

Control	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	16	23	43	0.34%	39.00%	LQVTNVLSQPLTQATVKLEHAK	2.83	2,418.37
Control	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	16	23	43	0.34%	39.00%	LSKEETVLATVQALQTASYLSQQADLR	6.11	2,963.57

Control	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	16	23	43	0.34%	39.00%	NFESLSEAFSVASAAAALSENR	3.08	2,271.09
Control	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	16	23	43	0.34%	39.00%	SIVEEIEDLVAR	3.53	1,372.73

Control	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	16	23	43	0.34%	39.00%	TGQEVVFVAEPDSK	4.83	1,505.75
Control	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	16	23	43	0.34%	39.00%	YIANTVELR	3.28	1,078.59

Control	6011	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	4	5	5	0.04%	16.00%	FGLGSIAGAVGATAVYPIDLVK	4.61	2,119.18
Control	6011	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	4	5	5	0.04%	16.00%	GLLPQLLGVAPEK	2.55	1,334.80
Control	6011	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	4	5	5	0.04%	16.00%	IAPLEEGTLPFNLAEAQR	4.45	1,969.04

Control	6011	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	4	5	5	0.04%	16.00%	LQVAGEITTGPR	3	1,241.69
Control	6011	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	4	5	5	0.04%	16.00%	LTVNDFVR	2.17	963.5258
Control	6011	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	4	5	5	0.04%	16.00%	TVELLSGVVDQTK	3.21	1,388.76

Control	6011	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	4	5	5	0.04%	16.00%	YEGFFGLYR	2.93	1,151.55
Control	6011	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	4	5	5	0.04%	16.00%	YLNIFGESQPNPK	3.51	1,506.76
Control	6011	BCL2-like 13 (apoptosis facilitator)	gi|115305268,gi|118151242	30,356.10	99.80%	2	2	2	0.02%	10.80%	APLLGALQTLLSRPVTYQAYR	3.13	2,331.32
Control	6011	BCL2-like 13 (apoptosis facilitator)	gi|115305268,gi|118151242	30,356.10	99.80%	2	2	2	0.02%	10.80%	ILVPLILLR	2.38	1,049.74
Control	6011	PREDICTED: interleukin enhancer binding factor 3, 90kDa isoform 2	gi|119894807	95,626.10	99.80%	2	2	2	0.02%	5.02%	GSSDHAESENVDVPAEDEGKEGAGEQK	3.72	2,771.19

Control	6011	PREDICTED: interleukin enhancer binding factor 3, 90kDa isoform 2	gi|119894807	95,626.10	99.80%	2	2	2	0.02%	5.02%	VLAGETLSVNDPPDVLDR	3.97	1,909.99
Control	6011	Synaptojanin 2 binding protein	gi|74354054,gi|78369420	15,792.00	99.80%	2	4	5	0.04%	19.30%	LQEGDKILSVNGQDLK	4.92	1,756.94
Control	6011	Synaptojanin 2 binding protein	gi|74354054,gi|78369420	15,792.00	99.80%	2	4	5	0.04%	19.30%	NLLHQDAVDLFR	3.62	1,440.76
Control	6011	ADPGK protein	gi|126010731,gi|126722892,gi|205686178	54,066.80	99.80%	2	2	3	0.02%	12.50%	FFSDKETFHDIAQVASEFPEAQHYVGGNAALIGQK	3.46	3,851.87
Control	6011	ADPGK protein	gi|126010731,gi|126722892,gi|205686178	54,066.80	99.80%	2	2	3	0.02%	12.50%	LLEVVTSISDIPTGVPVHLELASMTNK	3.27	2,879.54
Control	6011	Tumor protein D52-like 2	gi|74354962,gi|77736177	19,916.60	99.80%	2	2	2	0.02%	29.00%	GLLSDSMTDVPVDTAVAAQAPAVEGLTETEAEELRAELAK	5.41	4,114.04
Control	6011	Tumor protein D52-like 2	gi|74354962,gi|77736177	19,916.60	99.80%	2	2	2	0.02%	29.00%	TSAALSTMGSAISR	3.24	1,368.68
Control	6011	UBA1 protein	gi|126717459,gi|156523068,gi|182702190	117,813.30	100.00%	2	3	3	0.02%	2.84%	LAGTQPLEVLEAVQR	4.86	1,623.91
Control	6011	UBA1 protein	gi|126717459,gi|156523068,gi|182702190	117,813.30	100.00%	2	3	3	0.02%	2.84%	YDGQVAVFGSDLQER	3.17	1,683.80
Control	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	17	21	43	0.34%	25.40%	AGTQLLAGLR	2.91	999.5947
Control	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	17	21	43	0.34%	25.40%	FDLQIQSSNLFDK	4.48	1,554.78
Control	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	17	21	43	0.34%	25.40%	FDLQIQSSNLFDKVSPVVSYK	3.51	2,414.26
Control	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	17	21	43	0.34%	25.40%	FGSAIAPLGDLDQDGFNDIAIAAPYGGEDK	2.85	3,037.44
Control	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	17	21	43	0.34%	25.40%	FGSAIAPLGDLDQDGFNDIAIAAPYGGEDKK	5.09	3,165.54

Control	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	17	21	43	0.34%	25.40%	FSVHQQSEMDTSVK	4.52	1,638.74
Control	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	17	21	43	0.34%	25.40%	GALPTKLDFQVELLLDKLK	4.14	2,141.26
Control	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	17	21	43	0.34%	25.40%	GATDIDKNGYPDLIVGAFGVDR	4.48	2,293.15
Control	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	17	21	43	0.34%	25.40%	GIVYIFNGRPTGLNAVPSQILEGK	3.35	2,543.40
Control	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	17	21	43	0.34%	25.40%	IYIGDDNPLTLIVK	4.12	1,573.88
Control	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	17	21	43	0.34%	25.40%	MFLLVGAPK	3.58	991.5647
Control	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	17	21	43	0.34%	25.40%	PTGLNAVPSQILEGK	3.43	1,523.84
Control	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	17	21	43	0.34%	25.40%	RALFLHNR	2.61	1,026.60
Control	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	17	21	43	0.34%	25.40%	SSASFNVIEFPYK	3.3	1,488.74
Control	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	17	21	43	0.34%	25.40%	TAQAIFDDSYLGYSVAVGDFNGDGIDDFVSGVPR	3.66	3,567.66
Control	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	17	21	43	0.34%	25.40%	VRPPQEEQEREQLQPHENGEGNSET	2.32	2,917.33
Control	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	17	21	43	0.34%	25.40%	YKENPETEEDVGPVVQHIYELR	4.62	2,644.29
Control	6011	selenoprotein S	gi|144953869,gi|172045703,gi|86438358	21,367.70	99.80%	2	2	2	0.02%	17.90%	HLDQAAAALEPDIVVK	2.63	1,689.92
Control	6011	selenoprotein S	gi|144953869,gi|172045703,gi|86438358	21,367.70	99.80%	2	2	2	0.02%	17.90%	KPQEEDSPGPSTSVIPK	3.78	1,882.94
Control	6011	RecName: Full=Transaldolase	gi|110816439,gi|164420731,gi|83638723	37,668.70	99.80%	2	2	2	0.02%	11.30%	KLGGSQEEQITNAIDKLFVLFGAEILK	3.03	2,961.63
Control	6011	RecName: Full=Transaldolase	gi|110816439,gi|164420731,gi|83638723	37,668.70	99.80%	2	2	2	0.02%	11.30%	LSFDKDAMVAR	2.6	1,268.63
Control	6011	poly(A) binding protein, cytoplasmic 1	gi|41386798,gi|47117093,gi|74268035,gi|8979741	70,653.30	100.00%	3	3	3	0.02%	6.60%	ALDTMNFDVIK	2.23	1,282.64

Control	6011	poly(A) binding protein, cytoplasmic 1	gi|41386798,gi|47117093,gi|74268035,gi|8979741	70,653.30	100.00%	3	3	3	0.02%	6.60%	IVATKPLYVALAQR	3.31	1,542.94
Control	6011	poly(A) binding protein, cytoplasmic 1	gi|41386798,gi|47117093,gi|74268035,gi|8979741	70,653.30	100.00%	3	3	3	0.02%	6.60%	SLGYAYVNFQQPADAER	3.31	1,928.91
Control	6011	RecName: Full=Monocarboxylate transporter 1; Short=MCT 1; AltName: Full=Solute carrier family 16 member 1	gi|122139973,gi|77567740,gi|82617542	54,281.70	100.00%	3	3	3	0.02%	3.79%	GASDANTDLIGGNPK	3.72	1,429.69
Control	6011	RecName: Full=Monocarboxylate transporter 1; Short=MCT 1; AltName: Full=Solute carrier family 16 member 1	gi|122139973,gi|77567740,gi|82617542	54,281.70	100.00%	3	3	3	0.02%	3.79%	GASDANTDLIGGNPKEEK	4.23	1,815.87
Control	6011	RecName: Full=Monocarboxylate transporter 1; Short=MCT 1; AltName: Full=Solute carrier family 16 member 1	gi|122139973,gi|77567740,gi|82617542	54,281.70	100.00%	3	3	3	0.02%	3.79%	GASDANTDLIGGNPKEEKK	3.01	1,943.97
Control	6011	RecName: Full=L-lactate dehydrogenase B chain; Short=LDH-B	gi|118572666,gi|148744825,gi|154425698,gi|27806561,gi|59858383,gi|74353944,gi|8979739	36,679.70	100.00%	3	4	4	0.03%	10.80%	IVADKDYSVTANSK	3.03	1,510.77

Control	6011	RecName: Full=L-lactate dehydrogenase B chain; Short=LDH-B	gi|118572666,gi|148744825,gi|154425698,gi|27806561,gi|59858383,gi|74353944,gi|8979739	36,679.70	100.00%	3	4	4	0.03%	10.80%	LKDEEVAQLKK	3.37	1,300.75
Control	6011	RecName: Full=L-lactate dehydrogenase B chain; Short=LDH-B	gi|118572666,gi|148744825,gi|154425698,gi|27806561,gi|59858383,gi|74353944,gi|8979739	36,679.70	100.00%	3	4	4	0.03%	10.80%	MVVESAYEVIK	2.75	1,283.66
Control	6011	PREDICTED: similar to armadillo repeat containing, X-linked 3	gi|119922567	42,522.80	99.80%	2	2	2	0.02%	7.92%	ASPNSDDTILSPQELQK	2.98	1,842.91
Control	6011	PREDICTED: similar to armadillo repeat containing, X-linked 3	gi|119922567	42,522.80	99.80%	2	2	2	0.02%	7.92%	LLLNLAENPAMTR	4.23	1,471.79
Control	6011	PREDICTED: similar to programmed cell death 6 interacting protein isoform 1	gi|119914274	96,862.00	100.00%	5	5	5	0.04%	7.20%	LLDEEEATDNDLR	4.66	1,532.71
Control	6011	PREDICTED: similar to programmed cell death 6 interacting protein isoform 1	gi|119914274	96,862.00	100.00%	5	5	5	0.04%	7.20%	MVPVSVQQSLAAYNQR	4.14	1,806.92
Control	6011	PREDICTED: similar to programmed cell death 6 interacting protein isoform 1	gi|119914274	96,862.00	100.00%	5	5	5	0.04%	7.20%	NIQVSHQEFSK	3.44	1,316.66
Control	6011	PREDICTED: similar to programmed cell death 6 interacting protein isoform 1	gi|119914274	96,862.00	100.00%	5	5	5	0.04%	7.20%	STPVNVPISQK	2.52	1,169.65

Control	6011	PREDICTED: similar to programmed cell death 6 interacting protein isoform 1	gi|119914274	96,862.00	100.00%	5	5	5	0.04%	7.20%	TMQGSEVVNVLK	3.4	1,320.68
Control	6011	ACTR2 protein	gi|154425680,gi|156121073,gi|17943200,gi|182627520,gi|56966173,gi|56966193	44,743.70	99.80%	2	2	2	0.02%	12.20%	DLMVGDEASELR	3.03	1,350.62
Control	6011	ACTR2 protein	gi|154425680,gi|156121073,gi|17943200,gi|182627520,gi|56966173,gi|56966193	44,743.70	99.80%	2	2	2	0.02%	12.20%	FEAPEALFQPHLINVEGVGVAELLFNTIQAADIDTR	4.55	3,938.03
Control	6011	Sec61 alpha 1 subunit (S. cerevisiae)	gi|154426140,gi|59857767,gi|75060961,gi|94966817	52,208.90	100.00%	6	7	21	0.16%	21.60%	FLEVIKPFCVILPEIQKPER	4.51	2,398.36
Control	6011	Sec61 alpha 1 subunit (S. cerevisiae)	gi|154426140,gi|59857767,gi|75060961,gi|94966817	52,208.90	100.00%	6	7	21	0.16%	21.60%	GMEFEGAIIALFHLLATR	3.96	2,005.06
Control	6011	Sec61 alpha 1 subunit (S. cerevisiae)	gi|154426140,gi|59857767,gi|75060961,gi|94966817	52,208.90	100.00%	6	7	21	0.16%	21.60%	GQYNTYPIKLFYTSNIPIILQSALVSNLYVISQMLSAR	4.26	4,335.31
Control	6011	Sec61 alpha 1 subunit (S. cerevisiae)	gi|154426140,gi|59857767,gi|75060961,gi|94966817	52,208.90	100.00%	6	7	21	0.16%	21.60%	GTLMELGISPIVTSGLIMQLLAGAK	4.65	2,529.40
Control	6011	Sec61 alpha 1 subunit (S. cerevisiae)	gi|154426140,gi|59857767,gi|75060961,gi|94966817	52,208.90	100.00%	6	7	21	0.16%	21.60%	LFYTSNIPIILQSALVSNLYVISQMLSAR	5.86	3,270.78
Control	6011	Sec61 alpha 1 subunit (S. cerevisiae)	gi|154426140,gi|59857767,gi|75060961,gi|94966817	52,208.90	100.00%	6	7	21	0.16%	21.60%	YRGQYNTYPIK	4.04	1,402.71

Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	AVDSLVPIGR	3.09	1,026.59
Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	EAYPGDVFYLHSR	2.44	1,553.74
Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	EVAAFAQFGSDLDAATQQLLSR	4.45	2,338.17
Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	FENAFLSHVISQHQALLSK	4.15	2,169.15
Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	GIRPAINVGLSVSR	3.02	1,438.85
Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	GMSLNLEPDNVGVVVFGNDK	4.98	2,120.03

Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	GYLDKLEPSK	2.76	1,149.62
Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	HALIIYDDLSK	3.4	1,287.69
Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	ILGADTSVDLEETGR	4.82	1,575.79
Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	ISVREPMQTGIK	2.67	1,374.74
Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	ITKFENAFLSHVISQHQALLSK	2.89	2,511.37
Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	LKEIVTNFLAGFEA	4.36	1,551.84

Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	QGQYSPMAIEEQVAVIYAGVR	3.51	2,325.15
Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	QVAGTMKLELAQYR	2.6	1,607.86
Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	TGAIDVPVGEELLGR	4.48	1,624.89
Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	TGTAEVSSILEER	3.98	1,391.70
Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	TSIAIDTIINQK	3.21	1,316.74
Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	VGLKAPGIIPR	3.67	1,120.72

Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	VLSIGDGIAR	2.67	1,000.58
Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	VVDALGNAIDGK	3.69	1,171.63
Control	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	27	58	0.45%	54.50%	VVDALGNAIDGKGPIGSK	4.91	1,710.94
Control	6011	PREDICTED: similar to 60S ribosomal protein L9	gi|119904384,gi|119905715,gi|164420694,gi|76607197,gi|91207745	21,858.70	99.80%	2	2	2	0.02%	15.10%	FLDGIYVSEK	3.14	1,170.60
Control	6011	PREDICTED: similar to 60S ribosomal protein L9	gi|119904384,gi|119905715,gi|164420694,gi|76607197,gi|91207745	21,858.70	99.80%	2	2	2	0.02%	15.10%	TILSNQTVDIPENVDINLK	4.28	2,126.13
Control	6011	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	9	16	0.13%	41.40%	IMVANIEEVLQR	4.72	1,430.77
Control	6011	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	9	16	0.13%	41.40%	IMVANIEEVLQRGEALSALDSK	2.93	2,402.26
Control	6011	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	9	16	0.13%	41.40%	KLAFAYLEDLHSEFDEQHGK	4.74	2,377.15

Control	6011	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	9	16	0.13%	41.40%	NLGSINTELQDVQR	5.03	1,586.81
Control	6011	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	9	16	0.13%	41.40%	VADGLPLAASMQEDEQSGR	3.8	1,989.92
Control	6011	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	9	16	0.13%	41.40%	VADGLPLAASMQEDEQSGRDLQQYQSQAK	2.8	3,179.49
Control	6011	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	9	16	0.13%	41.40%	VPTVSRPYSFIEFDTYIQK	3.59	2,290.18
Control	6011	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	5	7	11	0.09%	27.20%	INVNEIFYDLVR	3.14	1,494.80
Control	6011	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	5	7	11	0.09%	27.20%	LVVLGSGGVGK	3.05	985.6042
Control	6011	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	5	7	11	0.09%	27.20%	SKINVNEIFYDLVR	4.07	1,709.92
Control	6011	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	5	7	11	0.09%	27.20%	VKDTDDVPMILVGNK	3.92	1,659.86
Control	6011	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	5	7	11	0.09%	27.20%	YDPTIEDSYR	2.82	1,258.56
Control	6011	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	5	6	8	0.06%	15.10%	DKVQSDSGSLDSTIPGIENTITVTTEQVTTASFPVGSK	2.87	3,909.95
Control	6011	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	5	6	8	0.06%	15.10%	EEAAAAAPAPAADDQGVLK	3.33	1,794.89
Control	6011	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	5	6	8	0.06%	15.10%	KREEAAAAAPAPAADDQGVLK	4.47	2,079.08
Control	6011	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	5	6	8	0.06%	15.10%	TISTSDPADALIK	3.22	1,331.71
Control	6011	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	5	6	8	0.06%	15.10%	TLPPAISTEPSVILSK	3.11	1,652.95

Control	6011	RecName: Full=Aconitate hydratase, mitochondrial; Short=Aconitase; AltName: Full=Citrate hydro-lyase; Flags: Precursor	gi|110282935,gi|1364216,gi|27806769,gi|74268076,gi|90970312	85,342.00	100.00%	3	3	3	0.02%	7.56%	AEFDPGQDTYQHPPKDSSGQQVDVSPTSQR	4.01	3,301.50
Control	6011	RecName: Full=Aconitate hydratase, mitochondrial; Short=Aconitase; AltName: Full=Citrate hydro-lyase; Flags: Precursor	gi|110282935,gi|1364216,gi|27806769,gi|74268076,gi|90970312	85,342.00	100.00%	3	3	3	0.02%	7.56%	FKLEAPDADELPR	4.65	1,500.77
Control	6011	RecName: Full=Aconitate hydratase, mitochondrial; Short=Aconitase; AltName: Full=Citrate hydro-lyase; Flags: Precursor	gi|110282935,gi|1364216,gi|27806769,gi|74268076,gi|90970312	85,342.00	100.00%	3	3	3	0.02%	7.56%	IVYGHLDDPANQEIER	4.2	1,868.91
Control	6011	PREDICTED: similar to Import inner membrane translocase subunit TIM44, mitochondrial	gi|119894845	51,429.40	100.00%	2	2	2	0.02%	6.17%	TEMSEVLTEILR	3.1	1,436.73

Control	6011	PREDICTED: similar to Import inner membrane translocase subunit TIM44, mitochondrial	gi|119894845	51,429.40	100.00%	2	2	2	0.02%	6.17%	VLTDKVTDLLGGLFSK	3.21	1,705.97
Control	6011	RecName: Full=ATP synthase subunit g, mitochondrial; Short=ATPase subunit g	gi|2493093,gi|74354012,gi|7579922,gi|94400870	11,604.00	100.00%	3	4	7	0.05%	33.70%	APALVNAAVTYSKPR	3.81	1,557.87
Control	6011	RecName: Full=ATP synthase subunit g, mitochondrial; Short=ATPase subunit g	gi|2493093,gi|74354012,gi|7579922,gi|94400870	11,604.00	100.00%	3	4	7	0.05%	33.70%	VELVPPTPAEIPTAIQSLK	3.06	2,003.14
Control	6011	RecName: Full=ATP synthase subunit g, mitochondrial; Short=ATPase subunit g	gi|2493093,gi|74354012,gi|7579922,gi|94400870	11,604.00	100.00%	3	4	7	0.05%	33.70%	VELVPPTPAEIPTAIQSLKK	3.01	2,131.24

Control	6011	RecName: Full=Heat shock protein 75 kDa, mitochondrial; Short=HSP 75; AltName: Full=Tumor necrosis factor type 1 receptor-associated protein; Short=TRAP-1; AltName: Full=TNFR-associated protein	gi|110287991,gi|83759104,gi|84579841	79,365.10	99.80%	2	2	2	0.02%	5.97%	AFLDALQNQAEAGSK	4.25	1,562.78
Control	6011	RecName: Full=Heat shock protein 75 kDa, mitochondrial; Short=HSP 75; AltName: Full=Tumor necrosis factor type 1 receptor-associated protein; Short=TRAP-1; AltName: Full=TNFR-associated protein	gi|110287991,gi|83759104,gi|84579841	79,365.10	99.80%	2	2	2	0.02%	5.97%	AQLLQPTLEINPR	2.66	1,492.85

Control	6011	RecName: Full=Heat shock protein 75 kDa, mitochondrial; Short=HSP 75; AltName: Full=Tumor necrosis factor type 1 receptor-associated protein; Short=TRAP-1; AltName: Full=TNFR-associated protein	gi|110287991,gi|83759104,gi|84579841	79,365.10	99.80%	2	2	2	0.02%	5.97%	GVVDSEDIPLNLSR	4.24	1,513.79
Control	6011	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	100.00%	3	3	4	0.03%	13.60%	VADPAYLPTQQDVLR	3.61	1,685.89
Control	6011	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	100.00%	3	3	4	0.03%	13.60%	VRVPTTGIIEYPFDLQSVIFR	4.24	2,450.34
Control	6011	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	100.00%	3	3	4	0.03%	13.60%	VSAFENPYVDAIK	3.41	1,452.74
Control	6011	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	100.00%	3	3	3	0.02%	6.25%	LPVPASAPIPFFHR	4.47	1,548.87
Control	6011	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	100.00%	3	3	3	0.02%	6.25%	NAELEAIPNSGMDHTHR	2.62	1,907.87

Control	6011	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	100.00%	3	3	3	0.02%	6.25%	VLMEFVENSR	3.56	1,239.60
Control	6011	RecName: Full=60S ribosomal protein L7a	gi|108860939,gi|146231828,gi|83638795,gi|94966839	30,008.40	99.80%	2	2	4	0.03%	10.20%	LKVPPAINQFTQALDR	5.42	1,811.02
Control	6011	RecName: Full=60S ribosomal protein L7a	gi|108860939,gi|146231828,gi|83638795,gi|94966839	30,008.40	99.80%	2	2	4	0.03%	10.20%	NFGIGQDIQPK	3.31	1,216.63
Control	6011	RecName: Full=Transgelin; AltName: Full=Smooth muscle protein 22-alpha; Short=SM22-alpha; AltName: Full=25 kDa F-actin-binding protein	gi|109940320,gi|114051586,gi|86823808	22,580.80	99.80%	2	2	2	0.02%	11.90%	EFTESQLQEGK	2.81	1,295.61
Control	6011	RecName: Full=Transgelin; AltName: Full=Smooth muscle protein 22-alpha; Short=SM22-alpha; AltName: Full=25 kDa F-actin-binding protein	gi|109940320,gi|114051586,gi|86823808	22,580.80	99.80%	2	2	2	0.02%	11.90%	TDMFQTVDLFEGK	2.91	1,546.71

Control	6011	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	5	7	7	0.05%	18.20%	DIETFYNTSIEEMPLNVADLI	2.79	2,443.16
Control	6011	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	5	7	7	0.05%	18.20%	GFKDQIYDIFQK	3.64	1,501.77
Control	6011	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	5	7	7	0.05%	18.20%	GIYAYGFEKPSAIQQR	4.61	1,827.94

Control	6011	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	5	7	7	0.05%	18.20%	LQMEAPHIIVGTPGR	3.53	1,634.87
Control	6011	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	5	7	7	0.05%	18.20%	VLITTDLLAR	3.41	1,114.68
Control	6011	RecName: Full=Mitochondrial Rho GTPase 1; Short=MIRO-1; AltName: Full=Ras homolog gene family member T1	gi|108860795,gi|114051724,gi|88682961	72,061.70	100.00%	6	7	9	0.07%	11.10%	FGYDDDLDLTPEYLFPLLK	2.56	2,274.12

Control	6011	RecName: Full=Mitochondrial Rho GTPase 1; Short=MIRO-1; AltName: Full=Ras homolog gene family member T1	gi|108860795,gi|114051724,gi|88682961	72,061.70	100.00%	6	7	9	0.07%	11.10%	ISDQDNDGTLNDAELNFFQR	4.4	2,312.04
Control	6011	RecName: Full=Mitochondrial Rho GTPase 1; Short=MIRO-1; AltName: Full=Ras homolog gene family member T1	gi|108860795,gi|114051724,gi|88682961	72,061.70	100.00%	6	7	9	0.07%	11.10%	LPLILVGNK	2.69	966.6348
Control	6011	RecName: Full=Mitochondrial Rho GTPase 1; Short=MIRO-1; AltName: Full=Ras homolog gene family member T1	gi|108860795,gi|114051724,gi|88682961	72,061.70	100.00%	6	7	9	0.07%	11.10%	NISELFYYAQK	3.4	1,375.69
Control	6011	RecName: Full=Mitochondrial Rho GTPase 1; Short=MIRO-1; AltName: Full=Ras homolog gene family member T1	gi|108860795,gi|114051724,gi|88682961	72,061.70	100.00%	6	7	9	0.07%	11.10%	RFGYDDDLDLTPEYLFPLLK	3.31	2,430.22

Control	6011	RecName: Full=Mitochondrial Rho GTPase 1; Short=MIRO-1; AltName: Full=Ras homolog gene family member T1	gi|108860795,gi|114051724,gi|88682961	72,061.70	100.00%	6	7	9	0.07%	11.10%	SGVLQALLGR	2.9	1,013.61
Control	6011	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	12	15	0.12%	27.20%	DVYVQLYLQHLTAR	4.09	1,718.92
Control	6011	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	12	15	0.12%	27.20%	GPPDFSSDEEREPTPVLGSGAAVAGR	5.86	2,598.24
Control	6011	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	12	15	0.12%	27.20%	HAAPILPITEFSDIPR	3.91	1,776.96
Control	6011	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	12	15	0.12%	27.20%	LKSELVANNVTLPAGEQR	5.59	1,939.06
Control	6011	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	12	15	0.12%	27.20%	LKSELVANNVTLPAGEQRK	4.39	2,067.16
Control	6011	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	12	15	0.12%	27.20%	SELVANNVTLPAGEQR	4.08	1,697.88
Control	6011	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	12	15	0.12%	27.20%	SSTPLPTISSSVENTR	3.43	1,675.85
Control	6011	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	12	15	0.12%	27.20%	YGVNPGPIVGTTR	2.71	1,330.71
Control	6011	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	12	13	14	0.11%	7.83%	ALSTDPAAPTLK	2.53	1,184.65
Control	6011	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	12	13	14	0.11%	7.83%	AVSSAIAQLLGEVAQGNENYAGIAAR	4.01	2,573.33
Control	6011	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	12	13	14	0.11%	7.83%	GLAGAVSELLR	3.41	1,085.63
Control	6011	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	12	13	14	0.11%	7.83%	GVGAAATAVTQALNELLQHVR	4.27	2,119.16
Control	6011	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	12	13	14	0.11%	7.83%	LAQAAQSSVATITR	3.63	1,416.78
Control	6011	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	12	13	14	0.11%	7.83%	LNEAAAGLNQAATELVQASR	2.68	2,027.05
Control	6011	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	12	13	14	0.11%	7.83%	NLGTALAELR	2.56	1,057.60

Control	6011	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	12	13	14	0.11%	7.83%	QAAASATQTIAAAQHATSTPK	3	2,025.04
Control	6011	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	12	13	14	0.11%	7.83%	TLSHPQQMALLDQTK	4.05	1,726.88
Control	6011	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	12	13	14	0.11%	7.83%	TMLESAGGLIQTAR	3.38	1,463.75
Control	6011	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	12	13	14	0.11%	7.83%	VLGEAMTGISQNAK	3.83	1,434.73
Control	6011	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	12	13	14	0.11%	7.83%	VSQMAQYFEPLTLAAVGAASK	4.27	2,198.12
Control	6011	TMEM214 protein	gi|133778127,gi|134085813,gi|205830924	77,001.60	99.90%	2	3	3	0.02%	4.95%	SLSPFAIAYLDR	3.39	1,352.72
Control	6011	TMEM214 protein	gi|133778127,gi|134085813,gi|205830924	77,001.60	99.90%	2	3	3	0.02%	4.95%	VLAFGAKPESTLHTYFPSFLSR	4.23	2,468.30
Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	DLGLFGLYK	2.21	1,025.57
Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	FGLYLPK	2.67	837.487
Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	FKPPSVAVVQPK	3.24	1,296.77
Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	FTLGSVAGAVGATAVYPIDLVK	4.01	2,149.19
Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	GLIPQLIGVAPEK	2.55	1,334.80
Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	GTGSVVGELMYK	3	1,256.62
Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	HLNYTEFTQFLQELQLEHAR	6.02	2,517.25
Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	IAPLAEGALPYNLAELQR	3.6	1,939.06
Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	IVQLLAGVADQTK	3.88	1,355.79
Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	KIYSTLAGTR	3.06	1,109.63
Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	LQVAGEITTGPR	3	1,241.69
Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	LTLADIER	2.33	930.5256
Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	LTVNDFVR	2.17	963.5258

Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	NIFLQYASTEVDGEHYMTPEDFVQR	4.43	3,005.36
Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	VSALNVLR	2.41	871.5359
Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	YEGFFGLYR	2.93	1,151.55
Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	YGQVTPLEIDILYQLSDLYNATGR	4.52	2,742.40
Control	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	18	19	25	0.20%	36.00%	YLGLYNDPNSNPK	3.66	1,494.72
Control	6011	RecName: Full=Electron transfer flavoprotein subunit alpha, mitochondrial; Short=Alpha-ETF; Flags: Precursor	gi|110808222,gi|115496196,gi|86823828	34,944.00	99.80%	2	3	3	0.02%	8.71%	GLLPEELTPLILATQK	2.84	1,736.02
Control	6011	RecName: Full=Electron transfer flavoprotein subunit alpha, mitochondrial; Short=Alpha-ETF; Flags: Precursor	gi|110808222,gi|115496196,gi|86823828	34,944.00	99.80%	2	3	3	0.02%	8.71%	LDVAPISDIIAIK	2.83	1,367.81
Control	6011	RecName: Full=Cytochrome b5	gi|117806,gi|1372997,gi|157830773,gi|27806667,gi|298,gi|79160196	15,311.60	100.00%	2	2	2	0.02%	25.40%	EQAGGDATENFEDVGHSTDAR	3.1	2,205.93
Control	6011	RecName: Full=Cytochrome b5	gi|117806,gi|1372997,gi|157830773,gi|27806667,gi|298,gi|79160196	15,311.60	100.00%	2	2	2	0.02%	25.40%	FLEEHPGGEEVLR	2.21	1,511.75
Control	6011	ALDH3A2 protein	gi|151557095,gi|156120617	54,059.30	100.00%	4	4	4	0.03%	10.30%	EKDILAAIGADLSK	3.39	1,443.81

Control	6011	ALDH3A2 protein	gi|151557095,gi|156120617	54,059.30	100.00%	4	4	4	0.03%	10.30%	HLTPVTLELGGK	2.92	1,264.73
Control	6011	ALDH3A2 protein	gi|151557095,gi|156120617	54,059.30	100.00%	4	4	4	0.03%	10.30%	IAFGGEMDEATR	2.71	1,312.58
Control	6011	ALDH3A2 protein	gi|151557095,gi|156120617	54,059.30	100.00%	4	4	4	0.03%	10.30%	NADEAIQFINER	3.44	1,419.69
Control	6011	IKK interacting protein	gi|126010633,gi|126165284,gi|193806036	39,199.60	99.80%	2	2	2	0.02%	6.59%	LEPLVNDLTLR	2.76	1,282.74
Control	6011	IKK interacting protein	gi|126010633,gi|126165284,gi|193806036	39,199.60	99.80%	2	2	2	0.02%	6.59%	METSEFQGLQSK	3.87	1,400.64
Control	6011	defender against cell death 1	gi|59858361,gi|73918963,gi|74354770,gi|77736467,gi|83286811	12,477.50	99.80%	2	2	5	0.04%	19.50%	ADFQGISPER	3.07	1,119.54
Control	6011	defender against cell death 1	gi|59858361,gi|73918963,gi|74354770,gi|77736467,gi|83286811	12,477.50	99.80%	2	2	5	0.04%	19.50%	FLEEYLSATPQR	3	1,453.73
Control	6011	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	14	16	18	0.14%	19.70%	ALGYFAVVTGK	3.1	1,125.63
Control	6011	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	14	16	18	0.14%	19.70%	DFFTTGSPGETAFR	2.96	1,532.70
Control	6011	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	14	16	18	0.14%	19.70%	EFDLTKEEDLAALR	3.48	1,649.84
Control	6011	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	14	16	18	0.14%	19.70%	ESVEQQADSFK	3.64	1,267.58
Control	6011	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	14	16	18	0.14%	19.70%	EVLEDFAEDSEK	3.01	1,410.63

Control	6011	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	14	16	18	0.14%	19.70%	GNSSESIEAIRDYEEEFFQNSK	4.05	2,579.15
Control	6011	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	14	16	18	0.14%	19.70%	IDQLQEELLHTQLK	2.85	1,707.93
Control	6011	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	14	16	18	0.14%	19.70%	LAPDFDKIAESLSLLKDFFTTGSPGETAFR	3.28	3,273.67
Control	6011	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	14	16	18	0.14%	19.70%	LDAFIEALHQEK	2.11	1,413.74
Control	6011	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	14	16	18	0.14%	19.70%	MLAITANTLR	3.14	1,119.62
Control	6011	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	14	16	18	0.14%	19.70%	SIVTDLVSQMDPHGR	2.24	1,670.82
Control	6011	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	14	16	18	0.14%	19.70%	SLIDMYSEVLDVLSDYDASYNTQDHLPR	4.36	3,275.51
Control	6011	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	14	16	18	0.14%	19.70%	TSVLEMIAQAR	3.68	1,218.65
Control	6011	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	14	16	18	0.14%	19.70%	VSDKEKIDQLQEELLHTQLK	4.85	2,394.29
Control	6011	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	9	13	22	0.17%	26.00%	ELQALTDAMYTNLR	3.44	1,654.81

Control	6011	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	9	13	22	0.17%	26.00%	EVVADLALPMADGR	3.37	1,472.74
Control	6011	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	9	13	22	0.17%	26.00%	GELETVLLGAEQPISQMTTLPQK	3.31	2,483.31
Control	6011	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	9	13	22	0.17%	26.00%	IFDVQLPHYNPGDEK	3.19	1,771.87
Control	6011	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	9	13	22	0.17%	26.00%	LLLFPFLSPQK	3.15	1,302.78
Control	6011	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	9	13	22	0.17%	26.00%	LLLFPFLSPQKDPEIYTDPEVFK	5.86	2,736.45
Control	6011	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	9	13	22	0.17%	26.00%	LTAAPFITR	2.96	989.5779
Control	6011	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	9	13	22	0.17%	26.00%	VLDSMPVLDSVLSESLR	5.07	1,875.97
Control	6011	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	9	13	22	0.17%	26.00%	YGFGLMQPEHDVPVR	2.73	1,760.84
Control	6011	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	3	3	3	0.02%	9.73%	AFITNIPFDVK	4	1,264.69
Control	6011	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	3	3	3	0.02%	9.73%	GDFFPPERPQQLPHGLGGIGMGLGPGGQPIDANHLNK	3.23	3,834.91
Control	6011	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	3	3	3	0.02%	9.73%	GNFGGSFAGSFGGAGGHAPGVAR	3.16	2,034.95

Control	6011	metalloproteinase	gi|1044811,gi|157742933,gi|27806209,gi|29839751	84,171.20	100.00%	3	3	3	0.02%	5.75%	AIDTIYQTTDFSGIR	3.68	1,700.85
Control	6011	metalloproteinase	gi|1044811,gi|157742933,gi|27806209,gi|29839751	84,171.20	100.00%	3	3	3	0.02%	5.75%	HYEGLSYDVDSLHQK	3.96	1,790.83
Control	6011	metalloproteinase	gi|1044811,gi|157742933,gi|27806209,gi|29839751	84,171.20	100.00%	3	3	3	0.02%	5.75%	LPPPKPLPGTLKR	1.79	1,413.89
Control	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	8	0.06%	44.60%	AILVDLEPGTMDSVR	3.87	1,631.83
Control	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	8	0.06%	44.60%	ALTVPELTQQVFDAK	4.32	1,659.90
Control	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	8	0.06%	44.60%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	3.41	3,213.49
Control	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	8	0.06%	44.60%	FPGQLNADLRK	3.12	1,258.69
Control	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	8	0.06%	44.60%	GHYTEGAELVDSVLDVVR	3.66	1,958.98
Control	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	8	0.06%	44.60%	GHYTEGAELVDSVLDVVRK	3.32	2,087.08
Control	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	8	0.06%	44.60%	IMNTFSVVPSPK	4.39	1,335.70
Control	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	8	0.06%	44.60%	ISEQFTAMFR	2.98	1,245.59
Control	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	8	0.06%	44.60%	ISVYYNEATGGK	2.93	1,301.64
Control	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	8	0.06%	44.60%	LAVNMVPFPR	3.55	1,159.63
Control	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	8	0.06%	44.60%	LHFFMPGFAPLTSR	3.66	1,620.84
Control	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	8	0.06%	44.60%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	4.94	4,479.06

Control	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	8	0.06%	44.60%	YLTVAAVFR	2.56	1,039.59
Control	6011	RecName: Full=T-complex protein 1 subunit beta; Short=TCP-1-beta; AltName: Full=CCT-beta	gi|115305838,gi|73586876,gi|77735435	57,458.70	100.00%	2	3	4	0.03%	7.10%	QALLNSAVDHGSDEVK	2.6	1,682.83
Control	6011	RecName: Full=T-complex protein 1 subunit beta; Short=TCP-1-beta; AltName: Full=CCT-beta	gi|115305838,gi|73586876,gi|77735435	57,458.70	100.00%	2	3	4	0.03%	7.10%	VQDDEVGDGTTSVTVLAAELLR	4.36	2,288.16
Control	6011	melanoma cell adhesion molecule	gi|2323281	9,468.30	99.80%	2	3	5	0.04%	22.10%	SDKLPEEMGLLQGSSGDK	5.52	1,906.91
Control	6011	melanoma cell adhesion molecule	gi|2323281	9,468.30	99.80%	2	3	5	0.04%	22.10%	SDKLPEEMGLLQGSSGDKR	4.18	2,063.01
Control	6011	RecName: Full=Ornithine aminotransferase, mitochondrial; AltName: Full=Ornithine--oxo-acid aminotransferase; Flags: Precursor	gi|122140925,gi|73586966,gi|77735431	48,058.30	100.00%	7	7	8	0.06%	30.80%	AFYNNVLGEYEEYVTK	3.06	1,938.91

Control	6011	RecName: Full=Ornithine aminotransferase, mitochondrial; AltName: Full=Ornithine--oxo-acid aminotransferase; Flags: Precursor	gi|122140925,gi|73586966,gi|77735431	48,058.30	100.00%	7	7	8	0.06%	30.80%	ALQDPNVAAFMVEPIQGEAGVVVPDPGYLVGVR	3.54	3,423.76
Control	6011	RecName: Full=Ornithine aminotransferase, mitochondrial; AltName: Full=Ornithine--oxo-acid aminotransferase; Flags: Precursor	gi|122140925,gi|73586966,gi|77735431	48,058.30	100.00%	7	7	8	0.06%	30.80%	GLLNAIVIR	2.87	968.6252
Control	6011	RecName: Full=Ornithine aminotransferase, mitochondrial; AltName: Full=Ornithine--oxo-acid aminotransferase; Flags: Precursor	gi|122140925,gi|73586966,gi|77735431	48,058.30	100.00%	7	7	8	0.06%	30.80%	NELMKLPSDVVTTVR	3.97	1,717.92

Control	6011	RecName: Full=Ornithine aminotransferase, mitochondrial; AltName: Full=Ornithine--oxo-acid aminotransferase; Flags: Precursor	gi|122140925,gi|73586966,gi|77735431	48,058.30	100.00%	7	7	8	0.06%	30.80%	SQVDKLTLTSR	3.48	1,247.70
Control	6011	RecName: Full=Ornithine aminotransferase, mitochondrial; AltName: Full=Ornithine--oxo-acid aminotransferase; Flags: Precursor	gi|122140925,gi|73586966,gi|77735431	48,058.30	100.00%	7	7	8	0.06%	30.80%	TLSAISSSTDPTSYDGFGPFMPGFEIIPYNDLPALER	3.34	4,021.91
Control	6011	RecName: Full=Ornithine aminotransferase, mitochondrial; AltName: Full=Ornithine--oxo-acid aminotransferase; Flags: Precursor	gi|122140925,gi|73586966,gi|77735431	48,058.30	100.00%	7	7	8	0.06%	30.80%	TVQGPPSSDYIFER	2.67	1,595.77
Control	6011	RAP2B protein	gi|134025188,gi|154425870,gi|156523174	20,470.40	99.80%	2	2	2	0.02%	14.80%	EIEVDSSPSVLEILDTAGTEQFASMR	4.31	2,840.35
Control	6011	RAP2B protein	gi|134025188,gi|154425870,gi|156523174	20,470.40	99.80%	2	2	2	0.02%	14.80%	KEIEVDSSPSVLEILDTAGTEQFASMR	3.55	2,968.45

Control	6011	RecName: Full=Transmembrane protein 111	gi|115311872,gi|73587331,gi|78050079	29,903.00	99.80%	2	2	2	0.02%	8.43%	LTQEQVSDSQVLIR	3.84	1,615.87
Control	6011	RecName: Full=Transmembrane protein 111	gi|115311872,gi|73587331,gi|78050079	29,903.00	99.80%	2	2	2	0.02%	8.43%	VPFPLTLR	2.17	942.5772
Control	6011	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	4	5	110	0.86%	38.60%	FFESFGDLSSADAILGNPK	3.51	2,014.98
Control	6011	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	4	5	110	0.86%	38.60%	LLGNVLVVVLAR	4.48	1,265.83
Control	6011	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	4	5	110	0.86%	38.60%	VKVDEVGGEALGR	3.2	1,328.72
Control	6011	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	4	5	110	0.86%	38.60%	VVTGVANALAHR	4.14	1,207.69
Control	6011	Ribosomal protein L6	gi|126717393,gi|58760432,gi|61553343,gi|61553350,gi|67461090,gi|72534798	32,672.90	99.80%	2	3	3	0.02%	11.10%	ASITPGTILIILTGR	4.18	1,525.93
Control	6011	Ribosomal protein L6	gi|126717393,gi|58760432,gi|61553343,gi|61553350,gi|67461090,gi|72534798	32,672.90	99.80%	2	3	3	0.02%	11.10%	QLGSGLLLVTGPLSLNR	4.33	1,738.02
Control	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	13	14	14	0.11%	9.18%	AFGPGLQGGSAGSPAR	4.82	1,429.72
Control	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	13	14	14	0.11%	9.18%	ANLPQSFQVDTSK	3.33	1,434.72

Control	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	13	14	14	0.11%	9.18%	ASGPGLNTTGVPASLPVEFTIDAK	3.58	2,342.22
Control	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	13	14	14	0.11%	9.18%	AYGPGIEPTGNMVK	3.37	1,449.70
Control	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	13	14	14	0.11%	9.18%	FADQHVPGSPFSVK	3.3	1,515.76
Control	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	13	14	14	0.11%	9.18%	FNEEHIPDSPFVVPVASPSGDAR	3.67	2,467.19
Control	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	13	14	14	0.11%	9.18%	GAGTGGLGLAVEGPSEAK	4.24	1,570.81
Control	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	13	14	14	0.11%	9.18%	IANLQTDLSDGLR	3.87	1,415.75
Control	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	13	14	14	0.11%	9.18%	LIALLEVLSQK	2.5	1,226.77
Control	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	13	14	14	0.11%	9.18%	SPFSVGVSPSLDLSK	3.75	1,519.80

Control	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	13	14	14	0.11%	9.18%	VAQPAITDNKDGTVTVR	2.4	1,784.95
Control	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	13	14	14	0.11%	9.18%	VSGQGLHEGHTFEPAEFIIDTR	3.57	2,440.19
Control	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	13	14	14	0.11%	9.18%	VTAQGPGLEPSGNIANK	4.83	1,652.86
Control	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	13	14	14	0.11%	9.18%	YTPVQQGPVGINVTYGGDAIPK	4.87	2,274.18
Control	6011	NRAS protein	gi|146186548,gi|148226664	21,211.30	100.00%	4	4	4	0.03%	24.90%	QGVEDAFYTLVR	3.18	1,397.71
Control	6011	NRAS protein	gi|146186548,gi|148226664	21,211.30	100.00%	4	4	4	0.03%	24.90%	SALTIQLIQNHFVDEYDPTIEDSYR	3.79	2,967.44
Control	6011	NRAS protein	gi|146186548,gi|148226664	21,211.30	100.00%	4	4	4	0.03%	24.90%	SALTIQLIQNHFVDEYDPTIEDSYRK	4.49	3,095.53
Control	6011	NRAS protein	gi|146186548,gi|148226664	21,211.30	100.00%	4	4	4	0.03%	24.90%	SFADINLYR	2.35	1,098.56
Control	6011	PI4K2A protein	gi|151554868,gi|154152033	54,067.10	100.00%	3	3	3	0.02%	7.10%	IYQGSSGSYFVKDPQGK	2.26	1,860.91
Control	6011	PI4K2A protein	gi|151554868,gi|154152033	54,067.10	100.00%	3	3	3	0.02%	7.10%	LELNIVPR	2.57	953.5779
Control	6011	PI4K2A protein	gi|151554868,gi|154152033	54,067.10	100.00%	3	3	3	0.02%	7.10%	LVVLDYIIR	2.55	1,103.68

Control	6011	similar to Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precursor (Succinyl-CoA synthetase, betaG chain) (SCS-betaG) (GTP-specific succinyl-CoA synthetase beta subunit)	gi|146231894,gi|75773452,gi|77736229,gi|91208175	46,647.10	99.80%	2	2	2	0.02%	7.41%	LEGTNVHEAQNILSNSGLPITSAVDLEDAAK	3.59	3,206.62
Control	6011	similar to Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precursor (Succinyl-CoA synthetase, betaG chain) (SCS-betaG) (GTP-specific succinyl-CoA synthetase beta subunit)	gi|146231894,gi|75773452,gi|77736229,gi|91208175	46,647.10	99.80%	2	2	2	0.02%	7.41%	LEGTNVHEAQNILSNSGLPITSAVDLEDAAKK	4.61	3,334.71
Control	6011	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	8	10	18	0.14%	37.00%	ANQVTDESLESTR	4.15	1,449.68
Control	6011	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	8	10	18	0.14%	37.00%	ANQVTDESLESTRR	2.62	1,605.78
Control	6011	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	8	10	18	0.14%	37.00%	ILGLAIESQDAGIK	4.62	1,427.81

Control	6011	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	8	10	18	0.14%	37.00%	NMALDMGNEIEAQNR	3.3	1,721.76
Control	6011	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	8	10	18	0.14%	37.00%	TITMLDEQGEQLK	3.67	1,521.75
Control	6011	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	8	10	18	0.14%	37.00%	TITMLDEQGEQLKR	2.72	1,677.85
Control	6011	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	8	10	18	0.14%	37.00%	VTNGQPQQATAGAASGGYIK	5.42	1,918.96
Control	6011	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	8	10	18	0.14%	37.00%	VTNGQPQQATAGAASGGYIKR	2.3	2,075.06
Control	6011	LBR protein	gi|151557087,gi|154152031	71,240.40	100.00%	3	4	4	0.03%	8.70%	APQDELSPASSGNAIYDFFIGR	5.1	2,355.13
Control	6011	LBR protein	gi|151557087,gi|154152031	71,240.40	100.00%	3	4	4	0.03%	8.70%	FHLSQESSYIPTQYSLR	2.87	2,056.01
Control	6011	LBR protein	gi|151557087,gi|154152031	71,240.40	100.00%	3	4	4	0.03%	8.70%	LTPLVLKPFGNSINR	3.21	1,668.98
Control	6011	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	gi|124828540,gi|126158903,gi|145566947	55,991.00	100.00%	3	3	3	0.02%	9.25%	ETVDSFLDLTR	2.36	1,295.65
Control	6011	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	gi|124828540,gi|126158903,gi|145566947	55,991.00	100.00%	3	3	3	0.02%	9.25%	NLFPSNLVVAAFR	2.8	1,447.81
Control	6011	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	gi|124828540,gi|126158903,gi|145566947	55,991.00	100.00%	3	3	3	0.02%	9.25%	SEEETSPLVTHPNPTGPAASTPESK	5.36	2,563.22

Control	6011	radical S-adenosylmethionine domain containin	gi|114052066,gi|122142787,gi|88682896	41,655.10	99.80%	2	2	3	0.02%	7.44%	FVISDEEFEAFLDR	3.3	1,716.81
Control	6011	radical S-adenosylmethionine domain containin	gi|114052066,gi|122142787,gi|88682896	41,655.10	99.80%	2	2	3	0.02%	7.44%	INFSGGEPFLQDR	3.38	1,479.72
Control	6011	RecName: Full=ATP-dependent RNA helicase A; AltName: Full=Nuclear DNA helicase II; Short=NDH II; AltName: Full=DEAH box protein 9	gi|2500541,gi|27806665,gi|577739	141,929.30	100.00%	4	4	4	0.03%	6.60%	ELDALDANDELTPLGR	2.87	1,741.86
Control	6011	RecName: Full=ATP-dependent RNA helicase A; AltName: Full=Nuclear DNA helicase II; Short=NDH II; AltName: Full=DEAH box protein 9	gi|2500541,gi|27806665,gi|577739	141,929.30	100.00%	4	4	4	0.03%	6.60%	GMTLVTPLQLLLFASK	3.48	1,748.00

Control	6011	RecName: Full=ATP-dependent RNA helicase A; AltName: Full=Nuclear DNA helicase II; Short=NDH II; AltName: Full=DEAH box protein 9	gi|2500541, gi|27806665,gi|577739	141,929.30	100.00%	4	4	4	0.03%	6.60%	QPGIISQLDPVNER	2.95	1,565.83
Control	6011	RecName: Full=ATP-dependent RNA helicase A; AltName: Full=Nuclear DNA helicase II; Short=NDH II; AltName: Full=DEAH box protein 9	gi|2500541, gi|27806665,gi|577739	141,929.30	100.00%	4	4	4	0.03%	6.60%	VNLSQDLEHQLQNIVQELNLEIVPIPEDPSVPVALNLGK	2.89	4,315.32
Control	6011	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	5	8	24	0.19%	7.97%	AKIQDKEGIPPDQQR	3.01	1,722.91
Control	6011	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	5	8	24	0.19%	7.97%	ESTLHLVLR	3.16	1,067.62
Control	6011	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	5	8	24	0.19%	7.97%	IQDKEGIPPDQQR	4.61	1,523.78
Control	6011	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	5	8	24	0.19%	7.97%	QLEDGRTLSDYNIQK	2.8	1,779.89

Control	6011	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	5	8	24	0.19%	7.97%	TITLEVEPSDTIENVK	4.79	1,787.93
Control	6011	TPA: predicted NADPH oxidase-5	gi|151427572,gi|155372001	86,454.40	99.80%	2	3	3	0.02%	3.71%	AIGLQMALDLLAK	3.71	1,372.79
Control	6011	TPA: predicted NADPH oxidase-5	gi|151427572,gi|155372001	86,454.40	99.80%	2	3	3	0.02%	3.71%	MAALHIVEVNLLPSK	4.11	1,650.92
Control	6011	RecName: Full=Small nuclear ribonucleoprotein Sm D1; Short=Sm-D1; AltName: Full=snRNP core protein D1	gi|109894869,gi|73586929,gi|78050059	13,263.90	99.80%	2	4	7	0.05%	27.70%	NREPVQLETLSIR	3.67	1,554.86
Control	6011	RecName: Full=Small nuclear ribonucleoprotein Sm D1; Short=Sm-D1; AltName: Full=snRNP core protein D1	gi|109894869,gi|73586929,gi|78050059	13,263.90	99.80%	2	4	7	0.05%	27.70%	YFILPDSLPLDTLLVDVEPK	4.75	2,287.25
Control	6011	RecName: Full=Syntaxin-4	gi|122140085,gi|74356383,gi|78050061	34,382.50	100.00%	4	4	4	0.03%	19.20%	AIEPQKEEADENYNSVNTR	4.32	2,207.02
Control	6011	RecName: Full=Syntaxin-4	gi|122140085,gi|74356383,gi|78050061	34,382.50	100.00%	4	4	4	0.03%	19.20%	NILSSADYVER	2.98	1,266.63
Control	6011	RecName: Full=Syntaxin-4	gi|122140085,gi|74356383,gi|78050061	34,382.50	100.00%	4	4	4	0.03%	19.20%	TQHGVLSQQFVELINK	3.63	1,840.99
Control	6011	RecName: Full=Syntaxin-4	gi|122140085,gi|74356383,gi|78050061	34,382.50	100.00%	4	4	4	0.03%	19.20%	VALVVHPGTAR	2.19	1,119.66

Control	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	15	20	38	0.30%	21.20%	AFTGREFDELSPSAQR	2.78	1,810.87
Control	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	15	20	38	0.30%	21.20%	AKDIVPGDIVEIAVGDKVPADIR	3.27	2,390.33
Control	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	15	20	38	0.30%	21.20%	AMGVVVATGVNTEIGK	4.88	1,561.83
Control	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	15	20	38	0.30%	21.20%	DIVPGDIVEIAVGDKVPADIR	4.12	2,191.20
Control	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	15	20	38	0.30%	21.20%	EEMNLEDSANFIK	3.08	1,555.69
Control	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	15	20	38	0.30%	21.20%	EFTLEFSR	1.79	1,028.50

Control	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	15	20	38	0.30%	21.20%	ISLPVILMDETLK	4.27	1,487.84
Control	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	15	20	38	0.30%	21.20%	KSEIGIAMGSGTAVAK	5.59	1,535.81
Control	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	15	20	38	0.30%	21.20%	MNVFDTELKGLSK	2.71	1,497.76
Control	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	15	20	38	0.30%	21.20%	NAENAIEALKEYEPEMGK	4.49	2,051.96
Control	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	15	20	38	0.30%	21.20%	NMLFSGTNIAAGK	3.35	1,339.67
Control	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	15	20	38	0.30%	21.20%	SEIGIAMGSGTAVAK	5.25	1,407.72

Control	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	15	20	38	0.30%	21.20%	TASEMVLADDNFSTIVAAVEEGR	4	2,441.15
Control	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	15	20	38	0.30%	21.20%	TVEEVLGHFGVNESTGLSLEQVKK	4.38	2,600.36
Control	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	15	20	38	0.30%	21.20%	VDQSILTGESVSVIK	4.19	1,574.86
Control	6011	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	100.00%	3	5	6	0.05%	6.08%	DEEDDDEDMYSDNINAATEEK	5.55	2,463.91
Control	6011	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	100.00%	3	5	6	0.05%	6.08%	HSLEGNPRDEEDDDEDMYSDNINAATEEK	6.04	3,354.35

Control	6011	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	100.00%	3	5	6	0.05%	6.08%	NLSLPFIFHEK	1.98	1,344.73
Control	6011	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	99.80%	2	2	3	0.02%	4.60%	FATLYSTQHR	1.97	1,223.62
Control	6011	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	99.80%	2	2	3	0.02%	4.60%	ILEVVNQVQDEER	4.35	1,570.81
Control	6011	PREDICTED: similar to L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit) (LDH-M)	gi|119920080,gi|126045,gi|148878492,gi|217588,gi|217592,gi|27806559	36,579.90	99.80%	2	2	2	0.02%	8.43%	DQLIQNLLKEEHVPQNK	4.16	2,046.10
Control	6011	PREDICTED: similar to L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit) (LDH-M)	gi|119920080,gi|126045,gi|148878492,gi|217588,gi|217592,gi|27806559	36,579.90	99.80%	2	2	2	0.02%	8.43%	QVVDSAYEVIK	3.13	1,250.66
Control	6011	Endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	gi|111308658,gi|115497382	32,554.10	99.80%	2	2	2	0.02%	11.40%	LSFGDTLQVHNVHGAFNALGGADR	4.72	2,496.24
Control	6011	Endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	gi|111308658,gi|115497382	32,554.10	99.80%	2	2	2	0.02%	11.40%	YDLSPITVK	2.44	1,035.57

Control	6011	PREDICTED: similar to hCG1980844	gi|194674945	298,419.90	100.00%	3	3	4	0.03%	1.21%	LVPFLVELR	2.37	1,085.67
Control	6011	PREDICTED: similar to hCG1980844	gi|194674945	298,419.90	100.00%	3	3	4	0.03%	1.21%	QLQPNEEADYLGVR	3	1,631.80
Control	6011	PREDICTED: similar to hCG1980844	gi|194674945	298,419.90	100.00%	3	3	4	0.03%	1.21%	YLLTQELLR	2.87	1,148.67
Control	6011	100 kDa coactivator	gi|30523262,gi|45429977,gi|60415927,gi|75517981	101,972.50	100.00%	3	3	3	0.02%	6.70%	EADGSETPEPFAAEAK	3.45	1,648.73
Control	6011	100 kDa coactivator	gi|30523262,gi|45429977,gi|60415927,gi|75517981	101,972.50	100.00%	3	3	3	0.02%	6.70%	NLPGLVQEGEPFSEEATLFTK	3.82	2,306.16
Control	6011	100 kDa coactivator	gi|30523262,gi|45429977,gi|60415927,gi|75517981	101,972.50	100.00%	3	3	3	0.02%	6.70%	VNVTVDYIRPASPATDTVPAFSER	3.19	2,605.33
Control	6011	PREDICTED: similar to karyopherin beta 1 isoform 2	gi|76644624	97,210.30	100.00%	4	5	5	0.04%	7.31%	GALQYLVPILTQTLTK	3.32	1,759.04
Control	6011	PREDICTED: similar to karyopherin beta 1 isoform 2	gi|76644624	97,210.30	100.00%	4	5	5	0.04%	7.31%	LAATNALLNSLEFTK	5.09	1,605.88
Control	6011	PREDICTED: similar to karyopherin beta 1 isoform 2	gi|76644624	97,210.30	100.00%	4	5	5	0.04%	7.31%	LLETTDRPDGHQNNLR	2.93	1,878.94
Control	6011	PREDICTED: similar to karyopherin beta 1 isoform 2	gi|76644624	97,210.30	100.00%	4	5	5	0.04%	7.31%	LQQVLQMESHIQSTSDR	3.84	2,015.98
Control	6011	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	100.00%	5	5	5	0.04%	21.90%	DLLSHENAATLNDVK	4.58	1,639.83
Control	6011	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	100.00%	5	5	5	0.04%	21.90%	DRQYLLFFHK	3.27	1,366.73

Control	6011	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	100.00%	5	5	5	0.04%	21.90%	LRDPLQVHLPLR	3.74	1,456.87
Control	6011	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	100.00%	5	5	5	0.04%	21.90%	VAASTGIDLLLLDDFKLVINDLTYHVRPPK	3.25	3,336.86
Control	6011	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	100.00%	5	5	5	0.04%	21.90%	VAIYSPDGVR	2.26	1,076.57
Control	6011	sorting and assembly machinery component 50 homolog	gi|114051051,gi|87578317,gi|95769210	52,025.30	100.00%	2	3	6	0.05%	5.33%	ETSYGLSFFKPQPGNFDR	2.57	2,090.00
Control	6011	sorting and assembly machinery component 50 homolog	gi|114051051,gi|87578317,gi|95769210	52,025.30	100.00%	2	3	6	0.05%	5.33%	LPNLLGR	2.02	782.4884
Control	6011	PREDICTED: similar to potassium-chloride cotransporter-1 isoform 2	gi|194675074	120,598.40	100.00%	3	3	3	0.02%	2.76%	DNIIPFLR	1.88	987.5623
Control	6011	PREDICTED: similar to potassium-chloride cotransporter-1 isoform 2	gi|194675074	120,598.40	100.00%	3	3	3	0.02%	2.76%	ELVHIKPDQSNVR	3.19	1,534.83
Control	6011	PREDICTED: similar to potassium-chloride cotransporter-1 isoform 2	gi|194675074	120,598.40	100.00%	3	3	3	0.02%	2.76%	LLTFASQLK	2.23	1,020.61

Control	6011	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	5	5	5	0.04%	6.67%	EKDGEFSVLQLVGMLR	3.93	1,836.95
Control	6011	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	5	5	5	0.04%	6.67%	FADIVSILDK	3.54	1,120.63
Control	6011	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	5	5	5	0.04%	6.67%	TYVDPHTYEDPNQAVLK	2.33	1,989.96
Control	6011	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	5	5	5	0.04%	6.67%	VIGAGEFGEVYK	3.09	1,268.65
Control	6011	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	5	5	5	0.04%	6.67%	YSEPPLGLTR	2.72	1,132.60
Control	6011	phospholipase D2	gi|110331871,gi|115304867,gi|115496504,gi|116248582	105,751.20	99.80%	2	2	2	0.02%	3.00%	FAVASSPAPEGDSR	3.51	1,390.66
Control	6011	phospholipase D2	gi|110331871,gi|115304867,gi|115496504,gi|116248582	105,751.20	99.80%	2	2	2	0.02%	3.00%	FLEDEYLLPSLGSK	2.84	1,610.83
Control	6011	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	3	4	6	0.05%	19.10%	GDQPAASDSDDDEPPPLPR	3.07	1,978.86
Control	6011	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	3	4	6	0.05%	19.10%	IVRGDQPAASDSDDDEPPPLPR	4.18	2,347.12
Control	6011	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	3	4	6	0.05%	19.10%	KFYGPEGPYGVFAGR	3.91	1,644.82
Control	6011	similar to ribosomal protein L27	gi|28189717,gi|47117099,gi|74268027,gi|77404275	15,780.40	100.00%	3	3	3	0.02%	30.10%	NIDDGTSDRPYSHALVAGIDR	3.72	2,272.10

Control	6011	similar to ribosomal protein L27	gi|28189717,gi|47117099,gi|74268027,gi|77404275	15,780.40	100.00%	3	3	3	0.02%	30.10%	VYNYNHLMPTR	2.8	1,423.68
Control	6011	similar to ribosomal protein L27	gi|28189717,gi|47117099,gi|74268027,gi|77404275	15,780.40	100.00%	3	3	3	0.02%	30.10%	YSVDIPLDK	2.76	1,049.55
Control	6011	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	8	11	13	0.10%	16.90%	GVMLAVDAVIAELKK	2.04	1,572.90
Control	6011	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	8	11	13	0.10%	16.90%	GYISPYFINTSK	3.07	1,389.70
Control	6011	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	8	11	13	0.10%	16.90%	IMQSSSEVGYDAMLGDFVNMVEK	3.2	2,566.15
Control	6011	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	8	11	13	0.10%	16.90%	ISSVQSIVPALEIANAHR	3.89	1,905.06
Control	6011	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	8	11	13	0.10%	16.90%	KISSVQSIVPALEIANAHR	4.37	2,033.15
Control	6011	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	8	11	13	0.10%	16.90%	LVQDVANNTNEEAGDGTTTATVLAR	4.89	2,560.25
Control	6011	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	8	11	13	0.10%	16.90%	TLNDELEIIEGMKFDR	2.33	1,938.95

Control	6011	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	8	11	13	0.10%	16.90%	VGLQVVAVK	3.2	912.5877
Control	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	11	18	37	0.29%	45.30%	DILLRPELEELR	2.18	1,495.85
Control	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	11	18	37	0.29%	45.30%	DILLRPELEELRNEHSAR	3.53	2,190.16
Control	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	11	18	37	0.29%	45.30%	FALPSPEHILGLPVGQHIYLSAR	3.76	2,515.38
Control	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	11	18	37	0.29%	45.30%	GPNGLLVYQGK	3.96	1,145.63
Control	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	11	18	37	0.29%	45.30%	IDGNLVIRPYTPVSSDDDKGFVDLVIK	5.4	2,975.57
Control	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	11	18	37	0.29%	45.30%	IGDTIEFR	2.99	950.4943
Control	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	11	18	37	0.29%	45.30%	LIDKEVISHDTR	3.12	1,425.77
Control	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	11	18	37	0.29%	45.30%	LIDKEVISHDTRR	2.61	1,581.87
Control	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	11	18	37	0.29%	45.30%	STPAITLENPDIK	3.87	1,398.75
Control	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	11	18	37	0.29%	45.30%	STPAITLENPDIKYPLR	4.66	1,928.05
Control	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	11	18	37	0.29%	45.30%	SVGMIAGGTGITPMLQVIR	6.02	1,917.03
Control	6011	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	10	10	10	0.08%	3.83%	EHLLMALADLDELLVR	3.12	1,867.00

Control	6011	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	10	10	10	0.08%	3.83%	GTLEPVQRPDVVLVGAGHR	3.81	2,000.10
Control	6011	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	10	10	10	0.08%	3.83%	HPTPLALGQFHTVTLLR	3.45	1,901.08
Control	6011	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	10	10	10	0.08%	3.83%	IPGDQVVSVVFIK	3.16	1,400.81
Control	6011	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	10	10	10	0.08%	3.83%	IQVVVLPGATTPPVR	3.94	1,546.93
Control	6011	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	10	10	10	0.08%	3.83%	LDVEFKPLAPDGVLLFSGGK	3.6	2,102.15
Control	6011	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	10	10	10	0.08%	3.83%	LRPGIVQSGGIVR	2.89	1,351.82
Control	6011	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	10	10	10	0.08%	3.83%	LRSPVISIDPPSSTVQQGQDASFK	5.85	2,557.33
Control	6011	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	10	10	10	0.08%	3.83%	SVVPQGGPHSLR	2.16	1,233.67
Control	6011	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	10	10	10	0.08%	3.83%	VVPYFTQTPYSFLPLPTIK	2.45	2,211.21
Control	6011	PTBP1 protein	gi|158454983	47,010.90	100.00%	2	2	2	0.02%	8.97%	KLPGDVTEGEVISLGLPFGK	2.86	2,056.13
Control	6011	PTBP1 protein	gi|158454983	47,010.90	100.00%	2	2	2	0.02%	8.97%	NNQFQALLQYADPVSAQHAK	3.4	2,243.12
Control	6011	Transmembrane protein 49	gi|111307060,gi|115496266,gi|122133514	46,165.40	100.00%	3	3	7	0.05%	13.50%	EQYNGNFTDPSSVNEK	2.88	1,828.80
Control	6011	Transmembrane protein 49	gi|111307060,gi|115496266,gi|122133514	46,165.40	100.00%	3	3	7	0.05%	13.50%	LAVQNLVQK	2.99	1,012.62

Control	6011	Transmembrane protein 49	gi|111307060,gi|115496266,gi|122133514	46,165.40	100.00%	3	3	7	0.05%	13.50%	LSGAEPDDEEYQEFEEMLEHAETAQDFASR	4.47	3,489.46
Control	6011	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	3	4	9	0.07%	5.16%	FASFIDKVR	1.87	1,082.60
Control	6011	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	3	4	9	0.07%	5.16%	NKYEDEINKR	2.43	1,308.65
Control	6011	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	3	4	9	0.07%	5.16%	SLDLDSIIAEVK	5.04	1,302.72
Control	6011	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	4	5	6	0.05%	6.67%	ALVQTEDHLLLFLQQLAGR	3.7	2,165.21
Control	6011	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	4	5	6	0.05%	6.67%	HLLVGLPSGAILSLPK	4.84	1,614.99
Control	6011	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	4	5	6	0.05%	6.67%	NFPQAALVSFATTGEK	4.58	1,680.86
Control	6011	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	4	5	6	0.05%	6.67%	RPVLQSLLLPIMDQDYAK	3.57	2,116.15
Control	6011	chloride intracellular channel 1	gi|59858371,gi|62751970,gi|74268283,gi|75040226	26,974.50	99.80%	2	2	2	0.02%	11.20%	GFSIPDVFR	2.11	1,037.54
Control	6011	chloride intracellular channel 1	gi|59858371,gi|62751970,gi|74268283,gi|75040226	26,974.50	99.80%	2	2	2	0.02%	11.20%	LAALNPESNTAGLDIFAK	2.88	1,844.98
Control	6011	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	100.00%	4	4	4	0.03%	16.80%	AQIQEQNPSIEVVYYNK	4.52	2,023.01
Control	6011	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	100.00%	4	4	4	0.03%	16.80%	ELQVGIPVTNEQGQR	3.12	1,667.87
Control	6011	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	100.00%	4	4	4	0.03%	16.80%	HFFTVTDPR	2.43	1,119.56
Control	6011	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	100.00%	4	4	4	0.03%	16.80%	NLLLSGAQLEASR	4.38	1,371.76

Control	6011	RecName: Full=Microsomal glutathione S-transferase 3; Short=Microsomal GST-3	gi|110279049,gi|74353862,gi|78042542	16,865.90	99.80%	2	2	5	0.04%	25.00%	AHQNTLEVYPPFLFFLAVGGVYHPR	2.92	2,872.49
Control	6011	RecName: Full=Microsomal glutathione S-transferase 3; Short=Microsomal GST-3	gi|110279049,gi|74353862,gi|78042542	16,865.90	99.80%	2	2	5	0.04%	25.00%	VLYAYGYYTGEPR	4.05	1,551.75
Control	6011	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	100.00%	3	4	9	0.07%	11.10%	LNQAVEFDVLPAFDALGQLTK	6.18	2,289.21
Control	6011	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	100.00%	3	4	9	0.07%	11.10%	PVILDPADPTGNVAGK	4.29	1,563.84
Control	6011	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	100.00%	3	4	9	0.07%	11.10%	QLAKPRPVILDPADPTGNVAGK	2.98	2,257.27
Control	6011	RecName: Full=Metaxin-1	gi|122137086,gi|83638781,gi|94967008	35,657.20	100.00%	3	3	4	0.03%	19.60%	FFFGDAPASLDAFVFSYLALLQQAK	4.46	2,766.42
Control	6011	RecName: Full=Metaxin-1	gi|122137086,gi|83638781,gi|94967008	35,657.20	100.00%	3	3	4	0.03%	19.60%	NQILTVLAGLAAMAGYALLSGIVSIQR	4.89	2,759.55
Control	6011	RecName: Full=Metaxin-1	gi|122137086,gi|83638781,gi|94967008	35,657.20	100.00%	3	3	4	0.03%	19.60%	YNADYDLSAR	3.37	1,187.53
Control	6011	ARP3 actin-related protein 3 homolog (yeast)	gi|115304856,gi|148744289,gi|149243031,gi|149243038,gi|149243045,gi|149243052,gi|149243059,gi|217422,gi|27806335,gi|47117646	47,353.80	100.00%	3	3	4	0.03%	10.50%	AEPEDHYFLLTEPPLNTPENR	2.94	2,482.19

Control	6011	ARP3 actin-related protein 3 homolog (yeast)	gi|115304856,gi|148744289,gi|149243031,gi|149243038,gi|149243045,gi|149243052,gi|149243059,gi|217422,gi|27806335,gi|47117646	47,353.80	100.00%	3	3	4	0.03%	10.50%	DITYFIQQLLR	2.46	1,409.78
Control	6011	ARP3 actin-related protein 3 homolog (yeast)	gi|115304856,gi|148744289,gi|149243031,gi|149243038,gi|149243045,gi|149243052,gi|149243059,gi|217422,gi|27806335,gi|47117646	47,353.80	100.00%	3	3	4	0.03%	10.50%	NIVLSGGSTMFR	3.92	1,297.66
Control	6011	KIAA1715	gi|111304578,gi|115496264	48,163.90	99.80%	2	2	2	0.02%	6.06%	IVEYLVGDGPQNR	3.86	1,459.75
Control	6011	KIAA1715	gi|111304578,gi|115496264	48,163.90	99.80%	2	2	2	0.02%	6.06%	TVTPALSSNVLPR	2.83	1,354.77
Control	6011	RecName: Full=GTP-binding protein SAR1a	gi|115311863,gi|74354052,gi|77735989	22,391.90	99.80%	2	2	2	0.02%	11.10%	LVFLGLDNAGK	3.08	1,146.65
Control	6011	RecName: Full=GTP-binding protein SAR1a	gi|115311863,gi|74354052,gi|77735989	22,391.90	99.80%	2	2	2	0.02%	11.10%	TTLLHMLKDDR	2.08	1,358.71
Control	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	23	65	0.51%	41.60%	AVFPSIVGR	2.37	945.5516
Control	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	23	65	0.51%	41.60%	AVFPSIVGRPR	3.1	1,198.71
Control	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	23	65	0.51%	41.60%	DLTDYLMK	1.87	1,014.48
Control	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	23	65	0.51%	41.60%	DLYANTVLSGGTTMYPGIADR	4.58	2,231.07
Control	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	23	65	0.51%	41.60%	EITALAPSTMK	3.03	1,161.62
Control	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	23	65	0.51%	41.60%	GYSFTTTAER	3.43	1,132.53

Control	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	23	65	0.51%	41.60%	IKIIAPPERK	2.5	1,164.75
Control	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	23	65	0.51%	41.60%	KDLYANTVLSGGTTMYPGIADR	4.74	2,359.16
Control	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	23	65	0.51%	41.60%	LDLAGRDLTDYLMK	2.75	1,639.84
Control	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	23	65	0.51%	41.60%	QEYDESGPSIVHR	2.59	1,516.70
Control	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	23	65	0.51%	41.60%	QEYDESGPSIVHRK	3	1,644.80
Control	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	23	65	0.51%	41.60%	SYELPDGQVITIGNER	4.51	1,790.89
Control	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	23	65	0.51%	41.60%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	6.32	3,183.61
Control	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	23	65	0.51%	41.60%	VAPEEHPVLLTEAPLNPK	4.43	1,954.06
Control	6011	RecName: Full=40S ribosomal protein S2	gi|108935889,gi|2293579,gi|74267604,gi|75812930	31,218.00	100.00%	3	3	3	0.02%	12.30%	GTGIVSAPVPK	2.54	1,025.60
Control	6011	RecName: Full=40S ribosomal protein S2	gi|108935889,gi|2293579,gi|74267604,gi|75812930	31,218.00	100.00%	3	3	3	0.02%	12.30%	SLEEIYLFSLPIK	2.14	1,551.87
Control	6011	RecName: Full=40S ribosomal protein S2	gi|108935889,gi|2293579,gi|74267604,gi|75812930	31,218.00	100.00%	3	3	3	0.02%	12.30%	SPYQEFTDHLVK	2.76	1,463.72

Control	6011	RecName: Full=Peptidyl-tRNA hydrolase 2, mitochondrial; Short=PTH 2; AltName: Full=Bcl-2 inhibitor of transcription; Flags: Precursor	gi|109892883,gi|116292141,gi|60650282,gi|73587109,gi|77735985	19,272.70	100.00%	3	3	3	0.02%	27.90%	APDEETLVELLTHAK	4.1	1,665.87
Control	6011	RecName: Full=Peptidyl-tRNA hydrolase 2, mitochondrial; Short=PTH 2; AltName: Full=Bcl-2 inhibitor of transcription; Flags: Precursor	gi|109892883,gi|116292141,gi|60650282,gi|73587109,gi|77735985	19,272.70	100.00%	3	3	3	0.02%	27.90%	TVLGIGPGPADLIDKVTGHLK	1.8	2,101.20
Control	6011	RecName: Full=Peptidyl-tRNA hydrolase 2, mitochondrial; Short=PTH 2; AltName: Full=Bcl-2 inhibitor of transcription; Flags: Precursor	gi|109892883,gi|116292141,gi|60650282,gi|73587109,gi|77735985	19,272.70	100.00%	3	3	3	0.02%	27.90%	VLGLTVSLIQDAGR	2.75	1,441.84
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	DLFSEAHSEFLK	3.75	1,422.69

Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	EATNPPVIQEEKPK	2.14	1,579.83
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	ELSDFISYLK	2.77	1,214.63
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	ELSDFISYLKR	2.55	1,370.73
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	FLEDYFDGNLK	3.29	1,360.64
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	FLEDYFDGNLKR	3.68	1,516.74
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	FVMQEEFSR	3.13	1,188.54
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	GFPTIYFSPANK	2.39	1,341.68
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	GFPTIYFSPANKK	3.3	1,469.78
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	IFRDGEESGAYDGPR	5.22	1,668.76
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	KLAPEYEAAATR	4.02	1,319.70
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	KLHFAVASR	2.39	1,028.60
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	KTFSHELSDFGLESTTGEIPVVAVR	2.57	2,719.39
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	LAPEYEAAATR	2.61	1,191.60
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	LRKDPNIVIAK	3.03	1,266.79
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	MDATANDVPSPYEVR	4.48	1,680.75
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	QAGPASVPLKSEEEFEK	2.62	1,845.92
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	TADGIVSHLKK	2.19	1,168.67
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	TFSHELSDFGLESTGEIPVVAVR	5.07	2,591.30
Control	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	20	24	37	0.29%	38.80%	YGVSGYPTLK	2.84	1,084.57
Control	6011	PECAM1 protein	gi|111308531	82,597.50	100.00%	5	8	20	0.16%	6.37%	APVHFTIEK	2.31	1,041.57
Control	6011	PECAM1 protein	gi|111308531	82,597.50	100.00%	5	8	20	0.16%	6.37%	FHIIPEGK	2.62	940.5252
Control	6011	PECAM1 protein	gi|111308531	82,597.50	100.00%	5	8	20	0.16%	6.37%	GTETVYSEIR	2.57	1,154.57
Control	6011	PECAM1 protein	gi|111308531	82,597.50	100.00%	5	8	20	0.16%	6.37%	PAVPLLNSNNEK	2.19	1,295.70

Control	6011	PECAM1 protein	gi|111308531	82,597.50	100.00%	5	8	20	0.16%	6.37%	QMPVEMSRPAVPLLNSNEK	2.66	2,270.13
Control	6011	RecName: Full=FAS-associated factor 2; AltName: Full=UBX domain-containing protein 8	gi|109896151,gi|116004259,gi|88683021	52,646.60	100.00%	3	3	3	0.02%	7.42%	FQIEANFPR	2.84	1,121.57
Control	6011	RecName: Full=FAS-associated factor 2; AltName: Full=UBX domain-containing protein 8	gi|109896151,gi|116004259,gi|88683021	52,646.60	100.00%	3	3	3	0.02%	7.42%	IYSYVVSRPQPR	2.99	1,464.80
Control	6011	RecName: Full=FAS-associated factor 2; AltName: Full=UBX domain-containing protein 8	gi|109896151,gi|116004259,gi|88683021	52,646.60	100.00%	3	3	3	0.02%	7.42%	QQQDEAYLASLR	2.8	1,421.70
Control	6011	RecName: Full=40S ribosomal protein S16	gi|108860953,gi|74354274,gi|75812950	16,427.90	100.00%	3	3	4	0.03%	21.90%	EIKDILIQYDR	3.09	1,405.77
Control	6011	RecName: Full=40S ribosomal protein S16	gi|108860953,gi|74354274,gi|75812950	16,427.90	100.00%	3	3	4	0.03%	21.90%	GPLQSVQVFGR	3.28	1,187.65
Control	6011	RecName: Full=40S ribosomal protein S16	gi|108860953,gi|74354274,gi|75812950	16,427.90	100.00%	3	3	4	0.03%	21.90%	LLEPVLLLGK	2.22	1,094.72
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	DGQVINETSQHHDDLE	2.97	1,836.80

Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	DNLAEDIMR	2.65	1,092.50
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	EEAESTLQSFR	2.97	1,296.61
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	EEAESTLQSFRQDVDNASLAR	4.07	2,366.12
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	EKLQEEMLQREEAESTLQSFR	4.37	2,597.25
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	EMEENFSVEAANYQDTIGR	3.39	2,218.96
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	ETNLDSLPLVDTHSK	3.36	1,668.84
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	ETNLDSLPLVDTHSKR	4.21	1,824.95
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	EYQDLLNVK	2.46	1,121.58
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	FADLSEAANR	3.8	1,093.53
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	FADLSEAANRNNDALR	2.39	1,776.86
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	FANYIDKVR	2.64	1,125.61
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	ILLAELEQLK	4.4	1,169.71
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	ILLAELEQLKGQGK	4.45	1,539.91
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	ISLPLPNFSSLNLR	4.65	1,570.90
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	KLHDEEIQELQAQIQEQHVQIDMDVSKPDLTAALR	6.67	4,085.06
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	KVESLQEEIAFLK	5.35	1,533.85
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	KVESLQEEIAFLKK	5.31	1,661.95
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	LGDLYEEEMR	2.48	1,254.57
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	LHDEEIQELQAQIQEQHVQIDMDVSKPDLTAALR	5.9	3,956.97
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	LLQDSVDFSLADAINTEFK	4.33	2,126.07
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	LQDEIQNMKEEMAR	3.85	1,750.81
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	LQEEMLQREEAESTLQSFR	5.03	2,340.11

Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	LQEEMLQREEAESTLQSFRQDVDNASLAR	4.05	3,409.63
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	MALDIEIATYR	3.45	1,311.66
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	MALDIEIATYRK	2.32	1,439.76
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	MFGGPGTASRPSSTR	2.57	1,508.73
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	NLQEAEEWYK	2.45	1,309.61
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	SRLGDLYEEEMR	3.84	1,513.70
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	TLYTSSPGGVYATR	4.24	1,472.74
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	TNEKVELQELNDR	4.35	1,587.80
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	TNEKVELQELNDRFANYIDK	4.33	2,439.22
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	TVETRDGQVINETSQHHDDLE	4.44	2,423.11
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	VELQELNDR	3.21	1,115.57
Control	6011	vimentin	gi|110347570	53,710.80	100.00%	35	52	130	1.01%	68.70%	VEVERDNLAEDIMR	4.05	1,688.83
Control	6011	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	7	11	20	0.16%	22.20%	DKLDGNELDLSLSDLNEVPVK	5.14	2,313.18
Control	6011	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	7	11	20	0.16%	22.20%	DKLDGNELDLSLSDLNEVPVKELAALPK	6.26	3,035.62
Control	6011	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	7	11	20	0.16%	22.20%	LDGNELDLSLSDLNEVPVK	4.38	2,070.06
Control	6011	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	7	11	20	0.16%	22.20%	LDGNELDLSLSDLNEVPVKELAALPK	2.98	2,792.49
Control	6011	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	7	11	20	0.16%	22.20%	LVNLQHLDLLNNR	2.94	1,561.88
Control	6011	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	7	11	20	0.16%	22.20%	LVTLPVSFAQLK	4.66	1,315.80
Control	6011	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	7	11	20	0.16%	22.20%	WLDLKDNPLDPVLAK	2.97	1,736.96

Control	6011	RecName: Full=CDGSH iron sulfur domain-containing protein 1; AltName: Full=MitoNEET	gi|110825757,gi|73587067,gi|77404223	11,964.80	99.80%	2	3	5	0.04%	26.40%	HNEETGDNVGPLIIK	4.87	1,635.83
Control	6011	RecName: Full=CDGSH iron sulfur domain-containing protein 1; AltName: Full=MitoNEET	gi|110825757,gi|73587067,gi|77404223	11,964.80	99.80%	2	3	5	0.04%	26.40%	VVHAFDMEDLGDK	3.93	1,491.68
Control	6011	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	8	9	11	0.09%	18.30%	DAGQISGLNVLR	3.86	1,242.68

Control	6011	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	8	9	11	0.09%	18.30%	EQQIVIQSSGGLSKDDIENMVK	3.37	2,434.21
Control	6011	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	8	9	11	0.09%	18.30%	LYSPSQIGAFVLMK	4.58	1,569.83

Control	6011	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	8	9	11	0.09%	18.30%	MKETAENYLGHTAK	4.19	1,608.77
Control	6011	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	8	9	11	0.09%	18.30%	NAVITVPAYFNDSQR	2.46	1,694.85

Control	6011	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	8	9	11	0.09%	18.30%	QAVTNPNNTFYATK	3.11	1,568.77
Control	6011	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	8	9	11	0.09%	18.30%	STNGDTFLGGEDFDQALLR	3.75	2,055.96

Control	6011	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	8	9	11	0.09%	18.30%	TTPSVVAFTADGER	2.9	1,450.72
Control	6011	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	7	9	12	0.09%	46.00%	ADLEAQRDVTYEEAK	3.82	1,737.83
Control	6011	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	7	9	12	0.09%	46.00%	GAAGALMVYDITR	3.75	1,353.68
Control	6011	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	7	9	12	0.09%	46.00%	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	4.26	3,150.56
Control	6011	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	7	9	12	0.09%	46.00%	KIYQNIQDGSLDLNAAESGVQHKPSAPQGGR	7.18	3,278.65
Control	6011	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	7	9	12	0.09%	46.00%	LQIWDTAGQER	2.59	1,316.66
Control	6011	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	7	9	12	0.09%	46.00%	NLTNPNTVIILIGNK	4.45	1,623.94
Control	6011	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	7	9	12	0.09%	46.00%	TGENVEDAFLEAAK	2.85	1,493.71
Control	6011	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	4	5	7	0.05%	27.50%	EHGLIFMETSAK	2.95	1,378.67
Control	6011	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	4	5	7	0.05%	27.50%	FQPVHDLTIGVEFGAR	3.44	1,785.93
Control	6011	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	4	5	7	0.05%	27.50%	GAAGALVYDITR	3.72	1,319.73

Control	6011	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	4	5	7	0.05%	27.50%	YIIIGDTGVGK	3.02	1,135.64
Control	6011	RecName: Full=Phosphoglycerate kinase 1	gi|108860885,gi|74353972,gi|77735551	44,520.20	100.00%	4	6	7	0.05%	15.30%	AHSSMVGVNLPK	3.71	1,255.65
Control	6011	RecName: Full=Phosphoglycerate kinase 1	gi|108860885,gi|74353972,gi|77735551	44,520.20	100.00%	4	6	7	0.05%	15.30%	ALESPERPFLAILGGAK	3.4	1,769.00
Control	6011	RecName: Full=Phosphoglycerate kinase 1	gi|108860885,gi|74353972,gi|77735551	44,520.20	100.00%	4	6	7	0.05%	15.30%	VDFNVPMKNNQITNNQR	3.18	2,048.00
Control	6011	RecName: Full=Phosphoglycerate kinase 1	gi|108860885,gi|74353972,gi|77735551	44,520.20	100.00%	4	6	7	0.05%	15.30%	VLNNMEIGTSLFDEEGSK	4.02	1,998.93
Control	6011	PREDICTED: LMBR1 domain containing 2	gi|119913265	81,156.60	99.80%	2	2	2	0.02%	7.05%	DRIELLQDAEPLDFNAETFTDDPLESESGR	4.38	3,422.59
Control	6011	PREDICTED: LMBR1 domain containing 2	gi|119913265	81,156.60	99.80%	2	2	2	0.02%	7.05%	NMDDYEDFDEKHNTYPSEK	2.76	2,392.95
Control	6011	RecName: Full=Spliceosome RNA helicase BAT1; AltName: Full=DEAD box protein UAP56; AltName: Full=56 kDa U2AF65-associated protein	gi|122140442,gi|27883545,gi|74353855,gi|75832045	48,947.00	99.80%	2	2	3	0.02%	6.78%	ILVATNLFGR	3.11	1,103.66

Control	6011	RecName: Full=Spliceosome RNA helicase BAT1; AltName: Full=DEAD box protein UAP56; AltName: Full=56 kDa U2AF65-associated protein	gi|122140442,gi|27883545,gi|74353855,gi|75832045	48,947.00	99.80%	2	2	3	0.02%	6.78%	VNIAFNYDMPEDSDTYLHR	3.12	2,316.02
Control	6011	FAP protein	gi|146186488,gi|148233352	87,719.00	99.80%	2	2	2	0.02%	3.55%	FMGLPTKDDNLK	2.23	1,394.70
Control	6011	FAP protein	gi|146186488,gi|148233352	87,719.00	99.80%	2	2	2	0.02%	3.55%	IFIIDATYPEHIGPR	3.12	1,741.93
Control	6011	PREDICTED: similar to endonuclease G-like 1 isoform 2	gi|119914318	41,059.10	99.80%	2	2	2	0.02%	7.61%	AVLEQFGFPLAGTETR	3.85	1,735.90
Control	6011	PREDICTED: similar to endonuclease G-like 1 isoform 2	gi|119914318	41,059.10	99.80%	2	2	2	0.02%	7.61%	LSGLVFFPHLDR	3.03	1,400.77
Control	6011	Chain R, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Reduced State	gi|149241523,gi|149241540,gi|149241553,gi|149241570,gi|149241583,gi|149241600,gi|149241613,gi|42564216,gi|50872151,gi|60391934,gi|81674705	16,717.40	100.00%	3	4	9	0.07%	35.50%	EIYPYVIQELRPTLNELGISTPEELGLDKV	6.97	3,428.82
Control	6011	Chain R, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Reduced State	gi|149241523,gi|149241540,gi|149241553,gi|149241570,gi|149241583,gi|149241600,gi|149241613,gi|42564216,gi|50872151,gi|60391934,gi|81674705	16,717.40	100.00%	3	4	9	0.07%	35.50%	GMNTLVGYDLVPEPK	4.06	1,648.83

Control	6011	Chain R, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Reduced State	gi|149241523,gi|149241540,gi|149241553,gi|149241570,gi|149241583,gi|149241600,gi|149241613,gi|42564216,gi|50872151,gi|60391934,gi|81674705	16,717.40	100.00%	3	4	9	0.07%	35.50%	LNDFASAVR	2.5	992.5159
Control	6011	nucleoside-diphosphate kinase NBR-A	gi|1064895,gi|1064897,gi|115311823,gi|115496892,gi|119224069,gi|151556410,gi|169658382,gi|169658384,gi|1709243,gi|74354800	17,307.40	99.80%	2	4	4	0.03%	19.10%	TFIAIKPDGVQR	2.38	1,344.76
Control	6011	nucleoside-diphosphate kinase NBR-A	gi|1064895,gi|1064897,gi|115311823,gi|115496892,gi|119224069,gi|151556410,gi|169658382,gi|169658384,gi|1709243,gi|74354800	17,307.40	99.80%	2	4	4	0.03%	19.10%	VMLGETNPADSKPGTIR	3.4	1,801.91
Control	6011	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	9	10	10	0.08%	21.10%	DRGSDVESLDKLMK	3.69	1,608.79
Control	6011	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	9	10	10	0.08%	21.10%	GTVGFSGAELENLVNQAALK	4.63	2,018.06
Control	6011	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	9	10	10	0.08%	21.10%	GVEEAKQELQEVVEFLK	4.47	1,975.04
Control	6011	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	9	10	10	0.08%	21.10%	GVEEAKQELQEVVEFLKNPQK	3.72	2,442.29
Control	6011	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	9	10	10	0.08%	21.10%	IKFDQSVDPEIIAR	3.89	1,630.88
Control	6011	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	9	10	10	0.08%	21.10%	LAETQHTAPSFVK	4.15	1,428.75
Control	6011	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	9	10	10	0.08%	21.10%	LSPETQSAIEQEIR	2.94	1,600.82

Control	6011	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	9	10	10	0.08%	21.10%	QTINQLLAEMDGFKPNEGVIIIGATNFPEALDNALIRPGR	3.17	4,352.27
Control	6011	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	9	10	10	0.08%	21.10%	TTTGLDSAVDPVQMK	4.06	1,578.77
Control	6011	RecName: Full=Vesicle-associated membrane protein 8; Short=VAMP-8	gi|122140420,gi|74353894,gi|77735533	11,339.40	99.80%	2	3	4	0.03%	24.00%	NKTEDLEATSEHFK	4.47	1,648.78
Control	6011	RecName: Full=Vesicle-associated membrane protein 8; Short=VAMP-8	gi|122140420,gi|74353894,gi|77735533	11,339.40	99.80%	2	3	4	0.03%	24.00%	NLRDEVEGVK	2.94	1,158.61
Control	6011	RecName: Full=Annexin A1; AltName: Full=Annexin-1; AltName: Full=Annexin I; AltName: Full=Lipocortin I; AltName: Full=Calpactin II; AltName: Full=Chromobindin-9; AltName: Full=p35; AltName: Full=Phospholipase A2	gi|118597373,gi|264182,gi|61553085,gi|73587269,gi|73853762,gi|74	38,881.20	99.90%	2	2	2	0.02%	8.96%	ALLGHLEEVVLALLK	4.18	1,617.99

Control	6011	RecName: Full=Annexin A1; AltName: Full=Annexin-1; AltName: Full=Annexin I; AltName: Full=Lipocortin I; AltName: Full=Calpactin II; AltName: Full=Chromobindin-9; AltName: Full=p35; AltName: Full=Phospholipase A2	gi|118597373,gi|264182,gi|61553085,gi|73587269,gi|73853762,gi|74	38,881.20	99.90%	2	2	2	0.02%	8.96%	GLGTDEDTLNEILASR	3.29	1,703.84
Control	6011	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	8	9	0.07%	10.20%	IEHFISILGK	3.74	1,156.67
Control	6011	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	8	9	0.07%	10.20%	IPQAVVDVSSHLQK	4.84	1,520.84
Control	6011	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	8	9	0.07%	10.20%	NLEELYLVGSLSHDISR	2.8	1,945.00
Control	6011	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	8	9	0.07%	10.20%	QFSEQQPAFR	2.71	1,237.60
Control	6011	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	8	9	0.07%	10.20%	SIEEIVSFQHLR	3.75	1,457.77
Control	6011	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	8	9	0.07%	10.20%	SNTTQSGPEGSLVNSQSLK	3.82	1,933.95
Control	6011	PREDICTED: similar to MYB binding protein 1a	gi|119911777	151,796.60	100.00%	4	5	5	0.04%	4.22%	LLGAALPLLSK	3.08	1,095.71
Control	6011	PREDICTED: similar to MYB binding protein 1a	gi|119911777	151,796.60	100.00%	4	5	5	0.04%	4.22%	LMGPVNLFSDENIPR	3.82	1,717.86
Control	6011	PREDICTED: similar to MYB binding protein 1a	gi|119911777	151,796.60	100.00%	4	5	5	0.04%	4.22%	QPENPLVLELLEPLLLVIR	4.51	2,198.32

Control	6011	PREDICTED: similar to MYB binding protein 1a	gi|119911777	151,796.60	100.00%	4	5	5	0.04%	4.22%	TAGDRVETLYAR	3.3	1,351.70
Control	6011	MGAT1 protein	gi|154426138,gi|59858237,gi|62751783	51,684.70	100.00%	5	5	5	0.04%	14.10%	GIVSFLYR	2.82	954.5407
Control	6011	MGAT1 protein	gi|154426138,gi|59858237,gi|62751783	51,684.70	100.00%	5	5	5	0.04%	14.10%	LAQDAEVELER	3.43	1,272.64
Control	6011	MGAT1 protein	gi|154426138,gi|59858237,gi|62751783	51,684.70	100.00%	5	5	5	0.04%	14.10%	LNQHFVPFTQLDLSYLR	4.42	2,091.10
Control	6011	MGAT1 protein	gi|154426138,gi|59858237,gi|62751783	51,684.70	100.00%	5	5	5	0.04%	14.10%	LPSDSALDDDPASLTR	5.09	1,672.80
Control	6011	MGAT1 protein	gi|154426138,gi|59858237,gi|62751783	51,684.70	100.00%	5	5	5	0.04%	14.10%	VYGAPLLQVEK	2.74	1,216.69
Control	6011	ribosomal protein S14	gi|118150778,gi|28189929,gi|74268249	15,659.00	99.80%	2	2	2	0.02%	15.90%	ADRDESSPYAAMLAAQDVAQR	3.02	2,281.05
Control	6011	ribosomal protein S14	gi|118150778,gi|28189929,gi|74268249	15,659.00	99.80%	2	2	2	0.02%	15.90%	VKADRDESSPYAAMLAAQDVAQR	2.73	2,508.21
Control	6011	RecName: Full=Transitional endoplasmic reticulum ATPase; Short=TER ATPase; AltName: Full=15S Mg(2+)-ATPase p97 subunit; AltName: Full=Valosin-containing protein; Short=VCP	gi|122140828,gi|73586667,gi|77735541	89,314.70	100.00%	3	3	3	0.02%	5.21%	GILLYGPPGTGK	2.46	1,172.67

Control	6011	RecName: Full=Transitional endoplasmic reticulum ATPase; Short=TER ATPase; AltName: Full=15S Mg(2+)-ATPase p97 subunit; AltName: Full=Valosin-containing protein; Short=VCP	gi|122140828,gi|73586667,gi|77735541	89,314.70	100.00%	3	3	3	0.02%	5.21%	LDQLIYIPLPDEK	3.41	1,556.86
Control	6011	RecName: Full=Transitional endoplasmic reticulum ATPase; Short=TER ATPase; AltName: Full=15S Mg(2+)-ATPase p97 subunit; AltName: Full=Valosin-containing protein; Short=VCP	gi|122140828,gi|73586667,gi|77735541	89,314.70	100.00%	3	3	3	0.02%	5.21%	NAPAIIFIDELDAIAPK	2.39	1,811.00

Control	6011	PREDICTED: similar to Thioredoxin domain-containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein ERp46) isoform 1	gi|119915902	45,792.10	100.00%	3	3	5	0.04%	8.37%	FFKPGQEAVK	2.98	1,150.63
Control	6011	PREDICTED: similar to Thioredoxin domain-containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein ERp46) isoform 1	gi|119915902	45,792.10	100.00%	3	3	5	0.04%	8.37%	GYPTLLLFR	2.31	1,079.62
Control	6011	PREDICTED: similar to Thioredoxin domain-containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein ERp46) isoform 1	gi|119915902	45,792.10	100.00%	3	3	5	0.04%	8.37%	VDCTQHYELCSGNQVR	3.8	1,851.81

Control	6011	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	4	6	17	0.13%	25.60%	FFDEESYSLLR	3.52	1,405.66
Control	6011	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	4	6	17	0.13%	25.60%	FFDEESYSLLRK	3.05	1,533.76

Control	6011	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	4	6	17	0.13%	25.60%	NNEDVSVIPPLFTVSVDHR	4.9	2,138.09
Control	6011	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	4	6	17	0.13%	25.60%	VQNMALYADVSGK	4.43	1,411.69
Control	6011	Transmembrane protein 30A	gi|109658458,gi|115497784	40,667.50	99.80%	2	2	2	0.02%	6.93%	FRNPPGTDPLEER	3.43	1,527.76
Control	6011	Transmembrane protein 30A	gi|109658458,gi|115497784	40,667.50	99.80%	2	2	2	0.02%	6.93%	KNDLHPTLPAGR	3.26	1,318.72
Control	6011	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	4	5	5	0.04%	10.80%	ASPAPGSGHPDGPGTHLEMNSLDR	2.33	2,416.10

Control	6011	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	4	5	5	0.04%	10.80%	LRPESALAQAQK	3.36	1,311.74
Control	6011	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	4	5	5	0.04%	10.80%	NREPLMPSPQFIK	3.76	1,572.82
Control	6011	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	4	5	5	0.04%	10.80%	SYFSSFTDDIISQPMLK	2.88	1,994.94
Control	6011	RecName: Full=Elongation factor 1-gamma; Short=EF-1-gamma; AltName: Full=eEF-1B gamma	gi|122146155,gi|74268360,gi|94966781,gi|95769122	50,360.80	99.80%	2	2	2	0.02%	4.55%	AKDPFAHLPK	2.37	1,123.63
Control	6011	RecName: Full=Elongation factor 1-gamma; Short=EF-1-gamma; AltName: Full=eEF-1B gamma	gi|122146155,gi|74268360,gi|94966781,gi|95769122	50,360.80	99.80%	2	2	2	0.02%	4.55%	ILGLLDAHLK	2.97	1,092.68
Control	6011	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	3	3	7	0.05%	5.16%	IPLNDIFR	3.11	987.5623

Control	6011	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	3	3	7	0.05%	5.16%	VALKIPLNDIFR	3.74	1,398.85
Control	6011	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	3	3	7	0.05%	5.16%	YLDFVFAVK	2.44	1,101.60
Control	6011	syndecan binding protein (syntenin)	gi|115497576,gi|146231800,gi|74267862	32,372.10	100.00%	3	4	5	0.04%	18.10%	DSQIADILSTAGNIVTITIMPAFIFEHIIK	2.98	3,287.76
Control	6011	syndecan binding protein (syntenin)	gi|115497576,gi|146231800,gi|74267862	32,372.10	100.00%	3	4	5	0.04%	18.10%	DSQIADILSTAGNIVTITIMPAFIFEHIIKR	3.34	3,443.86
Control	6011	syndecan binding protein (syntenin)	gi|115497576,gi|146231800,gi|74267862	32,372.10	100.00%	3	4	5	0.04%	18.10%	SIDNGIFVQLVQANSPSSLVGLR	4.61	2,414.30
Control	6011	Nicastrin	gi|74267600,gi|77735901	79,055.00	99.80%	2	2	3	0.02%	2.65%	ALAGVATVLAR	3.02	1,041.64
Control	6011	Nicastrin	gi|74267600,gi|77735901	79,055.00	99.80%	2	2	3	0.02%	2.65%	LLYGFLVR	2.27	980.5928
Control	6011	RecName: Full=ATP synthase subunit O, mitochondrial; AltName: Full=Oligomycin sensitivity conferral protein; Short=OSCP; Flags: Precursor	gi|143811365,gi|157881386,gi|159164706,gi|163451,gi|27806307,gi|28189911,gi|74268299	13,204.80	100.00%	4	5	6	0.05%	36.70%	EKFSPLTSNLINLLAENGR	3.47	2,116.14

Control	6011	RecName: Full=ATP synthase subunit O, mitochondrial; AltName: Full=Oligomycin sensitivity conferral protein; Short=OSCP; Flags: Precursor	gi|143811365,gi|157881386,gi|159164706,gi|163451,gi|27806307,gi|28189911,gi|74268299	13,204.80	100.00%	4	5	6	0.05%	36.70%	FSPLTSNLINLLAENGR	3.18	1,859.00
Control	6011	RecName: Full=ATP synthase subunit O, mitochondrial; AltName: Full=Oligomycin sensitivity conferral protein; Short=OSCP; Flags: Precursor	gi|143811365,gi|157881386,gi|159164706,gi|163451,gi|27806307,gi|28189911,gi|74268299	13,204.80	100.00%	4	5	6	0.05%	36.70%	LVRPPVQIYGIEGR	3.3	1,596.92
Control	6011	RecName: Full=ATP synthase subunit O, mitochondrial; AltName: Full=Oligomycin sensitivity conferral protein; Short=OSCP; Flags: Precursor	gi|143811365,gi|157881386,gi|159164706,gi|163451,gi|27806307,gi|28189911,gi|74268299	13,204.80	100.00%	4	5	6	0.05%	36.70%	YATALYSAASK	2.69	1,145.58
Control	6011	G-protein gamma-12 subunit	gi|1109682,gi|148743956,gi|1586681,gi|2494918,gi|27807509	8,039.60	99.80%	2	2	2	0.02%	26.40%	NDPLLMGIPTSENPFK	4.13	1,788.88

Control	6011	G-protein gamma-12 subunit	gi|1109682,gi|148743956,gi|1586681,gi|2494918,gi|27807509	8,039.60	99.80%	2	2	2	0.02%	26.40%	NDPLLMGIPTSENPFKDKK	2.76	2,160.10
Control	6011	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	5	10	0.08%	18.80%	DFSLEQLR	2.41	1,007.52
Control	6011	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	5	10	0.08%	18.80%	FYGPAGPYGIFAGR	3.49	1,472.73
Control	6011	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	5	10	0.08%	18.80%	GLGAGAGAGEESPAASLPR	4.74	1,667.83
Control	6011	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	5	10	0.08%	18.80%	RGLGAGAGAGEESPAASLPR	4.3	1,823.94
Control	6011	TXNDC13 protein	gi|148878448,gi|149642897	38,865.40	100.00%	3	4	4	0.03%	12.10%	FFVTTLPAFFHAK	2.61	1,525.82
Control	6011	TXNDC13 protein	gi|148878448,gi|149642897	38,865.40	100.00%	3	4	4	0.03%	12.10%	VDVIQEPGLSGR	4.47	1,269.68
Control	6011	TXNDC13 protein	gi|148878448,gi|149642897	38,865.40	100.00%	3	4	4	0.03%	12.10%	YRGPGVYEDLQNYILEK	5.57	2,057.03
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	AEDIPQMDDAFSQTVK	2.13	1,810.82
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	ALSQIHEAAVR	1.63	1,194.66
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	DNDSDDVESNLLLPAGIALR	3.09	2,127.06
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	DNYIPNTLNPVFGR	3.04	1,619.82
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	DQLKPTQLLQNVAR	4.85	1,623.92
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	FGKPDPIVSVIFKDEK	4.94	1,819.00

Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	FKGFPPPVLSEDGSSIR	5.52	1,832.95
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	GKSDENEDPSVVGEFK	3.72	1,736.80
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	GNNPFFDELFFYNVHLTPSELMDEIISIR	5.65	3,473.67
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	IDVGFVYDEPGHAVMR	3.89	1,820.86
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	ILHQHLGPPEER	3.04	1,425.76
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	ILVELSTLLEK	3.94	1,257.77
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	IPAHQVLYSTSGGDASGK	5.44	1,787.89
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	ISVYDYDTFTR	2.65	1,379.65
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	IYRAEDIPQMDDAFSQTVK	4.23	2,243.07
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	KMAPSETHGAAAIFK	2.79	1,574.80
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	LDAVNTLLVMAER	3.27	1,460.78

Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	NDVVGTTYLHLSK	3.84	1,446.76
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	NLGPPGPPFNITPR	3.16	1,476.80
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	NLVDPFVEVSFAGK	3.6	1,521.79
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	SLLTEADAGHTEFTDEVYQNESR	6.42	2,612.17
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	TLHSSFQPNISQGR	4.05	1,571.79
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	TQGLVPEHVETR	2.57	1,365.71
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	VFLPKEELYMPPLVIK	2.8	1,932.09
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	VIEDRDNYIPNTLNPVFGR	3.9	2,232.14
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	VIIELFDNDQVGKDEFLGR	5.49	2,207.13
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	VIVESASNIPK	3.5	1,156.66
Control	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	28	34	46	0.36%	20.00%	VSMFVLGTGDEPPPEKQDR	3.33	2,118.02

Control	6011	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	4	5	7	0.05%	24.30%	ADFREPNAEVPRPIPHIGADYIPTEEER	3.62	3,218.59
Control	6011	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	4	5	7	0.05%	24.30%	FKNLENSPLGEALR	3.28	1,587.85
Control	6011	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	4	5	7	0.05%	24.30%	NLENSPLGEALR	2.53	1,312.69
Control	6011	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	4	5	7	0.05%	24.30%	SVPLAATSMLITQGLISK	2.79	1,846.04
Control	6011	RecName: Full=Myosin-10; AltName: Full=Myosin heavy chain 10; AltName: Full=Myosin heavy chain, non-muscle IIb; AltName: Full=Non-muscle myosin heavy chain IIb; Short=NMMHC II-b;	gi|13431706,gi|27807325,gi|4115748	229,087.40	99.80%	2	2	2	0.02%	2.58%	KFDQLLAEEK	3.08	1,220.65
Control	6011	RecName: Full=Myosin-10; AltName: Full=Myosin heavy chain 10; AltName: Full=Myosin heavy chain, non-muscle IIb; AltName: Full=Non-muscle myosin heavy chain IIb; Short=NMMHC II-b;	gi|13431706,gi|27807325,gi|4115748	229,087.40	99.80%	2	2	2	0.02%	2.58%	LDPHLVLDQLR	3.05	1,318.75

Control	6011	RecName: Full=Myosin-10; AltName: Full=Myosin heavy chain 10; AltName: Full=Myosin heavy chain, non-muscle IIb; AltName: Full=Non-muscle myosin heavy chain IIb; Short=NMMHC II-b;	gi|13431706,gi|27807325,gi|4115748	229,087.40	99.80%	2	2	2	0.02%	2.58%	TQLEELEDELQATEDAK	3.8	1,961.92
Control	6011	RecName: Full=Myosin-10; AltName: Full=Myosin heavy chain 10; AltName: Full=Myosin heavy chain, non-muscle IIb; AltName: Full=Non-muscle myosin heavy chain IIb; Short=NMMHC II-b;	gi|13431706,gi|27807325,gi|4115748	229,087.40	99.80%	2	2	2	0.02%	2.58%	VIQYLAHVASSHK	2.11	1,452.80
Control	6011	PREDICTED: similar to Interferon-induced protein with tetratricopeptide repeats 1 (IFIT-1)	gi|194678915	54,815.90	99.80%	2	2	2	0.02%	5.23%	LQDVEQEAEGEK	4.16	1,374.64

Control	6011	PREDICTED: similar to Interferon-induced protein with tetratricopeptide repeats 1 (IFIT-1)	gi|194678915	54,815.90	99.80%	2	2	2	0.02%	5.23%	YNVGIYNLLAYVK	3.02	1,529.84
Control	6011	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	6	6	7	0.05%	20.70%	GSYGDLGGPIITTQVTIPK	3.18	1,917.03
Control	6011	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	6	6	7	0.05%	20.70%	IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK	5.7	3,829.95
Control	6011	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	6	6	7	0.05%	20.70%	IILDLISESPIK	3.58	1,340.80
Control	6011	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	6	6	7	0.05%	20.70%	IITITGTQDQIQNAQYLLQNSVK	4.64	2,589.39
Control	6011	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	6	6	7	0.05%	20.70%	RPAEDMEEEQAFKR	3.13	1,751.80

Control	6011	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	6	6	7	0.05%	20.70%	TDYNASVSVPDSSGPER	3.45	1,780.80
Control	6011	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	gi|74354758,gi|77735915	23,580.50	99.80%	2	2	3	0.02%	11.30%	MIDLSGNPVLR	3.65	1,230.65
Control	6011	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	gi|74354758,gi|77735915	23,580.50	99.80%	2	2	3	0.02%	11.30%	SLISVIHLITAAR	3.92	1,393.85
Control	6011	RecName: Full=DnaJ homolog subfamily C member 11	gi|110808198,gi|114050887,gi|84708894	63,220.40	100.00%	5	6	7	0.05%	16.30%	GIRPGLTTVLAR	3.37	1,253.77
Control	6011	RecName: Full=DnaJ homolog subfamily C member 11	gi|110808198,gi|114050887,gi|84708894	63,220.40	100.00%	5	6	7	0.05%	16.30%	GTISVGIDATDLFDRYEEEYEDVSGSGFPQIEINK	5.46	3,893.82
Control	6011	RecName: Full=DnaJ homolog subfamily C member 11	gi|110808198,gi|114050887,gi|84708894	63,220.40	100.00%	5	6	7	0.05%	16.30%	GVLHQVMALDSEALR	3.37	1,654.86
Control	6011	RecName: Full=DnaJ homolog subfamily C member 11	gi|110808198,gi|114050887,gi|84708894	63,220.40	100.00%	5	6	7	0.05%	16.30%	LFNLVHQAYEVLSDPQTR	2.89	2,130.10

Control	6011	RecName: Full=DnaJ homolog subfamily C member 11	gi|110808198,gi|114050887,gi|84708894	63,220.40	100.00%	5	6	7	0.05%	16.30%	TPAEIREEFER	1.99	1,376.68
Control	6011	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	9	11	13	0.10%	11.70%	KPLIGSVLAK	2.34	1,025.67
Control	6011	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	9	11	13	0.10%	11.70%	KPLIGSVLAKDPDAAQR	3.95	1,779.01
Control	6011	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	9	11	13	0.10%	11.70%	NLESPSSFTIK	2.5	1,222.63
Control	6011	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	9	11	13	0.10%	11.70%	TSDKGQFFGITK	2.55	1,328.68
Control	6011	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	9	11	13	0.10%	11.70%	VDKNTGDVYALER	4.5	1,479.74
Control	6011	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	9	11	13	0.10%	11.70%	VGSPLGSLFVEDPDEPQNR	2.44	2,056.00
Control	6011	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	9	11	13	0.10%	11.70%	VGSPLGSLFVEDPDEPQNRK	2.92	2,184.09
Control	6011	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	9	11	13	0.10%	11.70%	YSFVQGEYR	2.66	1,148.54
Control	6011	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	9	11	13	0.10%	11.70%	YTFSVPEDIR	2.73	1,226.61

Control	6011	RecName: Full=Alpha-enolase; AltName: Full=2-phospho-D-glycerate hydro-lyase; AltName: Full=Non-neural enolase; Short=NNE; AltName: Full=Enolase 1; AltName: Full=Phosphopyruvate hydratase	gi|109940077,gi|74354056,gi|87196501	47,309.10	100.00%	3	3	3	0.02%	9.45%	DATNVGDEGGFAPNILENK	3.92	1,960.92
Control	6011	RecName: Full=Alpha-enolase; AltName: Full=2-phospho-D-glycerate hydro-lyase; AltName: Full=Non-neural enolase; Short=NNE; AltName: Full=Enolase 1; AltName: Full=Phosphopyruvate hydratase	gi|109940077,gi|74354056,gi|87196501	47,309.10	100.00%	3	3	3	0.02%	9.45%	IGAEVYHNLK	2.42	1,143.62

Control	6011	RecName: Full=Alpha-enolase; AltName: Full=2-phospho-D-glycerate hydro-lyase; AltName: Full=Non-neural enolase; Short=NNE; AltName: Full=Enolase 1; AltName: Full=Phosphopyruvate hydratase	gi|109940077,gi|74354056,gi|87196501	47,309.10	100.00%	3	3	3	0.02%	9.45%	KLNVVEQEKIDK	3.99	1,442.82
Control	6011	EH-domain containing 1	gi|110331767,gi|158455084,gi|59858079,gi|62751751,gi|75070053	60,666.10	99.90%	2	2	2	0.02%	10.30%	IGPEPTTDSFIAVMHGPTEGVVPGNALVVDPR	3.66	3,288.66
Control	6011	EH-domain containing 1	gi|110331767,gi|158455084,gi|59858079,gi|62751751,gi|75070053	60,666.10	99.90%	2	2	2	0.02%	10.30%	LADVDRDGLLDDEEFALANHLIK	2.41	2,582.31
Control	6011	LOC515309 protein	gi|148878460,gi|149773584	31,548.40	100.00%	3	4	4	0.03%	15.20%	FAEVYFAQSQQK	3.1	1,445.71
Control	6011	LOC515309 protein	gi|148878460,gi|149773584	31,548.40	100.00%	3	4	4	0.03%	15.20%	KEEEEEEEEYDEGSNLKR	4.93	2,241.96
Control	6011	LOC515309 protein	gi|148878460,gi|149773584	31,548.40	100.00%	3	4	4	0.03%	15.20%	SNPEDQILYQTER	3.37	1,592.76
Control	6011	SCO cytochrome oxidase deficient homolog 1 (yeast)	gi|119223914,gi|122692513,gi|134035032	33,641.50	99.80%	2	2	2	0.02%	12.10%	LIGLTGTKEEIDQVAR	4.83	1,742.97
Control	6011	SCO cytochrome oxidase deficient homolog 1 (yeast)	gi|119223914,gi|122692513,gi|134035032	33,641.50	99.80%	2	2	2	0.02%	12.10%	SIGKPLLGGPFSLTTHTGEPK	3.66	2,137.17
Control	6011	LMAN1 protein	gi|148744096,gi|149773586	58,038.50	100.00%	3	3	3	0.02%	10.60%	EKYQEEFEHFQQELDK	2.71	2,126.97

Control	6011	LMAN1 protein	gi|148744096,gi|149773586	58,038.50	100.00%	3	3	3	0.02%	10.60%	GAGAPGQQGQTFQQELDTVVNTQHEILR	2.75	3,022.50
Control	6011	LMAN1 protein	gi|148744096,gi|149773586	58,038.50	100.00%	3	3	3	0.02%	10.60%	YVSSLTEEISK	3.05	1,255.64
Control	6011	PREDICTED: lamin B2	gi|194668843	70,532.10	100.00%	3	3	3	0.02%	12.30%	ETENGEEGEDEAAEFGEEDLFHQQGDPR	3.19	3,164.28
Control	6011	PREDICTED: lamin B2	gi|194668843	70,532.10	100.00%	3	3	3	0.02%	12.30%	KLLEGEEERLK	2.99	1,343.75
Control	6011	PREDICTED: lamin B2	gi|194668843	70,532.10	100.00%	3	3	3	0.02%	12.30%	LQEKEELRELNDR	2.84	1,671.87
Control	6011	PREDICTED: lamin B2	gi|194668843	70,532.10	100.00%	3	3	3	0.02%	12.30%	QVLEGEEISYK	2.78	1,294.65
Control	6011	PREDICTED: lamin B2	gi|194668843	70,532.10	100.00%	3	3	3	0.02%	12.30%	TTLVNADGEEVAMR	3.09	1,521.72
Control	6011	acyl-CoA synthetase long-chain family member 5	gi|115497154,gi|152941112,gi|94534758	76,013.10	100.00%	3	4	4	0.03%	5.86%	ALVLISNVEK	3.22	1,085.66
Control	6011	acyl-CoA synthetase long-chain family member 5	gi|115497154,gi|152941112,gi|94534758	76,013.10	100.00%	3	4	4	0.03%	5.86%	GAMLTHANIVSNASGFLK	4.41	1,846.95
Control	6011	acyl-CoA synthetase long-chain family member 5	gi|115497154,gi|152941112,gi|94534758	76,013.10	100.00%	3	4	4	0.03%	5.86%	TLKPTLFPTVPR	3.21	1,369.82
Control	6011	poly(rC) binding protein 1	gi|59858399,gi|62751650,gi|75040221	37,480.20	99.80%	2	3	3	0.02%	9.27%	ESTGAQVQVAGDMLPNSTER	4.65	2,105.98
Control	6011	poly(rC) binding protein 1	gi|59858399,gi|62751650,gi|75040221	37,480.20	99.80%	2	3	3	0.02%	9.27%	IITLTGPTNAIFK	3.58	1,388.82
Control	6011	PREDICTED: similar to ER lipid raft associated 1 isoform 2	gi|194678978	39,049.70	99.80%	2	2	2	0.02%	15.20%	DLNVMAPGLTIQAVR	3.31	1,613.87

Control	6011	PREDICTED: similar to ER lipid raft associated 1 isoform 2	gi|194678978	39,049.70	99.80%	2	2	2	0.02%	15.20%	EALEPSGESPIQNK	3.15	1,498.74
Control	6011	PREDICTED: similar to ER lipid raft associated 1 isoform 2	gi|194678978	39,049.70	99.80%	2	2	2	0.02%	15.20%	ISEIEDAAFLAR	3.48	1,334.70
Control	6011	PREDICTED: similar to ER lipid raft associated 1 isoform 2	gi|194678978	39,049.70	99.80%	2	2	2	0.02%	15.20%	SVQTTLQTDEVK	3.97	1,348.70
Control	6011	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	100.00%	4	5	5	0.04%	15.00%	LQTVQSADQVLVLR	4.68	1,569.90
Control	6011	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	100.00%	4	5	5	0.04%	15.00%	QVVLVGQEPVLFSGSVR	4	1,814.02
Control	6011	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	100.00%	4	5	5	0.04%	15.00%	STVAALLQNLYQPTEGQVLLDGKPVSEYEHHYLHR	3.31	4,006.05
Control	6011	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	100.00%	4	5	5	0.04%	15.00%	VNFQNVSFAYPSRPDQPALQGLTFTLSPGQMTALVGPNGSGK	3.85	4,408.20
Control	6011	Solute carrier family 39 (zinc transporter), member 7	gi|112362085,gi|115749633,gi|146231764,gi|63169171	42,835.10	99.80%	2	2	3	0.02%	8.77%	DGPVRPQNAEEEKAGSDLR	2.61	2,068.01
Control	6011	Solute carrier family 39 (zinc transporter), member 7	gi|112362085,gi|115749633,gi|146231764,gi|63169171	42,835.10	99.80%	2	2	3	0.02%	8.77%	EKQSSEEEEKEAGALR	2.83	1,819.87

Control	6011	glutaminyl-peptide cyclotransferase-like	gi|110331975,gi|110331977,gi|112362220,gi|115495265,gi|122146335,gi|95768579,gi|95769160	41,828.70	99.80%	2	2	3	0.02%	9.92%	GPLIGSLPEAR	2.75	1,109.63
Control	6011	glutaminyl-peptide cyclotransferase-like	gi|110331975,gi|110331977,gi|112362220,gi|115495265,gi|122146335,gi|95768579,gi|95769160	41,828.70	99.80%	2	2	3	0.02%	9.92%	IQAIELFMLLDLLGAPNPTFYSHFPR	3.49	3,019.58
Control	6011	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	6	7	9	0.07%	27.80%	AGAGSATLSMAYAGAR	4.23	1,470.70
Control	6011	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	6	7	9	0.07%	27.80%	ANAFVAELKDLDPAR	3.13	1,629.86
Control	6011	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	6	7	9	0.07%	27.80%	LTLYDIAHTPGVAADLSHIETR	5.4	2,393.25
Control	6011	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	6	7	9	0.07%	27.80%	MIAEAIPELK	2.37	1,130.61

Control	6011	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	6	7	9	0.07%	27.80%	VAVLGASGGIGQPLSLLLK	4.13	1,793.09
Control	6011	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	6	7	9	0.07%	27.80%	VNVPVIGGHAGK	3.04	1,147.66
Control	6011	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	7	22	0.17%	27.60%	FGLIPEEFFQFLYPK	3.09	1,874.97
Control	6011	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	7	22	0.17%	27.60%	HYLFDVQR	2.77	1,077.55
Control	6011	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	7	22	0.17%	27.60%	IAQLEEVKQASIK	4.54	1,456.84
Control	6011	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	7	22	0.17%	27.60%	NNIAMALEVTYR	4.28	1,410.70

Control	6011	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	7	22	0.17%	27.60%	PVPPLPEHGGK	1.58	1,127.62
Control	6011	Ribosomal protein S8	gi|119224110,gi|58760384,gi|59858489,gi|70778956,gi|74268417,gi|75070020	24,188.40	99.80%	2	3	4	0.03%	13.50%	IIDVVYNASNNELVR	4.95	1,718.91
Control	6011	Ribosomal protein S8	gi|119224110,gi|58760384,gi|59858489,gi|70778956,gi|74268417,gi|75070020	24,188.40	99.80%	2	3	4	0.03%	13.50%	ISSLLEEQFQQGK	4.34	1,506.78
Control	6011	PREDICTED: asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	gi|119908777,gi|41056704,gi|60391782	395,853.30	99.80%	2	2	2	0.02%	1.10%	SVPCMEVIRYAMQVLLNVAK	3.19	2,280.19
Control	6011	PREDICTED: asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	gi|119908777,gi|41056704,gi|60391782	395,853.30	99.80%	2	2	2	0.02%	1.10%	VVITYLSFLCARLLDLR	2.92	1,995.15
Control	6011	RPS17 protein	gi|148745739,gi|149642675,gi|151554859,gi|166219437	15,564.50	100.00%	3	3	3	0.02%	43.70%	IAGYVTHLMK	2.88	1,148.61
Control	6011	RPS17 protein	gi|148745739,gi|149642675,gi|151554859,gi|166219437	15,564.50	100.00%	3	3	3	0.02%	43.70%	LLDFGSLSNLQVTQPTVGMNFK	3.05	2,425.24
Control	6011	RPS17 protein	gi|148745739,gi|149642675,gi|151554859,gi|166219437	15,564.50	100.00%	3	3	3	0.02%	43.70%	RDNYVPEVSALDQEIIEVDPDTKEMLK	3.2	3,162.55

Control	6011	PREDICTED: similar to oxysterol 7alpha-hydroxylase	gi|194672764	90,479.20	100.00%	5	6	7	0.05%	9.43%	AMAVLRDEIDHLLQSTGQK	2.89	2,141.10
Control	6011	PREDICTED: similar to oxysterol 7alpha-hydroxylase	gi|194672764	90,479.20	100.00%	5	6	7	0.05%	9.43%	FLFGIPYPDSDVLFR	3.19	1,785.92
Control	6011	PREDICTED: similar to oxysterol 7alpha-hydroxylase	gi|194672764	90,479.20	100.00%	5	6	7	0.05%	9.43%	LSFQIFTNK	2.61	1,097.60
Control	6011	PREDICTED: similar to oxysterol 7alpha-hydroxylase	gi|194672764	90,479.20	100.00%	5	6	7	0.05%	9.43%	MLTDSDLIDEIHSTYQFLQGK	3.6	2,470.18
Control	6011	PREDICTED: similar to oxysterol 7alpha-hydroxylase	gi|194672764	90,479.20	100.00%	5	6	7	0.05%	9.43%	YYHLPFGLGVSK	4.67	1,380.73
Control	6011	RecName: Full=ER lumen protein retaining receptor 2; AltName: Full=KDEL endoplasmic reticulum protein retention receptor 2; Short=KDEL receptor 2	gi|116247777,gi|119331188,gi|86823931	24,437.80	99.80%	2	2	2	0.02%	16.00%	LTGDLSHLAAIVILLLK	5.44	1,790.12

Control	6011	RecName: Full=ER lumen protein retaining receptor 2; AltName: Full=KDEL endoplasmic reticulum protein retention receptor 2; Short=KDEL receptor 2	gi|116247777,gi|119331188,gi|86823931	24,437.80	99.80%	2	2	2	0.02%	16.00%	YLDLFTSFISLYNTSMK	3.63	2,059.01
Control	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	12	15	24	0.19%	37.70%	AVFVDLEPTVIDEVR	5.22	1,701.91
Control	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	12	15	24	0.19%	37.70%	DVNAAIATIK	3.03	1,015.58
Control	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	12	15	24	0.19%	37.70%	EIIDLVLDR	2.4	1,085.62
Control	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	12	15	24	0.19%	37.70%	FDGALNVDLTEFQTNLVPYPR	3.8	2,409.21
Control	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	12	15	24	0.19%	37.70%	IHFPLATYAPVISAEK	3.5	1,756.96
Control	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	12	15	24	0.19%	37.70%	LDHKFDLMYAK	2.14	1,396.69
Control	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	12	15	24	0.19%	37.70%	LISQIVSSITASLR	3.78	1,487.88
Control	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	12	15	24	0.19%	37.70%	NLDIERPTYTNLNR	3.6	1,718.88
Control	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	12	15	24	0.19%	37.70%	QLFHPEQLITGKEDAANNYAR	3.82	2,415.21
Control	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	12	15	24	0.19%	37.70%	RNLDIERPTYTNLNR	2.33	1,874.98
Control	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	12	15	24	0.19%	37.70%	TIGGGDDSFNTFFSETGAGK	3.3	2,007.89
Control	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	12	15	24	0.19%	37.70%	VGINYQPPTVVPGGDLAK	3.9	1,824.99
Control	6011	KTN1 protein	gi|154426114,gi|156121057	150,612.10	99.80%	2	2	2	0.02%	2.30%	AQQLSITSQVQELQNLLK	2.92	2,041.13
Control	6011	KTN1 protein	gi|154426114,gi|156121057	150,612.10	99.80%	2	2	2	0.02%	2.30%	SVEELLEAELLK	3.01	1,372.76

Control	6011	tricarboxylate carrier protein	gi|1765906,gi|2497986,gi|27807191	33,859.10	99.90%	2	2	2	0.02%	7.72%	GLSSLLYGSIPK	3.08	1,234.70
Control	6011	tricarboxylate carrier protein	gi|1765906,gi|2497986,gi|27807191	33,859.10	99.90%	2	2	2	0.02%	7.72%	GTYQGLTATVLK	2.77	1,251.69
Control	6011	PREDICTED: similar to transmembrane protein 165	gi|76619924	34,667.10	99.80%	2	3	4	0.03%	13.30%	MSPDEGQEELEEVQAELK	4.11	2,076.93
Control	6011	PREDICTED: similar to transmembrane protein 165	gi|76619924	34,667.10	99.80%	2	3	4	0.03%	13.30%	NKEPPAPAQQLQPQPAAVQGPEPAR	5.8	2,619.36
Control	6011	RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8; AltName: Full=NADH-ubiquinone oxidoreductase 19 kDa subunit; AltName: Full=Complex I-19kD;	gi|1171870,gi|28461275,gi|599681,gi|86827664	20,073.10	99.80%	2	3	3	0.02%	17.40%	ARPEPNPEVEGDLKPAR	5.96	1,874.97

Control	6011	RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8; AltName: Full=NADH-ubiquinone oxidoreductase 19 kDa subunit; AltName: Full=Complex I-19kD;	gi|1171870,gi|28461275,gi|599681,gi|86827664	20,073.10	99.80%	2	3	3	0.02%	17.40%	TDRPLPENPYHSR	2.21	1,581.78
Control	6011	Adaptor-related protein complex 2, beta 1 subunit	gi|115304848,gi|115497346,gi|122132354,gi|124028640	104,551.20	99.80%	2	2	2	0.02%	5.12%	LAPPLVTLLSGEPEVQYVALR	4.09	2,265.29
Control	6011	Adaptor-related protein complex 2, beta 1 subunit	gi|115304848,gi|115497346,gi|122132354,gi|124028640	104,551.20	99.80%	2	2	2	0.02%	5.12%	LASQANIAQVLAELKEYATEVDVDFVR	3.37	2,992.56
Control	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	12	17	24	0.19%	12.60%	ATILYASETGR	3.4	1,181.62

Control	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	12	17	24	0.19%	12.60%	AVDTRLEELGGER	2.78	1,444.74
Control	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	12	17	24	0.19%	12.60%	DFINQYYSSIK	3.15	1,377.67

Control	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	12	17	24	0.19%	12.60%	DFINQYYSSIKR	2.11	1,533.77
Control	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	12	17	24	0.19%	12.60%	ESSNTDSAGALGTLR	3.64	1,478.71

Control	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	12	17	24	0.19%	12.60%	LLSTLAEEPSEQQELETLSQDPR	5.21	2,613.29
Control	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	12	17	24	0.19%	12.60%	LSTQAEGLQLLPGLIHVHR	3.91	2,082.18

Control	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	12	17	24	0.19%	12.60%	SAITVFPQR	2.61	1,018.57
Control	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	12	17	24	0.19%	12.60%	TYVQDILR	2.78	1,007.55

Control	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	12	17	24	0.19%	12.60%	VEDPPPPTESVAVEQLEK	3.55	1,963.99
Control	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	12	17	24	0.19%	12.60%	VLTAFSREPDSPK	3.4	1,446.76

Control	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	12	17	24	0.19%	12.60%	YHEDIFGLTLR	3.17	1,363.70
Control	6011	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	4	7	12	0.09%	11.90%	IGGIGTVPVGR	3.15	1,025.61
Control	6011	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	4	7	12	0.09%	11.90%	LPLQDVYK	2.55	975.5511
Control	6011	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	4	7	12	0.09%	11.90%	VETGVLKPGMVVTFAPVNVTTEVK	4.46	2,531.38
Control	6011	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	4	7	12	0.09%	11.90%	YYVTIIDAPGHR	3	1,404.73

Control	6011	cell division cycle 42 (GTP binding protein, 25kDa)	gi|114052486,gi|122063301,gi|86821687	21,240.70	99.80%	2	3	8	0.06%	19.90%	NVFDEAILAALEPPEPK	4.51	1,852.97
Control	6011	cell division cycle 42 (GTP binding protein, 25kDa)	gi|114052486,gi|122063301,gi|86821687	21,240.70	99.80%	2	3	8	0.06%	19.90%	TPFLLVGTQIDLRDDPSTIEK	4.97	2,358.26
Control	6011	RecName: Full=Golgi SNAP receptor complex member 1	gi|108935998,gi|83638559,gi|84370083	28,524.90	99.90%	2	2	2	0.02%	13.60%	MNTLANRFPAVNSLIQR	2.85	1,961.04
Control	6011	RecName: Full=Golgi SNAP receptor complex member 1	gi|108935998,gi|83638559,gi|84370083	28,524.90	99.90%	2	2	2	0.02%	13.60%	NSDRLIEETISIAMATK	2.99	1,907.97
Control	6011	LOC535125	gi|110558977,gi|115496698	75,634.70	99.80%	2	2	2	0.02%	5.53%	IAESLGGSGYSVER	3.86	1,424.70
Control	6011	LOC535125	gi|110558977,gi|115496698	75,634.70	99.80%	2	2	2	0.02%	5.53%	VPVFGTSTHTLDISQLGDLGTRR	2.56	2,470.31
Control	6011	minor histocompatibility antigen 13	gi|164448616	41,537.10	100.00%	3	3	6	0.05%	15.60%	GEVTEMFSYEESNPKDPAAVTETR	3.52	2,703.21
Control	6011	minor histocompatibility antigen 13	gi|164448616	41,537.10	100.00%	3	3	6	0.05%	15.60%	LVFPQDLLEK	2.62	1,201.68
Control	6011	minor histocompatibility antigen 13	gi|164448616	41,537.10	100.00%	3	3	6	0.05%	15.60%	QYQLLFTQGSGENKEEIINYEFDTK	4.93	2,994.44
Control	6011	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	4	5	8	0.06%	31.20%	EDGNEEDKENQGDETQGQQPPQR	3.23	2,628.10
Control	6011	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	4	5	8	0.06%	31.20%	GAEAANVTGPGGVPVQGSK	4.31	1,695.87
Control	6011	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	4	5	8	0.06%	31.20%	NYQQNYQNSESGEKNEGSESAPEGQAQQR	5.62	3,257.40

Control	6011	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	4	5	8	0.06%	31.20%	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	4.81	3,239.53
Control	6011	PREDICTED: similar to vesicle amine transport protein 1 isoform 1	gi|76671278	42,822.00	100.00%	3	3	3	0.02%	10.20%	GVDIVMDPLGGSDTAK	3.8	1,590.77
Control	6011	PREDICTED: similar to vesicle amine transport protein 1 isoform 1	gi|76671278	42,822.00	100.00%	3	3	3	0.02%	10.20%	VLLVPGPEKEN	2.67	1,194.67
Control	6011	PREDICTED: similar to vesicle amine transport protein 1 isoform 1	gi|76671278	42,822.00	100.00%	3	3	3	0.02%	10.20%	VVTYGMANLLTGPK	3.28	1,479.79
Control	6011	RecName: Full=Adenosylhomocysteinase; Short=AdoHcyase; AltName: Full=S-adenosyl-L-homocysteine hydrolase	gi|118573856,gi|146231804,gi|75773598,gi|77735583	47,620.90	100.00%	4	4	5	0.04%	12.50%	DGPLNMILDDGGDLTNLIHTK	3.74	2,268.12
Control	6011	RecName: Full=Adenosylhomocysteinase; Short=AdoHcyase; AltName: Full=S-adenosyl-L-homocysteine hydrolase	gi|118573856,gi|146231804,gi|75773598,gi|77735583	47,620.90	100.00%	4	4	5	0.04%	12.50%	VAVVAGYGDVGK	3.29	1,134.62

Control	6011	RecName: Full=Adenosylhomocysteinase; Short=AdoHcyase; AltName: Full=S-adenosyl-L-homocysteine hydrolase	gi|118573856,gi|146231804,gi|75773598,gi|77735583	47,620.90	100.00%	4	4	5	0.04%	12.50%	VPAINVNDSVTK	4.01	1,256.68
Control	6011	RecName: Full=Adenosylhomocysteinase; Short=AdoHcyase; AltName: Full=S-adenosyl-L-homocysteine hydrolase	gi|118573856,gi|146231804,gi|75773598,gi|77735583	47,620.90	100.00%	4	4	5	0.04%	12.50%	YPQLLSGIR	3.15	1,046.60
Control	6011	glycosyltransferase 8 domain containing 1	gi|59858311,gi|62751968,gi|75040232,gi|88758687	41,941.60	100.00%	2	2	2	0.02%	7.28%	FYLPILVPR	3.04	1,117.68
Control	6011	glycosyltransferase 8 domain containing 1	gi|59858311,gi|62751968,gi|75040232,gi|88758687	41,941.60	100.00%	2	2	2	0.02%	7.28%	VKEDPDQGESIKPLTFAR	2.72	2,030.06
Control	6011	H3 histone, family 3A	gi|59858289,gi|62177168,gi|95769331	15,310.70	100.00%	3	4	8	0.06%	38.20%	EIAQDFKTDLR	3.26	1,335.69
Control	6011	H3 histone, family 3A	gi|59858289,gi|62177168,gi|95769331	15,310.70	100.00%	3	4	8	0.06%	38.20%	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	4.62	3,380.68
Control	6011	H3 histone, family 3A	gi|59858289,gi|62177168,gi|95769331	15,310.70	100.00%	3	4	8	0.06%	38.20%	YRPGTVALR	2.65	1,032.59
Control	6011	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A3	gi|194664564	39,691.20	99.80%	2	2	2	0.02%	11.30%	IFVGGIKEDTEEYNLRDYFEK	2.36	2,565.25

Control	6011	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A3	gi|194664564	39,691.20	99.80%	2	2	2	0.02%	11.30%	SSGSPYGGGYGSGGGSGGYGSR	4.69	1,910.79
Control	6011	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	100.00%	4	4	4	0.03%	13.70%	FTSLGLLPR	2.79	1,003.59
Control	6011	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	100.00%	4	4	4	0.03%	13.70%	LTEDGLPLGINLGK	4.37	1,439.81
Control	6011	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	100.00%	4	4	4	0.03%	13.70%	VFRLPEDQAIINR	3.8	1,570.87
Control	6011	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	100.00%	4	4	4	0.03%	13.70%	VPIVGVGGVSSGQDALEK	5.24	1,711.92
Control	6011	inositol monophosphatase domain containing 1	gi|114052460,gi|122136157,gi|86827736	38,905.90	99.80%	2	2	3	0.02%	8.84%	TREGADDKMTSGDVLSNR	3.19	1,967.91
Control	6011	inositol monophosphatase domain containing 1	gi|114052460,gi|122136157,gi|86827736	38,905.90	99.80%	2	2	3	0.02%	8.84%	VLALLDVPDKSQEK	2.01	1,554.87
Control	6011	MHC class I antigen	gi|72536869	40,311.10	99.80%	2	3	9	0.07%	18.20%	EGEDQTQDMELVETRPSGDGTFQK	2.99	2,713.19
Control	6011	MHC class I antigen	gi|72536869	40,311.10	99.80%	2	3	9	0.07%	18.20%	GYSQDAYDGRDYIALNEDLR	4.98	2,334.06
Control	6011	MHC class I antigen	gi|72536869	40,311.10	99.80%	2	3	9	0.07%	18.20%	PGLEEPRFIIVGYVDDTQFVR	3.05	2,450.27
Control	6011	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	4	6	9	0.07%	7.01%	AENLGEVLR	2.84	1,000.54
Control	6011	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	4	6	9	0.07%	7.01%	AENLGEVLRGDR	2.6	1,328.69

Control	6011	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	4	6	9	0.07%	7.01%	ISEDYYVHLIADNLPVATR	5.38	2,189.12
Control	6011	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	4	6	9	0.07%	7.01%	IVNTPFQVLMNSEK	3.75	1,635.84
Control	6011	PREDICTED: plexin A2	gi|194674254	210,938.30	99.90%	2	2	2	0.02%	1.80%	EAFAELQTDINELTSDLDR	2.95	2,180.04
Control	6011	PREDICTED: plexin A2	gi|194674254	210,938.30	99.90%	2	2	2	0.02%	1.80%	FVDDLFETLFSTVHR	2.98	1,825.91
Control	6011	STX12 protein	gi|154425559,gi|154425988,gi|155371837	31,338.20	99.80%	2	2	2	0.02%	10.60%	ELGSLPLPLSTSEQR	3.54	1,626.87
Control	6011	STX12 protein	gi|154425559,gi|154425988,gi|155371837	31,338.20	99.80%	2	2	2	0.02%	10.60%	QLEADILDVNQIFK	3.72	1,645.88
Control	6011	PREDICTED: similar to plexin B2 isoform 1	gi|194681262	204,931.90	100.00%	2	2	2	0.02%	1.68%	EAFEAYTDHATYK	2.93	1,545.69
Control	6011	PREDICTED: similar to plexin B2 isoform 1	gi|194681262	204,931.90	100.00%	2	2	2	0.02%	1.68%	NLDTVQGSPLLVGSDLLK	3.64	1,869.03
Control	6011	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	100.00%	4	5	7	0.05%	21.00%	AITIFQERDPANIK	2.06	1,615.88
Control	6011	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	100.00%	4	5	7	0.05%	21.00%	GAAQNIIPASTGAAK	3.96	1,369.74
Control	6011	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	100.00%	4	5	7	0.05%	21.00%	IVSNASCTTNCLAPLAK	2.29	1,705.86

Control	6011	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	100.00%	4	5	7	0.05%	21.00%	VIHDHFGIVEGLMTTVHAITATQK	4	2,634.37
Control	6011	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	gi|155371851	60,580.30	99.80%	2	2	2	0.02%	6.10%	GRVPYPGMVNR	3.13	1,261.65
Control	6011	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	gi|155371851	60,580.30	99.80%	2	2	2	0.02%	6.10%	LVPLYAVVSEEPIYIVTEFMSK	2.89	2,543.34
Control	6011	PREDICTED: similar to Dehydrogenase/reductase SDR family member 7B, partial	gi|119935978	29,227.90	99.80%	2	2	2	0.02%	10.70%	SPVQVAQDILAALGK	4.68	1,509.86
Control	6011	PREDICTED: similar to Dehydrogenase/reductase SDR family member 7B, partial	gi|119935978	29,227.90	99.80%	2	2	2	0.02%	10.70%	VMETNYFGPVALTK	4.04	1,585.79
Control	6011	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	100.00%	3	5	6	0.05%	12.70%	FFLSAGLIDKVDNFK	1.85	1,713.92
Control	6011	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	100.00%	3	5	6	0.05%	12.70%	LEDPHVDIIR	2.34	1,206.65
Control	6011	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	100.00%	3	5	6	0.05%	12.70%	VSFSYAGLSSDDPDLGPAHVVTVIAR	4.55	2,673.35
Control	6011	intergral membrane protein 1	gi|114051696,gi|122136222,gi|152941168,gi|86823970	80,641.10	99.90%	2	2	4	0.03%	2.55%	FYSLLDPSYAK	2.53	1,303.66

Control	6011	intergral membrane protein 1	gi|114051696,gi|122136222,gi|152941168,gi|86823970	80,641.10	99.90%	2	2	4	0.03%	2.55%	IIFDDFR	2.24	925.4779
Control	6011	Myeloid-associated differentiation marker	gi|111308557,gi|115497460	35,291.10	99.80%	2	3	7	0.05%	9.01%	LVFVRV	1.99	732.4766
Control	6011	Myeloid-associated differentiation marker	gi|111308557,gi|115497460	35,291.10	99.80%	2	3	7	0.05%	9.01%	TTVTTTMSSSSGLGSPTIVGSPR	4.17	2,240.11
Control	6011	ribosomal protein L24	gi|27806129,gi|28189314,gi|28189753,gi|28189757,gi|28189765,gi|3132823,gi|41019240,gi|74267598	17,630.30	99.80%	2	2	2	0.02%	13.50%	AITGASLADIMAK	4.41	1,277.68
Control	6011	ribosomal protein L24	gi|27806129,gi|28189314,gi|28189753,gi|28189757,gi|28189765,gi|3132823,gi|41019240,gi|74267598	17,630.30	99.80%	2	2	2	0.02%	13.50%	VFQFLNAK	2.14	966.5407
Control	6011	PREDICTED: similar to Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A) (Guanylate cyclase) (NPR-A) (Atrial natriuretic peptide A-type receptor)	gi|194665089	119,021.60	100.00%	3	3	3	0.02%	4.04%	IITYKEPDNPEYLEFLQK	3.19	2,240.15

Control	6011	PREDICTED: similar to Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A) (Guanylate cyclase) (NPR-A) (Atrial natriuretic peptide A-type receptor)	gi|194665089	119,021.60	100.00%	3	3	3	0.02%	4.04%	MALALLDAVR	3.37	1,088.61
Control	6011	PREDICTED: similar to Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A) (Guanylate cyclase) (NPR-A) (Atrial natriuretic peptide A-type receptor)	gi|194665089	119,021.60	100.00%	3	3	3	0.02%	4.04%	MEQYANNLEELVEER	3.71	1,882.85
Control	6011	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	6	7	8	0.06%	10.10%	DAEAWFNEK	2.6	1,109.49

Control	6011	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	6	7	8	0.06%	10.10%	IRLENEIQTYR	4.13	1,434.77
Control	6011	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	6	7	8	0.06%	10.10%	LENEIQTYR	3.44	1,165.58
Control	6011	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	6	7	8	0.06%	10.10%	QSLEASLAETEGR	4.14	1,390.68
Control	6011	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	6	7	8	0.06%	10.10%	SQYEQLAEKNR	3.05	1,365.68
Control	6011	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	6	7	8	0.06%	10.10%	VLDELTLTK	2.44	1,031.60

Control	6011	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	7	8	8	0.06%	16.50%	DLDELSRYPEDKITPENLPQILLQLK	4.88	3,080.65
Control	6011	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	7	8	8	0.06%	16.50%	DLSAAGIGLLAAATQSLSMPASLGR	2.26	2,387.26
Control	6011	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	7	8	8	0.06%	16.50%	DSFDDRGPSLNPVLDYDHGSR	4.95	2,362.07
Control	6011	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	7	8	8	0.06%	16.50%	SQESGYYDRMDYEDDRLR	2.39	2,313.97
Control	6011	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	7	8	8	0.06%	16.50%	VIHLSNLPHSGYSDSAVLK	3.51	2,037.08
Control	6011	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	7	8	8	0.06%	16.50%	VVHIMDFQR	3.07	1,160.59
Control	6011	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	7	8	8	0.06%	16.50%	YQLLQLVEPFGVISNHLILNK	3.46	2,438.38
Control	6011	PREDICTED: similar to dynein, cytoplasmic, heavy polypeptide 1 isoform 3	gi|194677009	531,935.00	100.00%	5	5	5	0.04%	2.35%	AHQANQLYPFAISLIESVR	3.82	2,157.15
Control	6011	PREDICTED: similar to dynein, cytoplasmic, heavy polypeptide 1 isoform 3	gi|194677009	531,935.00	100.00%	5	5	5	0.04%	2.35%	GIFEALRPLETLPVEGLIR	2.85	2,123.22
Control	6011	PREDICTED: similar to dynein, cytoplasmic, heavy polypeptide 1 isoform 3	gi|194677009	531,935.00	100.00%	5	5	5	0.04%	2.35%	KLVPLLLEDGGEAPAALEAALEEK	3.12	2,476.35
Control	6011	PREDICTED: similar to dynein, cytoplasmic, heavy polypeptide 1 isoform 3	gi|194677009	531,935.00	100.00%	5	5	5	0.04%	2.35%	LVAEDIPLLFSLLSDVFPGVQYHR	4.46	2,728.47

Control	6011	PREDICTED: similar to dynein, cytoplasmic, heavy polypeptide 1 isoform 3	gi|194677009	531,935.00	100.00%	5	5	5	0.04%	2.35%	VFYEEELDVPLVLFNEVLDHVLR	4.57	2,787.46
Control	6011	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	4	6	13	0.10%	23.30%	GKESEKELALLK	3.61	1,344.77
Control	6011	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	4	6	13	0.10%	23.30%	GVGDDQLGEESEERDDHLLPM	2.4	2,357.02
Control	6011	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	4	6	13	0.10%	23.30%	HTLADNFNPVSEER	4.86	1,628.77
Control	6011	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	4	6	13	0.10%	23.30%	SFESTVGQSPDMYSYVFR	3.9	2,115.93
Control	6011	ADP-ribosylation-like factor 6 interacting protein 5	gi|59858163,gi|62460474,gi|74354855,gi|75057806	21,648.60	99.80%	2	3	7	0.05%	13.80%	FARPDFR	1.77	908.4737
Control	6011	ADP-ribosylation-like factor 6 interacting protein 5	gi|59858163,gi|62460474,gi|74354855,gi|75057806	21,648.60	99.80%	2	3	7	0.05%	13.80%	TPMGIVLDALEQQEETITK	4.45	2,132.08
Control	6011	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	4	4	6	0.05%	10.50%	EKPYFPIPEDYTFIQNVPLEDR	4.18	2,710.34

Control	6011	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	4	4	6	0.05%	10.50%	LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR	4.99	3,142.43
Control	6011	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	4	4	6	0.05%	10.50%	NFILDQTNVSAAAQR	3.91	1,647.84
Control	6011	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	4	4	6	0.05%	10.50%	SSGPTSLFAVTVAPPGAR	2.25	1,714.91
Control	6011	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	gi|124829038,gi|125630707,gi|171769867	51,147.90	100.00%	3	4	5	0.04%	9.27%	ADYLQNYEFPHLQNFIK	4.7	2,140.05
Control	6011	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	gi|124829038,gi|125630707,gi|171769867	51,147.90	100.00%	3	4	5	0.04%	9.27%	LLLVSFDGFR	3.23	1,166.66
Control	6011	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	gi|124829038,gi|125630707,gi|171769867	51,147.90	100.00%	3	4	5	0.04%	9.27%	VLEEIDEHIGELVHR	3.05	1,787.93
Control	6011	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	6	6	6	0.05%	12.60%	DNFTAIPEGTNGVEER	2.26	1,748.81
Control	6011	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	6	6	6	0.05%	12.60%	EESREPAPASPAPAGVEIR	3.9	1,962.99
Control	6011	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	6	6	6	0.05%	12.60%	MDENQFVAVTSTNAAK	3.17	1,741.81
Control	6011	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	6	6	6	0.05%	12.60%	QIGDNLIVPGGVK	2.73	1,309.75

Control	6011	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	6	6	6	0.05%	12.60%	SAADLISQAR	2.82	1,031.55
Control	6011	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	6	6	6	0.05%	12.60%	TLDFDALSVGQR	3.13	1,321.67
Control	6011	RecName: Full=Receptor expression-enhancing protein 5	gi|109892956,gi|114053301,gi|88954091	21,400.00	99.80%	2	2	2	0.02%	12.20%	HESQVDNVVNDLKDK	3.59	1,739.86
Control	6011	RecName: Full=Receptor expression-enhancing protein 5	gi|109892956,gi|114053301,gi|88954091	21,400.00	99.80%	2	2	2	0.02%	12.20%	IIRPFFLK	2.52	1,033.66
Control	6011	TOMM22 protein	gi|151556851,gi|154152189	15,275.00	99.80%	2	3	4	0.03%	26.40%	LQMEQQQQLQQR	4.62	1,557.78
Control	6011	TOMM22 protein	gi|151556851,gi|154152189	15,275.00	99.80%	2	3	4	0.03%	26.40%	QILLGPNTGLSGGMPGALPSLPGKI	4.45	2,404.33
Control	6011	RecName: Full=Gap junction alpha-1 protein; AltName: Full=Connexin-43; Short=Cx43; AltName: Full=Vascular smooth muscle connexin-43	gi|117704,gi|162889,gi|27806607,gi|86827705	43,170.50	99.80%	2	2	2	0.02%	9.40%	KLDAGHELQPLAIVDQRPSSR	2.71	2,330.26

Control	6011	RecName: Full=Gap junction alpha-1 protein; AltName: Full=Connexin-43; Short=Cx43; AltName: Full=Vascular smooth muscle connexin-43	gi|117704,gi|162889,gi|27806607,gi|86827705	43,170.50	99.80%	2	2	2	0.02%	9.40%	SDPYHTTTGPLSPSK	2.4	1,587.77
Control	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	16	21	32	0.25%	55.80%	AIAELGIYPAVDPLDSTSR	4.73	1,988.03
Control	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	16	21	32	0.25%	55.80%	FLSQPFQVAEVFTGHLGK	3.37	2,005.05
Control	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	16	21	32	0.25%	55.80%	FTQAGSEVSALLGR	4.12	1,435.75
Control	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	16	21	32	0.25%	55.80%	IMDPNIVGSEHYDVAR	2.93	1,831.86

Control	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	16	21	32	0.25%	55.80%	IMNVIGEPIDERGPIK	3.25	1,796.96
Control	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	16	21	32	0.25%	55.80%	IPSAVGYQPTLATDMGTMQER	4.54	2,282.08
Control	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	16	21	32	0.25%	55.80%	IPVGPETLGR	3	1,038.59
Control	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	16	21	32	0.25%	55.80%	IVAVIGAVVDVQFDEGLPPILNALEVQGR	3.73	3,031.68
Control	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	16	21	32	0.25%	55.80%	LVLEVAQHLGESTVR	3.18	1,650.92

Control	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	16	21	32	0.25%	55.80%	QFAAIHAEAPEFVEMSVEQEILVTGIK	3.78	3,002.52
Control	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	16	21	32	0.25%	55.80%	SLQDIIAILGMDELSEEDKLTVSR	3.41	2,691.38
Control	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	16	21	32	0.25%	55.80%	TVLIMELINNVAK	4.15	1,473.83
Control	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	16	21	32	0.25%	55.80%	VALTGLTVAEYFR	4.18	1,439.79
Control	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	16	21	32	0.25%	55.80%	VALVYGQMNEPPGAR	3.21	1,617.81

Control	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	16	21	32	0.25%	55.80%	VLDSGAPIRIPVGPETLGR	3.34	1,947.10
Control	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	16	21	32	0.25%	55.80%	VVDLLAPYAK	2.53	1,088.64
Control	6011	C1H3ORF21 protein	gi|112180740,gi|115496384	43,819.80	99.80%	2	3	3	0.02%	9.16%	ELFEEFDNFLPGAIIGIAR	2.97	2,151.11
Control	6011	C1H3ORF21 protein	gi|112180740,gi|115496384	43,819.80	99.80%	2	3	3	0.02%	9.16%	LLEPAQVQQLADKYHFR	2.92	2,056.10
Control	6011	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	5	6	7	0.05%	21.90%	AEQINQAAGEASAVLAK	3.94	1,670.87
Control	6011	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	5	6	7	0.05%	21.90%	ASYGVEDPEYAVTQLAQTTMR	3.99	2,346.09
Control	6011	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	5	6	7	0.05%	21.90%	ILEPGLNILIPVLDR	3.23	1,675.02
Control	6011	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	5	6	7	0.05%	21.90%	QAQILASEAEKAEQINQAAGEASAVLAK	4.45	2,839.48

Control	6011	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	5	6	7	0.05%	21.90%	STDASLDEELDRVK	3.43	1,577.77
Control	6011	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	5	7	9	0.07%	6.82%	IEFPILDDSSELQVK	3.53	1,732.90
Control	6011	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	5	7	9	0.07%	6.82%	LGEVPITVTAVSPAASDAVTQR	5.03	2,182.17
Control	6011	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	5	7	9	0.07%	6.82%	SPVTLTAYIVTSLLGYK	4.67	1,826.03
Control	6011	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	5	7	9	0.07%	6.82%	SYSQSILLDLTDSTLQTTLK	3.74	2,227.17
Control	6011	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	5	7	9	0.07%	6.82%	VGSPFELVVIGNK	4.4	1,358.77
Control	6011	CHMP4B protein	gi|116874509,gi|190360743	24,919.20	99.80%	2	2	2	0.02%	10.70%	EALENANTNTEVLK	3.19	1,545.78
Control	6011	CHMP4B protein	gi|116874509,gi|190360743	24,919.20	99.80%	2	2	2	0.02%	10.70%	KIEQELTAAK	2.43	1,130.64
Control	6011	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	100.00%	4	5	14	0.11%	21.70%	FLVGFTNK	2.47	925.5142
Control	6011	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	100.00%	4	5	14	0.11%	21.70%	GEDFPANNIVK	3.24	1,203.60
Control	6011	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	100.00%	4	5	14	0.11%	21.70%	GTEDFIVESLDASFR	4.21	1,685.80
Control	6011	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	100.00%	4	5	14	0.11%	21.70%	QATFEYSFIPAEPMGGRPFGLVINLNYK	3.24	3,175.59
Control	6011	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	9	10	0.08%	25.60%	DKSKYDEIFYNLAPADGK	3.02	2,074.01
Control	6011	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	9	10	0.08%	25.60%	FGTFHSPALEDADFDGKPMVLVAGQYSTGK	3.32	3,201.52

Control	6011	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	9	10	0.08%	25.60%	GYDFPAVLR	2.16	1,037.54
Control	6011	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	9	10	0.08%	25.60%	KLNPFGNTFLNR	2.89	1,420.77
Control	6011	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	9	10	0.08%	25.60%	LEGHGLPTNLPR	2.86	1,303.71
Control	6011	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	9	10	0.08%	25.60%	LFELEEQDLFR	3.58	1,438.72
Control	6011	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	9	10	0.08%	25.60%	LFELEEQDLFRDIQGLPR	3.31	2,218.15
Control	6011	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	9	10	0.08%	25.60%	LLEALDEMLTHDIAK	3.66	1,727.89
Control	6011	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	9	10	0.08%	25.60%	LSDVDRDGMLDDEEFALASHLIEAK	2.53	2,805.33
Control	6011	Adaptor-related protein complex 2, alpha 2 subunit	gi|111304969,gi|115496658,gi|122142416	103,753.40	99.80%	2	2	2	0.02%	2.99%	GLAVFISDIR	3.32	1,090.63
Control	6011	Adaptor-related protein complex 2, alpha 2 subunit	gi|111304969,gi|115496658,gi|122142416	103,753.40	99.80%	2	2	2	0.02%	2.99%	VGGYILGEFGNLIAGDPR	2.36	1,847.97
Control	6011	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	5	7	11	0.09%	13.20%	ALGVEQDLALPAIAVIGDQSSGK	4.52	2,252.21
Control	6011	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	5	7	11	0.09%	13.20%	ATEELQQYGDDIPSDEGDKMFFLIEK	3.69	3,034.39
Control	6011	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	5	7	11	0.09%	13.20%	LTQAQQALYEFPHFKG	4.31	1,877.95
Control	6011	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	5	7	11	0.09%	13.20%	SSVLEALSGVALPR	4.36	1,398.80
Control	6011	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	5	7	11	0.09%	13.20%	VAVENQPQDIGLQIK	4.63	1,651.90
Control	6011	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	5	7	11	0.09%	11.00%	KQDAFYKEQLAR	3.93	1,496.79

Control	6011	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	5	7	11	0.09%	11.00%	RVAEELALEQAK	3.09	1,356.75
Control	6011	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	5	7	11	0.09%	11.00%	RVAEELALEQAKK	5.12	1,484.84
Control	6011	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	5	7	11	0.09%	11.00%	VAEELALEQAK	4.38	1,200.65
Control	6011	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	5	7	11	0.09%	11.00%	VAEELALEQAKK	3.59	1,328.74
Control	6011	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	8	11	26	0.20%	15.80%	AEDYPIDLYYLMDLSYSMKDDLENVK	3.04	3,159.44
Control	6011	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	8	11	26	0.20%	15.80%	IGFGSFVEK	2.25	983.5197
Control	6011	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	8	11	26	0.20%	15.80%	LPEGVTINYK	3.05	1,133.62
Control	6011	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	8	11	26	0.20%	15.80%	LQPEDITQIQPQQLVLQLR	5.83	2,260.27
Control	6011	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	8	11	26	0.20%	15.80%	LSENNIQTIFAVTEEFQPVYK	4.42	2,470.25
Control	6011	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	8	11	26	0.20%	15.80%	NVLSLTDKGEVFNELVGK	5.9	1,962.05
Control	6011	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	8	11	26	0.20%	15.80%	SLGTDLMNEMR	2.53	1,282.58
Control	6011	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	8	11	26	0.20%	15.80%	TVMPYISTTPAK	3.38	1,324.68

Control	6011	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	5	7	11	0.09%	20.10%	LSQNNFALGYK	4.01	1,254.65
Control	6011	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	5	7	11	0.09%	20.10%	LTLDTIFVPNTGK	3.42	1,418.79
Control	6011	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	5	7	11	0.09%	20.10%	LTLDTIFVPNTGKK	3.86	1,546.88

Control	6011	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	5	7	11	0.09%	20.10%	LTLSALIDGK	3.74	1,030.61
Control	6011	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	5	7	11	0.09%	20.10%	SKLSQNNFALGYK	4.17	1,469.77
Control	6011	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	5	7	11	0.09%	20.10%	VNNASLIGLGYTQTLRPGVK	4.61	2,101.18
Control	6011	SLC25A3 protein	gi|151556064	39,986.50	100.00%	5	9	22	0.17%	17.20%	FGFYEVFK	2.24	1,036.51
Control	6011	SLC25A3 protein	gi|151556064	39,986.50	100.00%	5	9	22	0.17%	17.20%	FYALCGFGGVLSCGLTHTAVVPLDLVK	3.62	2,780.45

Control	6011	SLC25A3 protein	gi|151556064	39,986.50	100.00%	5	9	22	0.17%	17.20%	IQTQPGYANTLR	3.82	1,361.72
Control	6011	SLC25A3 protein	gi|151556064	39,986.50	100.00%	5	9	22	0.17%	17.20%	LPRPPPPEMPESLK	4.98	1,603.85
Control	6011	SLC25A3 protein	gi|151556064	39,986.50	100.00%	5	9	22	0.17%	17.20%	LPRPPPPEMPESLKK	3.09	1,731.95
Control	6011	ALCAM/CD166	gi|13111304,gi|41386784,gi|47605539	64,749.10	100.00%	2	2	2	0.02%	4.29%	SSNTYTLTDVKR	2.73	1,384.71
Control	6011	ALCAM/CD166	gi|13111304,gi|41386784,gi|47605539	64,749.10	100.00%	2	2	2	0.02%	4.29%	VFKQPSKPEIVSK	2.62	1,486.86
Control	6011	Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	gi|109659140,gi|27806841,gi|28372116,gi|2920652,gi|3046232,gi|33111880,gi|68067472	74,789.50	100.00%	4	5	5	0.04%	9.57%	IEDIRLEQNEAEK	2.22	1,715.84
Control	6011	Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	gi|109659140,gi|27806841,gi|28372116,gi|2920652,gi|3046232,gi|33111880,gi|68067472	74,789.50	100.00%	4	5	5	0.04%	9.57%	QETINLVVVPANVDIATTEALR	3.46	2,366.29
Control	6011	Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	gi|109659140,gi|27806841,gi|28372116,gi|2920652,gi|3046232,gi|33111880,gi|68067472	74,789.50	100.00%	4	5	5	0.04%	9.57%	SKIEDIRLEQNEAEK	3.15	1,930.97
Control	6011	Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	gi|109659140,gi|27806841,gi|28372116,gi|2920652,gi|3046232,gi|33111880,gi|68067472	74,789.50	100.00%	4	5	5	0.04%	9.57%	SSVLEALSGVALPR	4.36	1,398.80

Control	6011	Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	gi|109659140,gi|27806841,gi|28372116,gi|2920652,gi|3046232,gi|33111880,gi|68067472	74,789.50	100.00%	4	5	5	0.04%	9.57%	TLPLLENQIK	2.01	1,168.69
Control	6011	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor 1; AltName: Full=p40; AltName: Full=Protein C10	gi|122066007,gi|28189773,gi|73587277	18,591.70	100.00%	4	5	5	0.04%	35.70%	AIVAIENPADVSVISSR	2.95	1,740.95
Control	6011	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor 1; AltName: Full=p40; AltName: Full=Protein C10	gi|122066007,gi|28189773,gi|73587277	18,591.70	100.00%	4	5	5	0.04%	35.70%	FAAATGATPIAGR	4.18	1,203.65

Control	6011	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor 1; AltName: Full=p40; AltName: Full=Protein C10	gi|122066007,gi|28189773,gi|73587277	18,591.70	100.00%	4	5	5	0.04%	35.70%	FLAAGTHLGGTNLDFQMEQYIYK	3.66	2,633.27
Control	6011	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor 1; AltName: Full=p40; AltName: Full=Protein C10	gi|122066007,gi|28189773,gi|73587277	18,591.70	100.00%	4	5	5	0.04%	35.70%	LLVVTDPR	1.77	912.5514
Control	6011	alpha isoform of regulatory subunit A, protein phosphatase 2	gi|146231714,gi|79153525,gi|82697383	65,273.60	99.80%	2	2	2	0.02%	5.60%	IGPILDNSTLQSEVKPVLEK	3.07	2,180.22
Control	6011	alpha isoform of regulatory subunit A, protein phosphatase 2	gi|146231714,gi|79153525,gi|82697383	65,273.60	99.80%	2	2	2	0.02%	5.60%	VLAMSGDPNYLHR	2.65	1,488.73

Control	6011	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	3	4	5	0.04%	19.60%	GIVDQSQQAYQEAFEISK	4.31	2,040.99
Control	6011	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	3	4	5	0.04%	19.60%	LAEQAERYDDMAACMK	4.71	1,860.79
Control	6011	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	3	4	5	0.04%	19.60%	SVTEQGAELSNEER	4.84	1,548.71
Control	6011	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	5	5	5	0.04%	16.50%	IALTDNALIAR	3.66	1,170.68
Control	6011	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	5	5	5	0.04%	16.50%	KVPAVPETLK	2.41	1,081.66
Control	6011	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	5	5	5	0.04%	16.50%	KVPAVPETLKK	3.12	1,209.76
Control	6011	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	5	5	5	0.04%	16.50%	TTHFVEGGDAGNREDQINR	3.43	2,115.98
Control	6011	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	5	5	5	0.04%	16.50%	VPAVPETLKK	2.36	1,081.66

Control	6011	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	5	6	6	0.05%	14.70%	ADLINNLGTIAK	3.99	1,242.71
Control	6011	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	5	6	6	0.05%	14.70%	GVVDSEDLPLNISR	4.24	1,513.79
Control	6011	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	5	6	6	0.05%	14.70%	HLEINPDHSIIETLR	3.21	1,786.94
Control	6011	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	5	6	6	0.05%	14.70%	HSQFIGYPITLFVEK	4.51	1,778.95
Control	6011	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	5	6	6	0.05%	14.70%	NPDDITNEEYGEFYK	3.82	1,833.78
Control	6011	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	5	6	6	0.05%	14.70%	RAPFDLFENR	2.91	1,264.64
Control	6011	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	5	6	6	0.05%	14.70%	TLTIVDTGIGMTK	4.26	1,365.73
Control	6011	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	5	6	6	0.05%	14.70%	YESLTDPSKLDSGK	4.04	1,539.75
Control	6011	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	2	2	6	0.05%	19.80%	AMGIMNSFVNDIFER	4.5	1,759.81
Control	6011	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	2	2	6	0.05%	19.80%	KESYSVYVYK	3.28	1,265.64
Control	6011	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	6	6	7	0.05%	15.00%	EATESFASDPILYRPVAVALDTK	2.23	2,493.29
Control	6011	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	6	6	7	0.05%	15.00%	EATESFASDPILYRPVAVALDTKGPEIR	4.96	3,045.59
Control	6011	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	6	6	7	0.05%	15.00%	GDLGIEIPAEK	3.1	1,141.61

Control	6011	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	6	6	7	0.05%	15.00%	IYVDDGLISLLVK	4.08	1,447.84
Control	6011	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	6	6	7	0.05%	15.00%	LDIDSPPITAR	3.34	1,197.65
Control	6011	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	6	6	7	0.05%	15.00%	LSPITSDPTEAAAVGAVEASFK	3.08	2,161.10
Control	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	9	11	30	0.23%	29.90%	AMGNLQIDFADPSR	4.15	1,550.73
Control	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	9	11	30	0.23%	29.90%	AMGNLQIDFADPSRADDAR	2.41	2,078.96
Control	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	9	11	30	0.23%	29.90%	AVVYSNTIQSIMAIVK	3.66	1,752.96
Control	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	9	11	30	0.23%	29.90%	EYQLNDSAAYYLNDLER	5.03	2,076.95
Control	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	9	11	30	0.23%	29.90%	IAQSDYIPTQQDVLR	3.58	1,746.90

Control	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	9	11	30	0.23%	29.90%	LLLLGAGESGK	3.47	1,057.63
Control	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	9	11	30	0.23%	29.90%	NVQFVFDAVTDVIIK	2.94	1,707.93
Control	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	9	11	30	0.23%	29.90%	SREYQLNDSAAYYLNDLER	5.19	2,320.08
Control	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	9	11	30	0.23%	29.90%	YDEAASYIQSK	2.76	1,274.59
Control	6011	Paraoxonase 2	gi|109939919,gi|61553203,gi|61888862,gi|71648804	39,404.60	100.00%	6	8	9	0.07%	22.90%	FEEEENSLLHLK	2.54	1,487.74
Control	6011	Paraoxonase 2	gi|109939919,gi|61553203,gi|61888862,gi|71648804	39,404.60	100.00%	6	8	9	0.07%	22.90%	LLALSLLGIALALLGER	3.93	1,736.10
Control	6011	Paraoxonase 2	gi|109939919,gi|61553203,gi|61888862,gi|71648804	39,404.60	100.00%	6	8	9	0.07%	22.90%	LLIGTLYHR	2.13	1,085.65
Control	6011	Paraoxonase 2	gi|109939919,gi|61553203,gi|61888862,gi|71648804	39,404.60	100.00%	6	8	9	0.07%	22.90%	NTVEIFKFEEEENSLLHLK	3.91	2,319.19
Control	6011	Paraoxonase 2	gi|109939919,gi|61553203,gi|61888862,gi|71648804	39,404.60	100.00%	6	8	9	0.07%	22.90%	VVAEGFDSANGINISPDKK	3.29	1,961.00

Control	6011	Paraoxonase 2	gi|109939919,gi|61553203,gi|61888862,gi|71648804	39,404.60	100.00%	6	8	9	0.07%	22.90%	YIYVADILAHEIHVLEK	2.71	2,026.10
Control	6011	FOLH1 protein	gi|151553958,gi|156120365	84,574.90	99.80%	2	2	2	0.02%	3.73%	IPHLAGTEQNFQLAK	3.29	1,666.89
Control	6011	FOLH1 protein	gi|151553958,gi|156120365	84,574.90	99.80%	2	2	2	0.02%	3.73%	LQDLDKNNPILLR	2.19	1,551.89
Control	6011	ILVBL protein	gi|151557079,gi|154426224,gi|166233819,gi|59857973,gi|62751470	68,205.30	99.80%	2	2	2	0.02%	5.85%	AAQGLGAQGLLLSR	3.85	1,354.78
Control	6011	ILVBL protein	gi|151557079,gi|154426224,gi|166233819,gi|59857973,gi|62751470	68,205.30	99.80%	2	2	2	0.02%	5.85%	NAQIAQSPVLLLGGAASTLLQNR	3.45	2,335.31
Control	6011	RecName: Full=Complement component 1 Q subcomponent-binding protein, mitochondrial; Flags: Precursor	gi|115311784,gi|74354078,gi|77736001	30,588.80	100.00%	3	5	6	0.05%	19.40%	AEEQEPELTSTPNFVVEVTK	3.13	2,247.10
Control	6011	RecName: Full=Complement component 1 Q subcomponent-binding protein, mitochondrial; Flags: Precursor	gi|115311784,gi|74354078,gi|77736001	30,588.80	100.00%	3	5	6	0.05%	19.40%	GVDNTFADELVELSTALEHQEYISFLEDLK	4.52	3,425.66

Control	6011	RecName: Full=Complement component 1 Q subcomponent-binding protein, mitochondrial; Flags: Precursor	gi|115311784,gi|74354078,gi|77736001	30,588.80	100.00%	3	5	6	0.05%	19.40%	GVDNTFADELVELSTALEHQEYISFLEDLKGFVK	5.9	3,856.92
Control	6011	Na/K-ATPase beta 1 subunit [synthetic construct]	gi|22094876	35,156.20	100.00%	3	4	7	0.05%	9.21%	AYGENIGYSEKDR	3.47	1,501.69
Control	6011	Na/K-ATPase beta 1 subunit [synthetic construct]	gi|22094876	35,156.20	100.00%	3	4	7	0.05%	9.21%	SYMTYVDNIDNFLK	2.36	1,738.80
Control	6011	Na/K-ATPase beta 1 subunit [synthetic construct]	gi|22094876	35,156.20	100.00%	3	4	7	0.05%	9.21%	SYMTYVDNIDNFLKK	2.73	1,866.89
Control	6011	plastin 3	gi|152941116	70,782.90	100.00%	3	3	3	0.02%	6.51%	AYFHLLNQIAPK	3.98	1,414.78
Control	6011	plastin 3	gi|152941116	70,782.90	100.00%	3	3	3	0.02%	6.51%	IDINMSGFNETDDLKR	3.46	1,883.88
Control	6011	plastin 3	gi|152941116	70,782.90	100.00%	3	3	3	0.02%	6.51%	MINLSVPDTIDER	3.33	1,518.75
Control	6011	PREDICTED: similar to ATPase, Cu++ transporting, alpha polypeptide	gi|119920263	163,335.40	99.80%	2	2	2	0.02%	2.53%	GTVEYDPLLTSPETLR	3.56	1,790.92
Control	6011	PREDICTED: similar to ATPase, Cu++ transporting, alpha polypeptide	gi|119920263	163,335.40	99.80%	2	2	2	0.02%	2.53%	ILAIVGTAESNSEHPLGAAITK	4.13	2,192.19
Control	6011	ARF1 protein	gi|146327384,gi|28603778,gi|59858233,gi|62751462	20,583.70	99.80%	2	2	2	0.02%	22.10%	MLAEDELRDAVLLVFANK	4.67	2,063.08

Control	6011	ARF1 protein	gi|146327384,gi|28603778,gi|59858233,gi|62751462	20,583.70	99.80%	2	2	2	0.02%	22.10%	QDLPNAMNAAEITDKLGLHSLR	2.91	2,423.24
Control	6011	H2A histone family, member X	gi|109659379,gi|119331192,gi|119889440	13,977.80	99.80%	2	3	3	0.02%	23.10%	LLGGVTIAQGGVLPNIQAVLLPK	4.52	2,271.38
Control	6011	H2A histone family, member X	gi|109659379,gi|119331192,gi|119889440	13,977.80	99.80%	2	3	3	0.02%	23.10%	NDEELNKLLGGVTIAQGGVLPNIQAVLLPK	2.99	3,113.76
Control	6011	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	99.80%	2	2	2	0.02%	5.57%	SEIDLLDIR	3.04	1,073.58
Control	6011	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	99.80%	2	2	2	0.02%	5.57%	TLISILTER	2.58	1,045.63
Control	6011	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	8	10	15	0.12%	17.30%	GLNTIPLFVQLLYSPIENIQR	4.94	2,428.36
Control	6011	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	8	10	15	0.12%	17.30%	HAVVNLINYQDDAELATR	4.26	2,042.03
Control	6011	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	8	10	15	0.12%	17.30%	LHYGLPVVVK	3.22	1,124.68
Control	6011	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	8	10	15	0.12%	17.30%	LIILASGGPQALVNIMR	3.75	1,782.03

Control	6011	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	8	10	15	0.12%	17.30%	LLNDEDQVVVNK	3.84	1,385.73
Control	6011	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	8	10	15	0.12%	17.30%	MLGSPVDSVLFYAITTLHNLLLHQEGAK	3.43	3,083.62
Control	6011	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	8	10	15	0.12%	17.30%	NEGVATYAAAVLFR	4.12	1,481.77
Control	6011	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	8	10	15	0.12%	17.30%	TSMGGTQQQFVEGVR	3.89	1,640.77
Control	6011	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	gi|117306519,gi|118151180,gi|158512477	51,340.60	100.00%	4	4	6	0.05%	15.30%	EPEAPPEDKESESEAKADGETASDSESR	2.1	2,977.27
Control	6011	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	gi|117306519,gi|118151180,gi|158512477	51,340.60	100.00%	4	4	6	0.05%	15.30%	LVQQFLTLRPDQQLHIFNTLK	3.59	2,552.44
Control	6011	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	gi|117306519,gi|118151180,gi|158512477	51,340.60	100.00%	4	4	6	0.05%	15.30%	SHLTDKGMLTAATEDK	3.3	1,733.84
Control	6011	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	gi|117306519,gi|118151180,gi|158512477	51,340.60	100.00%	4	4	6	0.05%	15.30%	VAREPEAPPEDKESESEAK	3.31	2,097.99
Control	6011	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	7	7	7	0.05%	3.47%	FNQMLNQIPNDYHSSR	2.96	1,979.90

Control	6011	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	7	7	7	0.05%	3.47%	GLTSSEPVSIMEK	3.41	1,393.69
Control	6011	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	7	7	7	0.05%	3.47%	GPGDLEAPSNLVLSER	3.96	1,653.84
Control	6011	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	7	7	7	0.05%	3.47%	ITYQPSTGEGNEQTTTIGGR	4.58	2,110.01
Control	6011	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	7	7	7	0.05%	3.47%	IVEVFEIGPK	2.79	1,130.65
Control	6011	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	7	7	7	0.05%	3.47%	LKPDTPYTITVSSLYPDGEGGR	3.68	2,366.19
Control	6011	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	7	7	7	0.05%	3.47%	NNVILQPLQPDTPYK	4.34	1,739.93
Control	6011	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	4	4	5	0.04%	20.40%	ANVDKVFFDLMR	3.98	1,470.74
Control	6011	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	4	4	5	0.04%	20.40%	SDLEDKRQVSVEEAK	3.13	1,732.87
Control	6011	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	4	4	5	0.04%	20.40%	VFFDLMR	2.39	943.4707

Control	6011	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	4	4	5	0.04%	20.40%	VKEDENVPFLLVGNK	4.53	1,700.92
Control	6011	ALDOA protein	gi|151554749,gi|156120479	39,418.80	99.80%	2	2	3	0.02%	7.97%	GILAADESTGSIAK	4.33	1,332.70
Control	6011	ALDOA protein	gi|151554749,gi|156120479	39,418.80	99.80%	2	2	3	0.02%	7.97%	RLQSIGTENTEENRR	3.39	1,802.91
Control	6011	PREDICTED: similar to small GTP binding protein RAB23	gi|194677545	37,951.40	99.80%	2	2	2	0.02%	9.91%	LKQQIAENPESMHSSSNK	2.98	2,043.98
Control	6011	PREDICTED: similar to small GTP binding protein RAB23	gi|194677545	37,951.40	99.80%	2	2	2	0.02%	9.91%	VVAEVGDIPTALVQNK	4.55	1,652.92
Control	6011	signal transducer and activator of transcription 3 (acute-phase response factor)	gi|162287361,gi|81674209	83,096.10	99.80%	2	2	2	0.02%	5.54%	AILSTKPPGTFLLR	2.43	1,513.91
Control	6011	signal transducer and activator of transcription 3 (acute-phase response factor)	gi|162287361,gi|81674209	83,096.10	99.80%	2	2	2	0.02%	5.54%	LLQTAATAAQQGGQANHPTAAVVTEK	4.12	2,576.34
Control	6011	RecName: Full=Transmembrane emp24 domain-containing protein 1; Flags: Precursor	gi|114152289,gi|83638714,gi|84370158	25,119.90	99.80%	2	2	3	0.02%	11.50%	KADGVHTVEPTEAGDYK	4.29	1,816.87

Control	6011	RecName: Full=Transmembrane emp24 domain-containing protein 1; Flags: Precursor	gi|114152289,gi|83638714,gi|84370158	25,119.90	99.80%	2	2	3	0.02%	11.50%	SIQVLTLLR	2.92	1,042.66
Control	6011	growth and transformation-dependent protein	gi|114051522,gi|126258169,gi|84201630	17,719.20	99.80%	2	2	2	0.02%	20.50%	FKKEDEIPETVSFEMLDAAK	3.47	2,343.14
Control	6011	growth and transformation-dependent protein	gi|114051522,gi|126258169,gi|84201630	17,719.20	99.80%	2	2	2	0.02%	20.50%	RNETLTSLNLEK	3.77	1,417.76
Control	6011	PREDICTED: similar to asparagine-linked glycosylation 9 protein	gi|194673194	61,870.50	99.80%	2	3	3	0.02%	6.53%	LKGSGGSGGDTASAADKLR	3.15	1,747.89
Control	6011	PREDICTED: similar to asparagine-linked glycosylation 9 protein	gi|194673194	61,870.50	99.80%	2	3	3	0.02%	6.53%	TVPTDMNDQNLEEPSR	1.8	1,861.82
Control	6011	NADH:ubiquinone oxidoreductase ASHI subunit [Homo sapiens]	gi|33150722	21,747.60	99.80%	2	2	3	0.02%	16.10%	QYPYNNLYLER	2.34	1,472.72
Control	6011	NADH:ubiquinone oxidoreductase ASHI subunit [Homo sapiens]	gi|33150722	21,747.60	99.80%	2	2	3	0.02%	16.10%	VEDYEPYPDDGMGYGDYPK	3.23	2,225.89
Control	6011	proteasome activator subunit 2	gi|59858279,gi|62460470,gi|73921837,gi|74267960	27,362.30	99.80%	2	3	4	0.03%	10.50%	QNLFQEAEEFLYR	4.02	1,686.81
Control	6011	proteasome activator subunit 2	gi|59858279,gi|62460470,gi|73921837,gi|74267960	27,362.30	99.80%	2	3	4	0.03%	10.50%	TKVEAFQTTISK	3.23	1,352.74

Control	6011	Membrane bound O-acyltransferase domain containing 7	gi|111308475,gi|115496722,gi|122143520	52,749.30	99.80%	2	2	2	0.02%	8.47%	ALSLLGLPTPTPFTNAVQLLLTLK	2.59	2,521.50
Control	6011	Membrane bound O-acyltransferase domain containing 7	gi|111308475,gi|115496722,gi|122143520	52,749.30	99.80%	2	2	2	0.02%	8.47%	LVSLASEVQDLHVAQR	3.26	1,764.96
Control	6011	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	5	5	8	0.06%	10.00%	DAFLGSFLYEYSR	3.73	1,567.74
Control	6011	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	5	5	8	0.06%	10.00%	HLVDEPQNLIK	2.91	1,305.72
Control	6011	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	5	5	8	0.06%	10.00%	KVPQVSTPTLVEVSR	4.42	1,639.94
Control	6011	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	5	5	8	0.06%	10.00%	LVNELTEFAK	2.99	1,163.63
Control	6011	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	5	5	8	0.06%	10.00%	TVMENFVAFVDK	3.32	1,415.69

Control	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	21	0.16%	26.90%	IIGAVDQIQLTQAQLEER	6.2	2,025.10
Control	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	21	0.16%	26.90%	IREGQVEVLK	3.49	1,170.68
Control	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	21	0.16%	26.90%	KLEVNEAELLR	4.23	1,313.74
Control	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	21	0.16%	26.90%	KSFTPDHVVYAR	3	1,419.74
Control	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	21	0.16%	26.90%	LEVNEAELLR	3.17	1,185.65
Control	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	21	0.16%	26.90%	QAEMEGAVQSIQGELSK	3.87	1,820.87
Control	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	21	0.16%	26.90%	SDQVNGVLVLSLLDK	3.75	1,599.90
Control	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	21	0.16%	26.90%	SDQVNGVLVLSLLDKIIGAVDQIQLTQAQLEER	3.75	3,605.98
Control	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	21	0.16%	26.90%	VMIYQDEVKLPAK	4.24	1,549.83
Control	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	21	0.16%	26.90%	VPPFTFHVK	1.89	1,071.60
Control	6011	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	100.00%	4	7	14	0.11%	21.60%	KYMEENDLLKK	4.51	1,426.72
Control	6011	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	100.00%	4	7	14	0.11%	21.60%	LEKAENEALAMR	4.09	1,390.70

Control	6011	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	100.00%	4	7	14	0.11%	21.60%	LQAAVDGPSDKKEE	2.4	1,486.74
Control	6011	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	100.00%	4	7	14	0.11%	21.60%	VNLQNNPGAVEHFHMK	3.66	1,850.90
Control	6011	ITGA3 protein	gi|151556279,gi|156120449	45,035.90	99.80%	2	2	3	0.02%	6.34%	EAGNPGSLFGYSVALHR	3.69	1,774.89
Control	6011	ITGA3 protein	gi|151556279,gi|156120449	45,035.90	99.80%	2	2	3	0.02%	6.34%	YLLLAGAPR	3.4	973.583
Control	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	16	44	0.34%	56.90%	AKDFSLILDDVAITELSFSR	3.51	2,240.18
Control	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	16	44	0.34%	56.90%	AQVSLLIR	2.26	899.5673
Control	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	16	44	0.34%	56.90%	DLQMVNISLR	3.35	1,204.64
Control	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	16	44	0.34%	56.90%	ESVFTVEGGHR	1.93	1,217.59
Control	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	16	44	0.34%	56.90%	FNASQLITQR	3.96	1,177.63
Control	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	16	44	0.34%	56.90%	IGGVQQDTILAEGLHFR	4.97	1,853.99
Control	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	16	44	0.34%	56.90%	IPWFQYPIIYDIR	3.89	1,723.92
Control	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	16	44	0.34%	56.90%	IVQAEGEAEAAR	3.93	1,243.63
Control	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	16	44	0.34%	56.90%	IYLTADNLVLNLQDESFTR	5.61	2,225.15
Control	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	16	44	0.34%	56.90%	LGLDYEER	2.92	994.4841
Control	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	16	44	0.34%	56.90%	LLLGAGAVAYGIR	4.48	1,273.76
Control	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	16	44	0.34%	56.90%	QKIVQAEGEAEAAR	3.66	1,499.78
Control	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	16	44	0.34%	56.90%	VLPSIVNEVLK	2.62	1,210.74

Control	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	16	44	0.34%	56.90%	VLSRPNAMELPSMYQR	2.79	1,907.95
Control	6011	Cancer susceptibility candidate 4	gi|126010717,gi|126165222,gi|150438872	43,181.70	99.80%	2	2	2	0.02%	7.11%	HVLLQEEVAELQGQVQR	3.33	1,976.06
Control	6011	Cancer susceptibility candidate 4	gi|126010717,gi|126165222,gi|150438872	43,181.70	99.80%	2	2	2	0.02%	7.11%	LADQFLQEQK	2.82	1,219.63
Control	6011	TAP1 protein	gi|151557007	81,933.30	100.00%	6	8	14	0.11%	10.80%	GVVGAALGFR	2.95	946.5469
Control	6011	TAP1 protein	gi|151557007	81,933.30	100.00%	6	8	14	0.11%	10.80%	IFEYLDR	2.45	955.4884
Control	6011	TAP1 protein	gi|151557007	81,933.30	100.00%	6	8	14	0.11%	10.80%	SFANEEGEAQKFR	4.26	1,512.71
Control	6011	TAP1 protein	gi|151557007	81,933.30	100.00%	6	8	14	0.11%	10.80%	SSQVAIEVLSAMPTVR	3.23	1,703.90
Control	6011	TAP1 protein	gi|151557007	81,933.30	100.00%	6	8	14	0.11%	10.80%	STVAALLQNLYQPTEGQVLLDGEPLPK	5.25	2,894.55
Control	6011	TAP1 protein	gi|151557007	81,933.30	100.00%	6	8	14	0.11%	10.80%	SVLFITQR	2.68	963.5622
Control	6011	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	99.80%	2	2	2	0.02%	8.06%	FASFIDKVR	1.87	1,082.60
Control	6011	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	99.80%	2	2	2	0.02%	8.06%	NKYEDEINKR	2.43	1,308.65
Control	6011	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	99.80%	2	2	2	0.02%	8.06%	NLDLDSIIAEVK	3.84	1,329.73
Control	6011	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	99.80%	2	2	2	0.02%	8.06%	QNLEPLFEQYINNLR	3.08	1,890.97
Control	6011	ribosomal protein L3	gi|1092507,gi|154426164,gi|27807287,gi|450499,gi|59858389,gi|7159574,gi|730564,gi|74267942	46,006.40	100.00%	3	3	3	0.02%	15.90%	DDSSKPVHLTAFLGYK	3.78	1,777.91

Control	6011	ribosomal protein L3	gi|1092507,gi|154426164,gi|27807287,gi|450499,gi|59858389,gi|7159574,gi|730564,gi|74267942	46,006.40	100.00%	3	3	3	0.02%	15.90%	ERLEQQVPVSQVFGQDEMIDVIGVTK	5.33	2,960.50
Control	6011	ribosomal protein L3	gi|1092507,gi|154426164,gi|27807287,gi|450499,gi|59858389,gi|7159574,gi|730564,gi|74267942	46,006.40	100.00%	3	3	3	0.02%	15.90%	SINPLGGFVHYGEVTNDFVMLK	4.03	2,453.22
Control	6011	MOSPD2 protein	gi|151556011,gi|155369632,gi|156120441	56,360.50	100.00%	3	4	5	0.04%	6.71%	ALIVLTNVTK	3.11	1,071.68
Control	6011	MOSPD2 protein	gi|151556011,gi|155369632,gi|156120441	56,360.50	100.00%	3	4	5	0.04%	6.71%	GPLLHISPAEELYFGSTDSGEK	2.9	2,347.15
Control	6011	MOSPD2 protein	gi|151556011,gi|155369632,gi|156120441	56,360.50	100.00%	3	4	5	0.04%	6.71%	GPLLHISPAEELYFGSTDSGEKK	5.41	2,475.24
Control	6011	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	13	15	0.12%	36.30%	AEDGSVIDYELIDQDAR	2.35	1,908.88

Control	6011	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	13	15	0.12%	36.30%	AYTNFDAERDALNIETAIK	4.07	2,155.07
Control	6011	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	13	15	0.12%	36.30%	GVDEVTIVNILTNR	4.54	1,542.85

Control	6011	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	13	15	0.12%	36.30%	LSLEGDHSTPPSAYGSVK	5.07	1,844.90
Control	6011	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	13	15	0.12%	36.30%	RAEDGSVIDYELIDQDAR	5.6	2,064.98

Control	6011	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	13	15	0.12%	36.30%	RAEDGSVIDYELIDQDARDLYDAGVK	2.35	2,926.41
Control	6011	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	13	15	0.12%	36.30%	SALSGHLETVILGLLK	4.17	1,650.98

Control	6011	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	13	15	0.12%	36.30%	SYSPYDMLESIKK	2.61	1,576.76
Control	6011	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	13	15	0.12%	36.30%	TDLEKDIVSDTSGDFRK	3.69	1,925.95
Control	6011	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	5	8	10	0.08%	16.00%	ELIEVLQPLIAEHQAR	3.12	1,859.04

Control	6011	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	5	8	10	0.08%	16.00%	GIDYDKLIVR	1.83	1,191.67
Control	6011	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	5	8	10	0.08%	16.00%	ISFPAIQAAPSFSNSFPQIFR	4.32	2,325.20
Control	6011	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	5	8	10	0.08%	16.00%	MSASDPNSSIFLTDTAK	4.23	1,800.83
Control	6011	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	5	8	10	0.08%	16.00%	NAAKDEIDSAVK	2.9	1,260.64

Control	6011	PREDICTED: similar to Transmembrane protein 16F	gi|119892265	106,290.10	100.00%	3	4	6	0.05%	6.70%	LLQVDESIIKPEQEFFTAPFEK	2.79	2,608.35
Control	6011	PREDICTED: similar to Transmembrane protein 16F	gi|119892265	106,290.10	100.00%	3	4	6	0.05%	6.70%	MNDFYIQDRDTFFNPATR	3.47	2,267.02
Control	6011	PREDICTED: similar to Transmembrane protein 16F	gi|119892265	106,290.10	100.00%	3	4	6	0.05%	6.70%	TPEFEEFNGKPDSLYFNDGQR	4.06	2,490.12
Control	6011	Vesicle-associated membrane protein 7	gi|109658341,gi|115495041,gi|122144644	24,944.90	100.00%	3	3	3	0.02%	11.40%	AFNFLNEIK	2.8	1,095.58
Control	6011	Vesicle-associated membrane protein 7	gi|109658341,gi|115495041,gi|122144644	24,944.90	100.00%	3	3	3	0.02%	11.40%	GLDKVMETQAQVDELK	3.66	1,819.91
Control	6011	Vesicle-associated membrane protein 7	gi|109658341,gi|115495041,gi|122144644	24,944.90	100.00%	3	3	3	0.02%	11.40%	VMETQAQVDELK	3.32	1,406.68
Control	6011	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	4	5	6	0.05%	16.90%	ALSSSLDDTEVKK	4.29	1,392.72
Control	6011	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	4	5	6	0.05%	16.90%	FRGPFTDVVTTNLK	4.66	1,594.86
Control	6011	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	4	5	6	0.05%	16.90%	GPFTDVVTTNLK	3.99	1,291.69
Control	6011	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	4	5	6	0.05%	16.90%	VEQVLSLEPQHELK	3.47	1,648.89
Control	6011	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	6	7	7	0.05%	15.10%	APDFVFYAPR	3.75	1,182.59
Control	6011	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	6	7	7	0.05%	15.10%	FYPEDVSEELIQDITQR	3	2,082.00
Control	6011	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	6	7	7	0.05%	15.10%	GMLREDAVLEYLK	3.59	1,552.80

Control	6011	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	6	7	7	0.05%	15.10%	KAPDFVFYAPR	2.03	1,310.69
Control	6011	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	6	7	7	0.05%	15.10%	TAMSTPHVAEPAENEQDEQDENGAEASAELR	5.12	3,342.43
Control	6011	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	6	7	7	0.05%	15.10%	TQEQLALEMAELTAR	3.64	1,719.86
Control	6011	PREDICTED: similar to Keratin, type I cytoskeletal 24 (Cytokeratin-24) (Keratin-24) (Type I keratin-24)	gi|194676109	55,111.70	99.80%	2	3	4	0.03%	5.33%	KVLDDLTMTR	2.72	1,207.64
Control	6011	PREDICTED: similar to Keratin, type I cytoskeletal 24 (Cytokeratin-24) (Keratin-24) (Type I keratin-24)	gi|194676109	55,111.70	99.80%	2	3	4	0.03%	5.33%	SDLEMQIESLTEELAYLK	3.96	2,112.04
Control	6011	H2A histone family, member Y	gi|114052404,gi|87578157	39,516.80	100.00%	2	4	5	0.04%	13.70%	AASADSTTEGTPADGFTVLSTK	3.7	2,127.01
Control	6011	H2A histone family, member Y	gi|114052404,gi|87578157	39,516.80	100.00%	2	4	5	0.04%	13.70%	IGVGAPVYMAAVLEYLTAEILELAGNAAR	4.33	2,991.59
Control	6011	PREDICTED: transmembrane protein 33 isoform 2	gi|119893815,gi|119922774	27,968.00	99.80%	2	2	3	0.02%	8.10%	ALLANALTSALR	5.08	1,213.73
Control	6011	PREDICTED: transmembrane protein 33 isoform 2	gi|119893815,gi|119922774	27,968.00	99.80%	2	2	3	0.02%	8.10%	LPHFQLSR	2.64	997.5578

Control	6011	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	8	14	0.11%	45.00%	DSLLQDGEFTMDLR	3.84	1,655.76
Control	6011	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	8	14	0.11%	45.00%	SSFFVNGLTLGGQK	3.91	1,454.76
Control	6011	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	8	14	0.11%	45.00%	STGGAPTFNITVTMTAK	4.04	1,712.85
Control	6011	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	8	14	0.11%	45.00%	TFVNITPAEVGILVGK	4.62	1,657.95
Control	6011	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	8	14	0.11%	45.00%	TFVNITPAEVGILVGKDR	3.23	1,929.08

Control	6011	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 precursor	gi|146231842,gi|194678667	85,878.90	99.80%	2	2	2	0.02%	4.39%	FLNSGGFIGFAPTIHQIVR	2.72	2,074.12
Control	6011	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 precursor	gi|146231842,gi|194678667	85,878.90	99.80%	2	2	2	0.02%	4.39%	LVGPEEALTPGEAR	3.05	1,438.75
Control	6011	PREDICTED: ATPase type 13A1 isoform 1	gi|76620985	132,577.20	99.90%	2	3	4	0.03%	2.92%	FLPVAFPVGNAFSFYQSNR	4.81	2,161.09
Control	6011	PREDICTED: ATPase type 13A1 isoform 1	gi|76620985	132,577.20	99.90%	2	3	4	0.03%	2.92%	SIDGSISEPLAQGSPK	3.93	1,585.81
Control	6011	PREDICTED: similar to intercellular adhesion molecule-2 isoform 1	gi|119912562	30,746.10	99.80%	2	3	5	0.04%	12.00%	DEELLCSFTCAGKQEMK	2.98	1,931.86
Control	6011	PREDICTED: similar to intercellular adhesion molecule-2 isoform 1	gi|119912562	30,746.10	99.80%	2	3	5	0.04%	12.00%	VPAVAPLEGLTVTLLR	4.22	1,649.00
Control	6011	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	6	8	9	0.07%	25.60%	ALNLPSSGEGLAFFTFPNIASATK	4.26	2,453.27
Control	6011	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	6	8	9	0.07%	25.60%	ENPVYTPLYFPEELHR	3.06	2,003.99
Control	6011	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	6	8	9	0.07%	25.60%	LVMASLYHIYVALEEEIER	3.45	2,294.17
Control	6011	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	6	8	9	0.07%	25.60%	NKENPVYTPLYFPEELHR	6.32	2,246.12

Control	6011	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	6	8	9	0.07%	25.60%	YLGDLSGGQVLK	2.94	1,249.68
Control	6011	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	6	8	9	0.07%	25.60%	YLGDLSGGQVLKK	3.51	1,377.77
Control	6011	HADHA protein	gi|74268185	83,232.60	100.00%	4	5	5	0.04%	10.90%	DTTASAVDVGLR	3.43	1,204.62
Control	6011	HADHA protein	gi|74268185	83,232.60	100.00%	4	5	5	0.04%	10.90%	MQLLEIITTEK	3.77	1,334.72
Control	6011	HADHA protein	gi|74268185	83,232.60	100.00%	4	5	5	0.04%	10.90%	SAVLISTKPGCFIAGADLNMLNSCTTSQEVTQISQEAQK	4.9	4,084.00
Control	6011	HADHA protein	gi|74268185	83,232.60	100.00%	4	5	5	0.04%	10.90%	TVLGSPEVLLGILPGAGATQR	4.03	2,049.17
Control	6011	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	3	3	3	0.02%	3.50%	FVFGTTPEDILR	3.1	1,394.73
Control	6011	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	3	3	3	0.02%	3.50%	GGVNDNFQGVLQNVR	3.38	1,616.81
Control	6011	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	3	3	3	0.02%	3.50%	KVTEENKELANELR	4.28	1,672.89
Control	6011	annexin 5	gi|119936560,gi|120474983,gi|260137,gi|73586525	36,057.60	99.80%	2	2	3	0.02%	9.97%	DLLDDLKSELTGKFEK	2.75	1,850.98
Control	6011	annexin 5	gi|119936560,gi|120474983,gi|260137,gi|73586525	36,057.60	99.80%	2	2	3	0.02%	9.97%	GLGTDEESILTLLTSR	4.3	1,704.90
Control	6011	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	100.00%	4	4	6	0.05%	24.10%	FSQMLHPIFEEASNVIKEEYPNANQVVFAR	5.12	3,523.73

Control	6011	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	100.00%	4	4	6	0.05%	24.10%	HMYVFGDFRDVLIPGK	2.54	1,909.96
Control	6011	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	100.00%	4	4	6	0.05%	24.10%	LHREFHHGPDPTDTAPGEEVQDVASSPPESSFQK	2.21	3,728.72
Control	6011	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	100.00%	4	4	6	0.05%	24.10%	SDPIQELHDLAEITTPDR	5.08	2,050.01
Control	6011	RecName: Full=Apolipoprotein O-like; AltName: Full=Protein FAM121A; Flags: Precursor	gi|125987581,gi|74268422,gi|78042526	29,097.30	99.80%	2	2	2	0.02%	11.70%	KAYATSQQMYEAVK	3.16	1,633.79
Control	6011	RecName: Full=Apolipoprotein O-like; AltName: Full=Protein FAM121A; Flags: Precursor	gi|125987581,gi|74268422,gi|78042526	29,097.30	99.80%	2	2	2	0.02%	11.70%	YVEEQPGHLQMGFASIR	2.7	1,977.95

Control	6011	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32, gi|59857977	33,881.70	100.00%	4	6	7	0.05%	22.50%	AVIGMTAGATGAFVGTPAEVALIR	4.75	2,289.23
Control	6011	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32, gi|59857977	33,881.70	100.00%	4	6	7	0.05%	22.50%	AVVVNAAQLASYSQSK	4.12	1,635.87
Control	6011	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32, gi|59857977	33,881.70	100.00%	4	6	7	0.05%	22.50%	FLFGGLAGMGATVFVQPLDLVK	3.78	2,296.24

Control	6011	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32,gi|59857977	33,881.70	100.00%	4	6	7	0.05%	22.50%	NVFNALFR	2.38	980.5311
Control	6011	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	6	6	7	0.05%	28.70%	GGALLTSTSGPGFHLMLPFITSYK	3.12	2,511.30
Control	6011	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	6	6	7	0.05%	28.70%	IEVVNFLVPHAVYDIVK	3.14	1,955.10
Control	6011	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	6	6	7	0.05%	28.70%	ISEIEDAAFLAR	3.48	1,334.70
Control	6011	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	6	6	7	0.05%	28.70%	LALQQDLTSMAPGLVIQAVR	4.95	2,140.18
Control	6011	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	6	6	7	0.05%	28.70%	SVQTTLQTDEVK	3.97	1,348.70
Control	6011	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	6	6	7	0.05%	28.70%	VAQVAEITFGQK	3.02	1,290.71
Control	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	10	13	19	0.15%	22.50%	AAEHRQTILESIRTAGTLFGEGFR	1.9	2,660.39
Control	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	10	13	19	0.15%	22.50%	ATLNAFLHR	2.64	1,042.58
Control	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	10	13	19	0.15%	22.50%	GLLLFVDEADAFLR	3.45	1,578.85
Control	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	10	13	19	0.15%	22.50%	ITVLEALR	2.76	914.567
Control	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	10	13	19	0.15%	22.50%	LKEYEAAVEQLKGDQIR	4.87	1,990.06
Control	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	10	13	19	0.15%	22.50%	MYFDKYVLKPATEGK	2.27	1,805.91

Control	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	10	13	19	0.15%	22.50%	NVLMYGPPGTGK	3.14	1,249.62
Control	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	10	13	19	0.15%	22.50%	QQQLLNEENLR	2.44	1,384.72
Control	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	10	13	19	0.15%	22.50%	RLLSKPQDALEGVVLSPSLEAR	2.94	2,378.34
Control	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	10	13	19	0.15%	22.50%	TAGTLFGEGFR	3.92	1,155.58
Control	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	11	12	14	0.11%	17.90%	AQAYQTGKDISTNYYASQK	4.67	2,137.02
Control	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	11	12	14	0.11%	17.90%	ELISNASDALDKIR	3.91	1,544.83
Control	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	11	12	14	0.11%	17.90%	EVEEDEYKAFYK	3.11	1,549.71
Control	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	11	12	14	0.11%	17.90%	FQSSHHPSDMTSLDQYVER	5.58	2,280.00
Control	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	11	12	14	0.11%	17.90%	GLFDEYGSK	2.08	1,015.47
Control	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	11	12	14	0.11%	17.90%	GVVDSDDLPLNVSR	4.21	1,485.75
Control	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	11	12	14	0.11%	17.90%	LIINSLYK	2.32	963.5874
Control	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	11	12	14	0.11%	17.90%	LISLTDENALAGNEELTVK	3.23	2,030.07
Control	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	11	12	14	0.11%	17.90%	NLLHVTDTGVGMTR	4.45	1,529.77

Control	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	11	12	14	0.11%	17.90%	NLLHVTDTGVGMTREELVK	3.23	2,128.11
Control	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	11	12	14	0.11%	17.90%	SILFVPTSAPR	3.68	1,187.68
Control	6011	PREDICTED: similar to FXYD domain-containing ion transport regulator 5 isoform 1	gi|76641186	18,921.80	99.80%	2	2	2	0.02%	10.40%	EDDPFFYDEDTLR	3.17	1,661.70
Control	6011	PREDICTED: similar to FXYD domain-containing ion transport regulator 5 isoform 1	gi|76641186	18,921.80	99.80%	2	2	2	0.02%	10.40%	QPGSKEDDPFFYDEDTLR	3.08	2,158.96
Control	6011	ALDH4A1 protein	gi|157278942,gi|157785571,gi|193806687	61,478.10	99.80%	2	2	2	0.02%	5.86%	STGSVVGQQPFGGAR	3.68	1,447.73
Control	6011	ALDH4A1 protein	gi|157278942,gi|157785571,gi|193806687	61,478.10	99.80%	2	2	2	0.02%	5.86%	TVIQAEIDAAAELIDFFR	3.72	2,022.05
Control	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	10	12	13	0.10%	13.90%	ALSAIADLLTNEHER	4.67	1,652.86
Control	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	10	12	13	0.10%	13.90%	APSRQDVYGPQPQVR	4.95	1,697.87
Control	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	10	12	13	0.10%	13.90%	DMDLTEVITGTLWNLSSHDSIK	3.65	2,491.20
Control	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	10	12	13	0.10%	13.90%	FHPEPYGLEDDQR	3.09	1,602.72
Control	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	10	12	13	0.10%	13.90%	KPTEDPTNDTVDFPK	3.33	1,703.81

Control	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	10	12	13	0.10%	13.90%	KPTEDPTNDTVDFPKR	5.69	1,859.91
Control	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	10	12	13	0.10%	13.90%	NFHYPPDGYSR	2.97	1,352.60
Control	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	10	12	13	0.10%	13.90%	QDVYGPQPQVR	2.63	1,286.65
Control	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	10	12	13	0.10%	13.90%	SLDNNYSTLNER	2.69	1,425.66
Control	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	10	12	13	0.10%	13.90%	TVQPVPMGPDGLPVDASAVSNSYIQTLGR	2.93	2,985.50
Control	6011	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	4	5	12	0.09%	14.80%	DPLVIELGQK	3.6	1,111.64
Control	6011	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	4	5	12	0.09%	14.80%	IFDTSLTRDPLVIELGQK	4.73	2,045.13
Control	6011	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	4	5	12	0.09%	14.80%	RVIIPSHLAYGK	3.58	1,353.80
Control	6011	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	4	5	12	0.09%	14.80%	VIIPSHLAYGK	3.04	1,197.70
Control	6011	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	7	7	9	0.07%	20.80%	EEQKDFVSLYQDFENFYTR	4.35	2,458.12
Control	6011	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	7	7	9	0.07%	20.80%	GVVDYFGLDPEDVDIMMGTFTK	2.42	2,465.13
Control	6011	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	7	7	9	0.07%	20.80%	LLKDAIVYGQPR	2.69	1,372.79
Control	6011	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	7	7	9	0.07%	20.80%	LPEVIALK	2.48	882.566
Control	6011	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	7	7	9	0.07%	20.80%	NIGVVVVGFPATPIIESR	5.57	1,868.06
Control	6011	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	7	7	9	0.07%	20.80%	QEIGNLDKHEELEK	2.42	1,681.84

Control	6011	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	7	7	9	0.07%	20.80%	SSAAAAAAAAGQIHHVTENGGLYK	3.62	2,295.15
Control	6011	endoglin	gi|115497110,gi|92097469	69,885.10	99.80%	2	3	5	0.04%	3.25%	FSFLLR	1.95	782.4559
Control	6011	endoglin	gi|115497110,gi|92097469	69,885.10	99.80%	2	3	5	0.04%	3.25%	LQAPGIPLQLAYDSK	4.31	1,613.89
Control	6011	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	7	0.05%	10.30%	DKLNPQSTYSEA	3.52	1,352.63
Control	6011	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	7	0.05%	10.30%	FVTAVGTQGAISK	3.52	1,278.71
Control	6011	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	7	0.05%	10.30%	IAPSSFVSSGPFLFIK	4.31	1,696.93
Control	6011	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	7	0.05%	10.30%	NLSALENYNFELVDGVK	2.72	1,924.97
Control	6011	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	7	0.05%	10.30%	SFEGNNNYDTPELR	2.83	1,655.73
Control	6011	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	7	0.05%	10.30%	TGPIQDHTGDGNFIYSQADENQK	5.31	2,535.14
Control	6011	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	4	4	4	0.03%	9.07%	LFEAEAQDLFR	3	1,338.67
Control	6011	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	4	4	4	0.03%	9.07%	LIEAVDNMLTNK	3.44	1,376.71
Control	6011	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	4	4	4	0.03%	9.07%	SISIIDSPGILSGEK	4.02	1,515.83
Control	6011	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	4	4	4	0.03%	9.07%	YLLEQDFPGMR	2.81	1,384.66

Control	6011	RPS7 protein	gi|148877374,gi|149642623,gi|205806695	22,109.50	100.00%	2	2	2	0.02%	7.73%	DVNFEFPEFQL	2.69	1,384.64
Control	6011	RPS7 protein	gi|148877374,gi|149642623,gi|205806695	22,109.50	100.00%	2	2	2	0.02%	7.73%	LTGKDVNFEFPEFQL	2.83	1,783.89
Control	6011	RRAS2 protein	gi|148743916,gi|149944707	23,381.60	100.00%	2	2	2	0.02%	13.70%	LDILDTAGQEEFGAMR	3.81	1,781.84
Control	6011	RRAS2 protein	gi|148743916,gi|149944707	23,381.60	100.00%	2	2	2	0.02%	13.70%	MNVDQAFHELVR	2.99	1,474.71
Control	6011	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	2	27	0.21%	34.20%	AAYFGIYDTAK	4.01	1,219.60
Control	6011	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	2	27	0.21%	34.20%	DFLAGGVAAAISK	5.16	1,219.67
Control	6011	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	2	27	0.21%	34.20%	EQGVLSFWR	2.58	1,121.57
Control	6011	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	2	27	0.21%	34.20%	GLYQGFNVSVQGIIIYR	2.63	1,927.04
Control	6011	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	2	27	0.21%	34.20%	GMGGAFVLVLYDEIK	4.27	1,627.84
Control	6011	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	2	27	0.21%	34.20%	GMGGAFVLVLYDEIKK	3.05	1,755.94
Control	6011	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	2	27	0.21%	34.20%	GMGGAFVLVLYDEIKKFT	3.12	2,004.05
Control	6011	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	2	27	0.21%	34.20%	LLLQVQHASK	2.8	1,136.68
Control	6011	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	2	27	0.21%	34.20%	QIFLGGVDKR	1.84	1,132.65
Control	6011	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	2	27	0.21%	34.20%	YFPTQALNFAFK	3.99	1,446.74
Control	6011	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	2	27	0.21%	34.20%	YFPTQALNFAFKDK	3.69	1,689.86

Control	6011	PREDICTED: similar to interferon-induced protein 44-like	gi|194665691,gi|194685057	49,925.50	99.80%	2	2	2	0.02%	5.90%	AMISQSQIQNVNK	4.53	1,476.75
Control	6011	PREDICTED: similar to interferon-induced protein 44-like	gi|194665691,gi|194685057	49,925.50	99.80%	2	2	2	0.02%	5.90%	VEGIKDEAGYINR	3.17	1,463.75
Control	6011	STX6 protein	gi|126010683,gi|126723527	29,055.10	99.80%	2	2	2	0.02%	14.10%	AVNTAQGLFQR	3.58	1,204.64
Control	6011	STX6 protein	gi|126010683,gi|126723527	29,055.10	99.80%	2	2	2	0.02%	14.10%	IGGELEEQAVMLDDFSHELESTQSR	3.24	2,836.29
Control	6011	ERGIC and golgi 2	gi|113912114,gi|115497448	42,596.10	99.80%	2	2	2	0.02%	9.28%	IDHLSFGELVPGIINPLDGTEK	3.12	2,364.25
Control	6011	ERGIC and golgi 2	gi|113912114,gi|115497448	42,596.10	99.80%	2	2	2	0.02%	9.28%	ISADTHQFAVTER	3.16	1,474.73
Control	6011	heme oxygenase (decycling) 2	gi|164448721	37,538.70	100.00%	4	5	6	0.05%	19.80%	AFEFNMQVFNELDQAGSLLAK	3.23	2,388.15
Control	6011	heme oxygenase (decycling) 2	gi|164448721	37,538.70	100.00%	4	5	6	0.05%	19.80%	IHEVGQNEPELLVAHAYTR	5	2,176.11
Control	6011	heme oxygenase (decycling) 2	gi|164448721	37,538.70	100.00%	4	5	6	0.05%	19.80%	LPTQDGLPVHDGK	2.56	1,376.72
Control	6011	heme oxygenase (decycling) 2	gi|164448721	37,538.70	100.00%	4	5	6	0.05%	19.80%	YMGDLSGGQVLKK	2.68	1,411.73
Control	6011	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	gi|59858119,gi|60650208,gi|60650268,gi|61889066,gi|75070049,gi|88954151	42,933.90	100.00%	3	3	4	0.03%	11.30%	FTRPIIAGMEFSR	3.84	1,540.79
Control	6011	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	gi|59858119,gi|60650208,gi|60650268,gi|61889066,gi|75070049,gi|88954151	42,933.90	100.00%	3	3	4	0.03%	11.30%	SDNSSHPQKDDGDNPETIMSSGNVNSSS	3.94	2,922.19

Control	6011	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	gi|59858119,gi|60650208,gi|60650268,gi|61889066,gi|75070049,gi|88954151	42,933.90	100.00%	3	3	4	0.03%	11.30%	SKSDNSSHPQKDDGDNPETIMSSGNVNSSS	3.72	3,137.32
Control	6011	Chromosome 20 open reading frame 108 ortholog	gi|119224079,gi|122692571	20,430.00	99.80%	2	2	2	0.02%	12.50%	ISITLVSVPLIVR	3.47	1,409.91
Control	6011	Chromosome 20 open reading frame 108 ortholog	gi|119224079,gi|122692571	20,430.00	99.80%	2	2	2	0.02%	12.50%	VGIFKPPAAKP	2.65	1,124.68
Control	6011	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	5	7	10	0.08%	11.10%	DAFVYAIK	2.05	926.4982
Control	6011	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	5	7	10	0.08%	11.10%	KLEIGFNGNR	3.08	1,147.62
Control	6011	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	5	7	10	0.08%	11.10%	SISHYHETLGEALQGVELEFSGLDIK	4.12	2,872.44
Control	6011	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	5	7	10	0.08%	11.10%	VNAVPRPIPEK	3.11	1,219.72
Control	6011	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	5	7	10	0.08%	11.10%	YLDPSFFQHR	2.15	1,309.63

Control	6011	PREDICTED: similar to Transmembrane emp24 domain-containing protein 2 precursor (Membrane protein p24A)	gi|194674620	22,715.40	99.80%	2	2	8	0.06%	12.40%	IVMFTIDIGEAPK	3.46	1,449.77
Control	6011	PREDICTED: similar to Transmembrane emp24 domain-containing protein 2 precursor (Membrane protein p24A)	gi|194674620	22,715.40	99.80%	2	2	8	0.06%	12.40%	YTFAAHMDGTYK	3.25	1,420.62
Control	6011	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	6	7	12	0.09%	9.18%	EATSTFTNITYR	3.33	1,403.68
Control	6011	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	6	7	12	0.09%	9.18%	GTGDSSQITQVSPQR	4.21	1,560.76
Control	6011	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	6	7	12	0.09%	9.18%	HVLTLTDQVTR	3.25	1,282.71

Control	6011	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	6	7	12	0.09%	9.18%	IGFGAFVDKPVSPYMYISPPEAIR	3.82	2,670.36
Control	6011	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	6	7	12	0.09%	9.18%	ILEARPLSDKGTGDSSQITQVSPQR	7.09	2,683.40
Control	6011	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	6	7	12	0.09%	9.18%	PLSDKGTGDSSQITQVSPQR	5.55	2,101.05
Control	6011	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	8	8	12	0.09%	16.90%	ADLVNNLGTIAK	3.6	1,228.69
Control	6011	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	8	8	12	0.09%	16.90%	ELISNASDALDKIR	3.91	1,544.83
Control	6011	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	8	8	12	0.09%	16.90%	GVVDSEDLPLNISR	4.24	1,513.79
Control	6011	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	8	8	12	0.09%	16.90%	HLEINPDHPIVETLR	3.96	1,782.95
Control	6011	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	8	8	12	0.09%	16.90%	HSQFIGYPITLYLEK	3.08	1,808.96
Control	6011	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	8	8	12	0.09%	16.90%	NPDDITQEEYGEFYK	3.34	1,847.80
Control	6011	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	8	8	12	0.09%	16.90%	SIYYITGESK	2.42	1,160.58
Control	6011	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	8	8	12	0.09%	16.90%	TLTLVDTGIGMTK	4.26	1,365.73

Control	6011	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	8	8	12	0.09%	16.90%	YESLTDPSKLDSGK	4.04	1,539.75
Control	6011	NADH dehydrogenase subunit 1	gi|33321662,gi|70988001,gi|70988015,gi|70988029,gi|70988043,gi|70988057,gi|70988071,gi|70988085,gi|70988099,gi|70988113,gi|70988127	35,655.00	100.00%	3	3	3	0.02%	8.81%	GPNVVGPYGLLQPIADAIK	4.06	1,922.07
Control	6011	NADH dehydrogenase subunit 1	gi|33321662,gi|70988001,gi|70988015,gi|70988029,gi|70988043,gi|70988057,gi|70988071,gi|70988085,gi|70988099,gi|70988113,gi|70988127	35,655.00	100.00%	3	3	3	0.02%	8.81%	KGPNVVGPYGLLQPIADAIK	3.63	2,050.17
Control	6011	NADH dehydrogenase subunit 1	gi|33321662,gi|70988001,gi|70988015,gi|70988029,gi|70988043,gi|70988057,gi|70988071,gi|70988085,gi|70988099,gi|70988113,gi|70988127	35,655.00	100.00%	3	3	3	0.02%	8.81%	YALIGALR	2.36	876.5302

Control	6011	RecName: Full=Adiponectin; AltName: Full=Adipocyte, C1q and collagen domain-containing protein; AltName: Full=30 kDa adipocyte complement-related protein; AltName: Full=Adipocyte complement-related 30	gi|114158576,gi|146186777,gi|73697558	26,115.60	100.00%	3	3	4	0.03%	15.00%	ALLFTHDQFQDK	3.07	1,462.73
Control	6011	RecName: Full=Adiponectin; AltName: Full=Adipocyte, C1q and collagen domain-containing protein; AltName: Full=30 kDa adipocyte complement-related protein; AltName: Full=Adipocyte complement-related 30	gi|114158576,gi|146186777,gi|73697558	26,115.60	100.00%	3	3	4	0.03%	15.00%	IFYNQQNHYDGTTGK	2.89	1,785.82

Control	6011	RecName: Full=Adiponectin; AltName: Full=Adipocyte, C1q and collagen domain-containing protein; AltName: Full=30 kDa adipocyte complement-related protein; AltName: Full=Adipocyte complement-related 30	gi|114158576,gi|146186777,gi|73697558	26,115.60	100.00%	3	3	4	0.03%	15.00%	SAFSVGLER	2.44	965.505
Control	6011	Solute carrier family 1 (neutral amino acid transporter), member 5	gi|115305216,gi|15145909,gi|21541958,gi|27807087	56,431.20	99.80%	2	2	3	0.02%	4.45%	EVLDSFLDLVR	3.57	1,305.71
Control	6011	Solute carrier family 1 (neutral amino acid transporter), member 5	gi|115305216,gi|15145909,gi|21541958,gi|27807087	56,431.20	99.80%	2	2	3	0.02%	4.45%	NIFPSNLVSAAFR	3.17	1,435.77
Control	6011	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	4	4	6	0.05%	11.50%	ALDLFSDNAPPPELLEIINEDVAK	4.09	2,623.35
Control	6011	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	4	4	6	0.05%	11.50%	GSFSEQGINEFLR	3.58	1,483.72

Control	6011	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	4	4	6	0.05%	11.50%	GSTAPVGGGAFPTISTR	4.6	1,575.81
Control	6011	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	4	4	6	0.05%	11.50%	TGEAIVDAALSALR	2.75	1,386.76
Control	6011	Deoxyribonuclease I-like 1	gi|151553571	35,175.30	99.80%	2	2	2	0.02%	8.86%	IVLHGEHLQSLLR	2.51	1,514.88
Control	6011	Deoxyribonuclease I-like 1	gi|151553571	35,175.30	99.80%	2	2	2	0.02%	8.86%	VLPSLVLVPLHTTPK	3.76	1,614.00
Control	6018	TIMM23 protein	gi|134025149,gi|139947578,gi|215274655	21,809.90	100.00%	3	3	4	0.04%	32.50%	NVQILNMVTR	3.2	1,203.65
Control	6018	TIMM23 protein	gi|134025149,gi|139947578,gi|215274655	21,809.90	100.00%	3	3	4	0.04%	32.50%	TTGGLAGFFGAGGAGYSHADLAGVPLTGMNPLSPYLNVDPR	5.36	4,034.97
Control	6018	TIMM23 protein	gi|134025149,gi|139947578,gi|215274655	21,809.90	100.00%	3	3	4	0.04%	32.50%	YLVQDTDEFILPTGANK	3.64	1,923.97
Control	6018	similar to translationally controlled tumor protein	gi|28189813,gi|59858437,gi|62177164,gi|62901141,gi|74356483	19,564.00	99.80%	2	3	3	0.03%	15.70%	DLISHDEMFSDIYK	2.85	1,728.78
Control	6018	similar to translationally controlled tumor protein	gi|28189813,gi|59858437,gi|62177164,gi|62901141,gi|74356483	19,564.00	99.80%	2	3	3	0.03%	15.70%	VKPFMTGAAEQIK	2.37	1,435.76
Control	6018	Chain B, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591027,gi|110591030,gi|114686,gi|27807305,gi|599873,gi|74356487	18,544.10	100.00%	3	4	10	0.10%	32.50%	IQEYEKELEK	3.62	1,308.67

Control	6018	Chain B, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591027,gi|110591030,gi|114686,gi|27807305,gi|599873,gi|74356487	18,544.10	100.00%	3	4	10	0.10%	32.50%	NIIPFDQMTIEDLNEVFPETK	3.55	2,509.22
Control	6018	Chain B, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591027,gi|110591030,gi|114686,gi|27807305,gi|599873,gi|74356487	18,544.10	100.00%	3	4	10	0.10%	32.50%	VPIPEDKYTAQVDAEEKEDVK	2.19	2,403.19
Control	6018	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	6	8	15	0.15%	10.10%	AQILLDCGEDNICVPDLQLEVFGEQNHVYLGDK	3.68	3,687.77
Control	6018	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	6	8	15	0.15%	10.10%	DLDGNGYPDLIVGSFGVDK	5.13	1,980.96
Control	6018	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	6	8	15	0.15%	10.10%	LAGMEPTPTLTLTGQDEFGR	5.39	2,150.04
Control	6018	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	6	8	15	0.15%	10.10%	QATLTQTLLIQNGAR	3.06	1,627.91

Control	6018	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	6	8	15	0.15%	10.10%	TIQFDFQILSK	2.81	1,339.73
Control	6018	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	6	8	15	0.15%	10.10%	VTAPPEAEYSGLVR	3.03	1,488.77
Control	6018	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	2	3	12	0.12%	14.00%	YVDSEGHLYTVPIR	3.18	1,648.83
Control	6018	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	2	3	12	0.12%	14.00%	YVDSEGHLYTVPIREQGNIYKPNNK	3.97	2,934.47
Control	6018	RTN3 protein	gi|115305093,gi|122132179,gi|146231798,gi|151554368,gi|32880223,gi|38327594	25,478.60	99.80%	2	4	4	0.04%	5.49%	TQIDHYVGIAR	2.17	1,272.67
Control	6018	RTN3 protein	gi|115305093,gi|122132179,gi|146231798,gi|151554368,gi|32880223,gi|38327594	25,478.60	99.80%	2	4	4	0.04%	5.49%	YKTQIDHYVGIAR	3.19	1,563.83
Control	6018	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	4	6	8	0.08%	17.00%	DNFHGLAIFLDTYPNDETTER	5.08	2,468.14
Control	6018	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	4	6	8	0.08%	17.00%	DNVDDPTGNFR	3.16	1,249.54
Control	6018	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	4	6	8	0.08%	17.00%	LPTGYYFGASAGTGDLSDNHDIISMK	5.56	2,746.27
Control	6018	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	4	6	8	0.08%	17.00%	SPKDNVDDPTGNFR	4.29	1,561.72

Control	6018	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	2	2	2	0.02%	6.30%	EIILVDDYSNDPEDGALLGK	3.93	2,176.07
Control	6018	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	2	2	2	0.02%	6.30%	QHPYTFPGGSGTVFAR	4.3	1,721.84
Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	ADIGVAMGIAGSDVSK	4.79	1,506.75
Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	AVAGDASESALLK	4.23	1,231.65
Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	AVFQANQDNLPILK	4.08	1,570.86
Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	DKYEPAAVSEHGDK	3.99	1,545.72
Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	EQPLDEELKDAFQNAYLELGGLGER	3.46	2,834.38
Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	GGDRIPADLR	2.37	1,069.58
Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	GVGIISEGNETVEDIAAR	6.21	1,829.92

Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	IVEIPFNSTNK	2.76	1,261.68
Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	KADIGVAMGIAGSDVSK	6.23	1,634.84
Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	LNIPVSQVNPR	3.37	1,236.71
Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	LSLDELHR	2.39	982.5317
Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	MSINAEEVVVGDLVEVK	4.18	1,846.95
Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	NMVPQQALVIR	2.56	1,284.71
Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	QAADMILLDDNFASIVTGVEEGR	4.24	2,480.20
Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	QGAIVAVTGDGVNDSPALK	5.06	1,811.95
Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	QGAIVAVTGDGVNDSPALKK	3.2	1,940.05
Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	SPDFTNENPLETR	4.97	1,519.70

Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	VDNSSLTGESEPQTR	4.35	1,619.75
Control	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	19	27	50	0.49%	24.70%	VIMVTGDHPITAK	4.44	1,397.75
Control	6018	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	4	4	4	0.04%	27.80%	AFDLLVDRPVTLVR	2.09	1,613.94
Control	6018	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	4	4	4	0.04%	27.80%	DYKVDQEIVNIIQER	4.99	1,861.97
Control	6018	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	4	4	4	0.04%	27.80%	RTPAPSPQTSLPNPITYLTK	2.57	2,182.19
Control	6018	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	4	4	4	0.04%	27.80%	TPAPSPQTSLPNPITYLTK	4.96	2,026.09
Control	6018	ribosomal protein L18	gi|59858459,gi|62752012,gi|75060915,gi|75775560,gi|89573893	21,518.10	100.00%	3	3	5	0.05%	18.10%	ILTFDQLALDSPK	4.75	1,460.80
Control	6018	ribosomal protein L18	gi|59858459,gi|62752012,gi|75060915,gi|75775560,gi|89573893	21,518.10	100.00%	3	3	5	0.05%	18.10%	TNRPPLSLSR	3.4	1,140.65
Control	6018	ribosomal protein L18	gi|59858459,gi|62752012,gi|75060915,gi|75775560,gi|89573893	21,518.10	100.00%	3	3	5	0.05%	18.10%	TNSTFNQVVLK	2.57	1,250.67

Control	6018	RecName: Full=Isocitrate dehydrogenase [NADP], mitochondrial; Short=IDH; AltName: Full=Oxalosuccinate decarboxylase; AltName: Full=NADP(+)-specific ICDH; AltName: Full=IDP; AltName:	gi|109891934,gi|28461205,gi|430,gi|73587323	50,807.00	100.00%	3	3	3	0.03%	8.85%	LILPHVDVQLK	2.18	1,274.78
Control	6018	RecName: Full=Isocitrate dehydrogenase [NADP], mitochondrial; Short=IDH; AltName: Full=Oxalosuccinate decarboxylase; AltName: Full=NADP(+)-specific ICDH; AltName: Full=IDP; AltName:	gi|109891934,gi|28461205,gi|430,gi|73587323	50,807.00	100.00%	3	3	3	0.03%	8.85%	LNEHFLNTSDFLDTIK	3.79	1,906.95

Control	6018	RecName: Full=Isocitrate dehydrogenase [NADP], mitochondrial; Short=IDH; AltName: Full=Oxalosuccinate decarboxylase; AltName: Full=NADP(+)-specific ICDH; AltName: Full=IDP; AltName:	gi|109891934,gi|28461205,gi|430,gi|73587323	50,807.00	100.00%	3	3	3	0.03%	8.85%	TIEAEAAHGTVTR	4.06	1,355.69
Control	6018	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	6	9	15	0.15%	10.70%	AFEESLSTLK	2.92	1,124.58
Control	6018	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	6	9	15	0.15%	10.70%	ELDKVFNDYTAVPDLYFENAMR	5.25	2,666.24
Control	6018	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	6	9	15	0.15%	10.70%	HTLGENIADNGGLK	4.42	1,438.73
Control	6018	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	6	9	15	0.15%	10.70%	NEIVFPAGILQAPFYTR	5.43	1,936.03

Control	6018	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	6	9	15	0.15%	10.70%	TPESSHEGLITDPHSPSR	4.91	1,946.92
Control	6018	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	6	9	15	0.15%	10.70%	VFNDYTAVPDLYFENAMR	3.66	2,181.00
Control	6018	RecName: Full=60S ribosomal protein L5	gi|108862056,gi|119900687,gi|119905361,gi|61552973,gi|75775327,gi|78369655	34,327.50	99.80%	2	2	2	0.02%	8.75%	GAVDGGLSIPHSTK	4.05	1,338.70
Control	6018	RecName: Full=60S ribosomal protein L5	gi|108862056,gi|119900687,gi|119905361,gi|61552973,gi|75775327,gi|78369655	34,327.50	99.80%	2	2	2	0.02%	8.75%	YLIEEDEDAYKK	3.37	1,515.72
Control	6018	secretory carrier membrane protein 3 isoform 1	gi|61553277,gi|71649517,gi|73586519,gi|78369651	38,348.80	100.00%	3	3	3	0.03%	15.00%	AQQEFAAGVFSNPAVR	3.35	1,691.85
Control	6018	secretory carrier membrane protein 3 isoform 1	gi|61553277,gi|71649517,gi|73586519,gi|78369651	38,348.80	100.00%	3	3	3	0.03%	15.00%	NYGSYSTQASTAAATAELK	5.73	2,047.00
Control	6018	secretory carrier membrane protein 3 isoform 1	gi|61553277,gi|71649517,gi|73586519,gi|78369651	38,348.80	100.00%	3	3	3	0.03%	15.00%	TAAANAAAGAAENAFR	3.74	1,476.72
Control	6018	ANO10 protein	gi|154425799,gi|156120985	76,294.20	99.80%	2	2	2	0.02%	3.79%	ETLENQNLYLVGASK	3.25	1,678.86
Control	6018	ANO10 protein	gi|154425799,gi|156120985	76,294.20	99.80%	2	2	2	0.02%	3.79%	LEFESLEALK	3.05	1,178.63
Control	6018	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	5	7	11	0.11%	23.10%	GHAAPTPTPVKPPR	2.9	1,425.80
Control	6018	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	5	7	11	0.11%	23.10%	LATMLETLR	2.87	1,063.58

Control	6018	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	5	7	11	0.11%	23.10%	LEANHGLLVAR	3.6	1,192.68
Control	6018	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	5	7	11	0.11%	23.10%	RIQSNLGALSR	3.43	1,214.70
Control	6018	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	5	7	11	0.11%	23.10%	SHDTTSNTLAQLLAK	5.44	1,599.83
Control	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	172	1.68%	56.30%	DAVTYTEHAK	2.69	1,134.54
Control	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	172	1.68%	56.30%	DNIQGITKPAIR	3.61	1,325.75
Control	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	172	1.68%	56.30%	ISGLIYEETR	4.16	1,180.62
Control	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	172	1.68%	56.30%	KTVTAMDVVYALK	3.92	1,454.79
Control	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	172	1.68%	56.30%	KTVTAMDVVYALKR	4.7	1,610.89

Control	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	172	1.68%	56.30%	RISGLIYEETR	2.96	1,336.72
Control	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	172	1.68%	56.30%	TVTAMDVVYALK	4.75	1,310.70
Control	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	172	1.68%	56.30%	TVTAMDVVYALKR	3.63	1,482.80
Control	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	172	1.68%	56.30%	VFLENVIR	3.17	989.5778
Control	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	172	1.68%	56.30%	VFLENVIRDAVTYTEHAK	5.26	2,105.10
Control	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	172	1.68%	56.30%	VLRDNIQGITKPAIR	4.39	1,694.01
Control	6018	RecName: Full=Cleft lip and palate transmembrane protein 1 homolog	gi|110278913,gi|114051439,gi|84708720	75,864.60	99.80%	2	4	4	0.04%	4.63%	ALNTFIDDLFAFVIK	3.9	1,726.94

Control	6018	RecName: Full=Cleft lip and palate transmembrane protein 1 homolog	gi|110278913,gi|114051439,gi|84708720	75,864.60	99.80%	2	4	4	0.04%	4.63%	NLLTGETEADPEMIKR	3.92	1,832.91
Control	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	16	19	33	0.32%	29.40%	AVDEAADALLK	2.52	1,115.59
Control	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	16	19	33	0.32%	29.40%	ELDSITPEVLPGWK	4.42	1,583.83
Control	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	16	19	33	0.32%	29.40%	KVEEVRDAMENEMR	2.62	1,751.81
Control	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	16	19	33	0.32%	29.40%	LAEQELQFR	3.02	1,133.60
Control	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	16	19	33	0.32%	29.40%	LSADDLNALIAHAHR	2.57	1,616.85
Control	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	16	19	33	0.32%	29.40%	LSQEQVDNFTLDINTAYAR	5.05	2,198.07
Control	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	16	19	33	0.32%	29.40%	MKTASADLPTVPLGSAVEAIR	3	2,143.14
Control	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	16	19	33	0.32%	29.40%	QHIALALEK	3.93	1,022.60
Control	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	16	19	33	0.32%	29.40%	QKGDTSASTTAGDTLSVPAPVVQHEELIK	3.76	2,979.53
Control	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	16	19	33	0.32%	29.40%	TASADLPTVPLGSAVEAIR	5.24	1,868.01
Control	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	16	19	33	0.32%	29.40%	TDHPETGEGKPKPATSEEASSTSVR	4.51	2,598.23
Control	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	16	19	33	0.32%	29.40%	TIPYSDKLFEMVLGSPPYTVPLPK	3.53	2,708.43

Control	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	16	19	33	0.32%	29.40%	VQEQELKYEFEQDLSEK	3.42	2,142.02
Control	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	16	19	33	0.32%	29.40%	VQEQELKYEFEQDLSEKLAEQELQFR	3.61	3,256.60
Control	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	16	19	33	0.32%	29.40%	VVSQYHELVVQAR	4.48	1,527.83
Control	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	16	19	33	0.32%	29.40%	YEFEQDLSEKLAEQELQFR	3.57	2,402.15
Control	6018	ATAD1 protein	gi|154426126,gi|76671592	41,750.40	99.80%	2	4	4	0.04%	11.40%	EYVNSTSEESHDEDEIRPVQQQDLHR	4	3,140.42
Control	6018	ATAD1 protein	gi|154426126,gi|76671592	41,750.40	99.80%	2	4	4	0.04%	11.40%	LQPSIIFIDEIDSFLR	3.88	1,906.03
Control	6018	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	3	4	6	0.06%	13.50%	GLFTGLTPR	2.23	961.5467
Control	6018	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	3	4	6	0.06%	13.50%	SAATLITHPFHVITLR	1.72	1,777.01
Control	6018	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	3	4	6	0.06%	13.50%	VLIQVGYEPLAPTVGR	3.82	1,711.97
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	AAALRPEEDGAFRPSEAFETLQK	3.47	2,533.27
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	AEESAAHLPEEIR	3.42	1,451.71
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	AEESAAHLPEEIRR	2.45	1,607.81

Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	ASVGQVESDLK	3.72	1,132.58
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	DLSDGIHVVK	2.94	1,082.58
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	EAADSEHHTLQALTEK	2.06	1,779.85
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	EELGQGLQGVEQK	3.75	1,414.72
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	ELVSLKQEQQR	2.26	1,357.74
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	ERDFTSLENTVEER	4.58	1,724.81
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	EVVKEIQTSVK	3.42	1,259.72
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	FKEAADSEHHTLQALTEK	4.1	2,055.01

Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	GLGEAQLSLAGDVDELK	5.08	1,714.89
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	GLGEAQLSLAGDVDELKR	4.62	1,870.99
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	GLLEDLRNDLDR	2.43	1,428.74
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	IETNENNLESAK	3.52	1,361.65
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	LEEELGQLK	3.2	1,058.57
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	LQNEILKDLSDGIHVVK	5.04	1,921.08
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	LQSVEDGVQAAR	4.12	1,272.65
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	QREELGQGLQGVEQK	5.32	1,698.88

Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	QREELGQGLQGVEQKVQSLQATFGTFESLVR	3.73	3,462.80
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	RLEEELGQLK	3.52	1,214.67
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	SINDNIAIFTDVQK	4.83	1,577.82
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	SINDNIAIFTDVQKR	4.05	1,733.92
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	STIQTMESDVYTEVK	3.58	1,746.81
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	TAVDSLVAYSVK	3.59	1,252.68
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	VQEQVHTLLGR	4.07	1,279.71
Control	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	27	40	92	0.90%	45.20%	VQSLQATFGTFESLVR	4.07	1,782.94
Control	6018	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	6	7	9	0.09%	24.90%	KQYDSYTFTASK	3.41	1,438.68
Control	6018	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	6	7	9	0.09%	24.90%	LEDPDGNVLYK	3.27	1,262.63

Control	6018	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	6	7	9	0.09%	24.90%	LEDPDGNVLYKEMKK	2.5	1,794.89
Control	6018	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	6	7	9	0.09%	24.90%	QYDSYTFTASK	2.12	1,310.59
Control	6018	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	6	7	9	0.09%	24.90%	SVIDYQTHFR	3	1,265.63
Control	6018	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	6	7	9	0.09%	24.90%	TVYFDFQVGEDPPLFPSENR	3.36	2,357.11
Control	6018	similar to peptidylprolyl isomerase A (cyclophilin A)	gi|28189771,gi|58760424,gi|75948300	17,851.80	100.00%	3	4	4	0.04%	16.50%	SIYGEKFDDENFILK	4.09	1,817.90
Control	6018	similar to peptidylprolyl isomerase A (cyclophilin A)	gi|28189771,gi|58760424,gi|75948300	17,851.80	100.00%	3	4	4	0.04%	16.50%	VSFELFADK	2.71	1,055.54
Control	6018	similar to peptidylprolyl isomerase A (cyclophilin A)	gi|28189771,gi|58760424,gi|75948300	17,851.80	100.00%	3	4	4	0.04%	16.50%	VSFELFADKVPK	2.77	1,379.76
Control	6018	Clusterin	gi|109939936,gi|116530,gi|146231734,gi|151555910,gi|163115,gi|27806907	51,096.70	100.00%	2	2	2	0.02%	9.79%	LFNSFPITVTVPQEVSSPNFMENVAEK	3.86	3,040.50
Control	6018	Clusterin	gi|109939936,gi|116530,gi|146231734,gi|151555910,gi|163115,gi|27806907	51,096.70	100.00%	2	2	2	0.02%	9.79%	RPQDTQYYSPFSSFPR	3.35	1,975.93
Control	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	34	0.33%	55.90%	AAELIANSLATAGDGLIELR	5.27	1,998.09
Control	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	34	0.33%	55.90%	AATFGLILDDVSLTHLTFGK	2.9	2,119.14
Control	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	34	0.33%	55.90%	DLQNVNITLR	3.96	1,185.66
Control	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	34	0.33%	55.90%	FDAGELITQR	4.02	1,149.59

Control	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	34	0.33%	55.90%	FGLALAVAGGVVNSALYNVDAGHR	4.11	2,371.25
Control	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	34	0.33%	55.90%	IFTSIGEDYDER	3.63	1,444.66
Control	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	34	0.33%	55.90%	ILFRPVASQLPR	2.25	1,396.84
Control	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	34	0.33%	55.90%	KLEAAEDIAYQLSR	4.25	1,606.84
Control	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	34	0.33%	55.90%	NITYLPAGQSVLLQLPQ	4.7	1,855.03
Control	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	34	0.33%	55.90%	SRNITYLPAGQSVLLQLPQ	4.96	2,098.17
Control	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	34	0.33%	55.90%	VLPSITTEILK	2.4	1,213.74
Control	6018	ras-related C3 botulinum toxin substrate 1	gi|27806443,gi|51702785,gi|6007014,gi|73587375	21,432.60	99.90%	2	3	3	0.03%	7.81%	KLTPITYPQGLAMAK	2.71	1,647.91
Control	6018	ras-related C3 botulinum toxin substrate 1	gi|27806443,gi|51702785,gi|6007014,gi|73587375	21,432.60	99.90%	2	3	3	0.03%	7.81%	LTPITYPQGLAMAK	3.38	1,519.82
Control	6018	Interferon induced transmembrane protein 1 (9-27)	gi|112362418,gi|118151192,gi|118151350,gi|118151354,gi|119919513,gi|14279576,gi|14279578,gi|148744152,gi|32480628,gi|73586549,gi|73587371	13,629.20	99.80%	2	3	5	0.05%	13.70%	KMVGDITGAQSYASTAK	5.09	1,743.86

Control	6018	Interferon induced transmembrane protein 1 (9-27)	gi|112362418,gi|118151192,gi|118151350,gi|118151354,gi|119919513,gi|14279576,gi|14279578,gi|148744152,gi|32480628,gi|73586549,gi|73587371	13,629.20	99.80%	2	3	5	0.05%	13.70%	MVGDITGAQSYASTAK	5.59	1,615.76
Control	6018	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	5	5	7	0.07%	42.30%	ALAAAGYDVEK	3.09	1,107.57
Control	6018	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	5	5	7	0.07%	42.30%	ALAAAGYDVEKNNSR	4.15	1,578.79
Control	6018	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	5	5	7	0.07%	42.30%	ASGPPVSELITK	2.68	1,198.67
Control	6018	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	5	5	7	0.07%	42.30%	KALAAAGYDVEK	2.62	1,235.66
Control	6018	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	5	5	7	0.07%	42.30%	SETAPAAPAAAPPAEK	3.1	1,478.75
Control	6018	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	99.90%	2	2	2	0.02%	11.90%	ILHVNGFNGEGGEEDPQAAR	4.03	2,110.00
Control	6018	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	99.90%	2	2	2	0.02%	11.90%	LLLLGAGESGK	3.36	1,057.63
Control	6018	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	99.90%	2	2	2	0.02%	11.90%	YTTPEDATPEPGEDPR	2.94	1,774.78

Control	6018	PREDICTED: similar to Transmembrane 9 superfamily member 2 precursor (p76), partial	gi|194671915	72,962.00	100.00%	3	4	5	0.05%	4.40%	IYYHVVETGSMGAR	4.3	1,598.76
Control	6018	PREDICTED: similar to Transmembrane 9 superfamily member 2 precursor (p76), partial	gi|194671915	72,962.00	100.00%	3	4	5	0.05%	4.40%	PSENLGQVLFGER	3.96	1,445.74
Control	6018	PREDICTED: similar to Transmembrane 9 superfamily member 2 precursor (p76), partial	gi|194671915	72,962.00	100.00%	3	4	5	0.05%	4.40%	RPSENLGQVLFGER	3.82	1,601.84
Control	6018	interferon stimulated gene 17 [Ovis aries]	gi|12082402,gi|57619183	17,482.10	99.80%	2	2	2	0.02%	17.20%	EVLQEGVPLVHQGLK	4.36	1,645.93
Control	6018	interferon stimulated gene 17 [Ovis aries]	gi|12082402,gi|57619183	17,482.10	99.80%	2	2	2	0.02%	17.20%	MLGGEEILVPLR	2.66	1,342.74
Control	6018	UPF0404 protein C11orf59 homolog	gi|122140364,gi|74267677,gi|77736483	17,713.10	99.80%	2	2	2	0.02%	26.70%	LPPLPSLTSQPHQVLASEPVPFSDLQQVSR	4.91	3,267.74
Control	6018	UPF0404 protein C11orf59 homolog	gi|122140364,gi|74267677,gi|77736483	17,713.10	99.80%	2	2	2	0.02%	26.70%	TDEQALLSSILAK	3.69	1,388.76
Control	6018	RPL12 protein	gi|148744191,gi|42564206,gi|45430019,gi|47117092,gi|74354972	17,801.10	99.80%	2	2	2	0.02%	18.80%	HSGNITFDEIVNIAR	4.1	1,685.86
Control	6018	RPL12 protein	gi|148744191,gi|42564206,gi|45430019,gi|47117092,gi|74354972	17,801.10	99.80%	2	2	2	0.02%	18.80%	QAQIEVVPSASALIIK	3.59	1,666.97

Control	6018	Nucleobindin 2	gi|113912161,gi|115496067	49,171.70	99.80%	2	2	2	0.02%	8.19%	LHDVNSDGFLDEQELEALFTK	4.87	2,420.16
Control	6018	Nucleobindin 2	gi|113912161,gi|115496067	49,171.70	99.80%	2	2	2	0.02%	8.19%	QVIDVLETDSHFR	3.06	1,558.79
Control	6018	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	gi|111304648,gi|115496338,gi|121957506	27,838.90	99.80%	2	4	7	0.07%	11.20%	FKGPFTDVVTTNLK	4.15	1,566.85
Control	6018	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	gi|111304648,gi|115496338,gi|121957506	27,838.90	99.80%	2	4	7	0.07%	11.20%	GPFTDVVTTNLK	4.12	1,291.69
Control	6018	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	gi|111304648,gi|115496338,gi|121957506	27,838.90	99.80%	2	4	7	0.07%	11.20%	HEQILVLDPPTDLK	3.6	1,617.89
Control	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	14	0.14%	23.60%	AEVQNLGGELVVSGVDSAMSLIQAAK	4.6	2,602.34
Control	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	14	0.14%	23.60%	AIMAQLPQEQK	2.97	1,272.66
Control	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	14	0.14%	23.60%	ALKPEVDKLNIMAAK	2.61	1,656.94
Control	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	14	0.14%	23.60%	ESQFLKEELVAAVEDVRK	4.56	2,090.11
Control	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	14	0.14%	23.60%	FTEQVEAAVEALSSDPAQPMDENEFIDASR	3.25	3,312.49

Control	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	14	0.14%	23.60%	HVNPVQALSEFK	3.02	1,368.73
Control	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	14	0.14%	23.60%	IAEQVASFQEEK	3.44	1,378.68
Control	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	14	0.14%	23.60%	NAGTEQDLGIQYK	3.27	1,436.70
Control	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	14	0.14%	23.60%	NLMNAVVQTVK	2.78	1,232.67
Control	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	14	0.14%	23.60%	TSVQTEDDQLIAGQSAR	4.43	1,818.88
Control	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	14	0.14%	23.60%	VIHVVTSEMDNYEPGVYTEK	3.59	2,326.09
Control	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	12	12	14	0.14%	23.60%	VLTDAVDDITSIDDFLAVSENHILEDVNK	3.25	3,200.58
Control	6018	RecName: Full=Transmembrane and coiled-coil domain-containing protein 1	gi|109895213,gi|74354058,gi|77736477	21,158.30	99.80%	2	2	2	0.02%	15.40%	LPFTPLSYIQGLSHR	3.23	1,728.94
Control	6018	RecName: Full=Transmembrane and coiled-coil domain-containing protein 1	gi|109895213,gi|74354058,gi|77736477	21,158.30	99.80%	2	2	2	0.02%	15.40%	QAGGFLGPPPPSGK	2.88	1,309.69
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	AKFEELNMDLFR	4.9	1,528.75

Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	DAGTIAGLNVMR	3.72	1,233.63
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	DNHLLGTFDLTGIPPAPR	2.86	1,934.01
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	EFFNGKEPSR	2.85	1,210.59
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	ELEEIVQPIISK	3.99	1,397.79
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	IDTRNELESYAYSLK	3.94	1,801.90
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	IEIESFYEGEDFSETLTR	4.43	2,164.99
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	IINEPTAAAIAYGLDK	3.81	1,659.90
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	IINEPTAAAIAYGLDKR	4.02	1,816.00

Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	ITPSYVAFTPEGER	3.86	1,566.78
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	KKELEEIVQPIISK	4.02	1,653.98
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	KSQIFSTASDNQPTVTIK	3.6	1,965.03
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	KVTHAVVTVPAYFNDAQR	3.01	2,016.07
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	MKETAEAYLGKK	3.35	1,384.71
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	MVNDAEKFAEEDKK	3.72	1,669.77
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	NELESYAYSLK	2.89	1,316.64
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	NQLTSNPENTVFDAK	4.11	1,677.81

Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	NQLTSNPENTVFDAKR	4.04	1,833.91
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	SQIFSTASDNQPTVTIK	5.03	1,836.93
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	TFAPEEISAMVLTK	4.98	1,552.79
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	TKPYIQVDVGGGQTK	3.35	1,590.85
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	TWNDPSVQQDIK	3.44	1,430.69
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	VLEDSDLKKSDIDEIVLVGGSTR	3.21	2,488.31
Control	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	24	34	51	0.50%	41.40%	VTHAVVTVPAYFNDAQR	4.26	1,887.97
Control	6018	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	3	4	5	0.05%	6.71%	LLNDEDPVVVTK	3.37	1,341.73

Control	6018	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	3	4	5	0.05%	6.71%	LNTIPLFVQLLYSSVENIQR	4.57	2,347.30
Control	6018	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	3	4	5	0.05%	6.71%	TLVTQNSGVEALIHAILR	2.62	1,935.10
Control	6018	RecName: Full=60S ribosomal protein L11	gi|108860925,gi|115497634,gi|74268362	20,235.20	99.80%	2	2	2	0.02%	12.90%	VLEQLTGQTPVFSK	4.11	1,546.85
Control	6018	RecName: Full=60S ribosomal protein L11	gi|108860925,gi|115497634,gi|74268362	20,235.20	99.80%	2	2	2	0.02%	12.90%	YDGIILPGK	2.5	975.5512
Control	6018	syntaxin 7	gi|118150840,gi|122140829,gi|73586654	29,638.60	99.80%	2	2	3	0.03%	10.70%	EFGSLPTTPSDQR	2.73	1,434.69
Control	6018	syntaxin 7	gi|118150840,gi|122140829,gi|73586654	29,638.60	99.80%	2	2	3	0.03%	10.70%	TLNQLGTPQDSPELR	4.16	1,668.86
Control	6018	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	4	5	9	0.09%	19.60%	GDLLFLTNR	3.24	1,048.58
Control	6018	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	4	5	9	0.09%	19.60%	GDLLFLTNRVEDPIR	3.31	1,757.95
Control	6018	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	4	5	9	0.09%	19.60%	MLSLDFLDDVRR	2	1,495.76
Control	6018	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	4	5	9	0.09%	19.60%	VGEIVVFR	2.64	918.5407

Control	6018	RecName: Full=Acyl-protein thioesterase 1; AltName: Full=Lysophospholipase 1; AltName: Full=Lysophospholipase I	gi|115311636,gi|75948308,gi|77736321	24,578.40	99.80%	2	2	2	0.02%	10.40%	ASFPQGPIGGVNR	2.73	1,299.68
Control	6018	RecName: Full=Acyl-protein thioesterase 1; AltName: Full=Lysophospholipase 1; AltName: Full=Lysophospholipase I	gi|115311636,gi|75948308,gi|77736321	24,578.40	99.80%	2	2	2	0.02%	10.40%	TLVNPANVTFR	2.98	1,231.68
Control	6018	PREDICTED: brain protein 44	gi|119889010,gi|194665199	14,264.40	99.90%	2	4	7	0.07%	18.90%	LRPLYNHPAGPR	2.94	1,390.77
Control	6018	PREDICTED: brain protein 44	gi|119889010,gi|194665199	14,264.40	99.90%	2	4	7	0.07%	18.90%	VLDKVELLLPEK	4.03	1,395.85
Control	6018	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	10	16	0.16%	21.30%	EDFESLLHSAK	2.91	1,275.62
Control	6018	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	10	16	0.16%	21.30%	FLVVLNFGDVGQLAR	5.03	1,647.92
Control	6018	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	10	16	0.16%	21.30%	FTGLSKEELLK	3.23	1,264.71
Control	6018	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	10	16	0.16%	21.30%	LLIAGTDSSDLQQILR	4.77	1,742.97
Control	6018	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	10	16	0.16%	21.30%	NQEDDLTETNLEQIDPIFGSK	5.71	2,406.13

Control	6018	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	10	16	0.16%	21.30%	SLLHGDFYDLSSGPDLFSYIR	4.03	2,402.17
Control	6018	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	10	16	0.16%	21.30%	SVSEDRLLIAGTDSSDLQQILR	4.19	2,416.27
Control	6018	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	10	16	0.16%	21.30%	VDLLLSTQPGR	3.25	1,198.68
Control	6018	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	10	16	0.16%	21.30%	VILDLTPNYK	2.91	1,175.67
Control	6018	MHC class I antigen	gi|84095083	40,657.50	100.00%	7	9	85	0.83%	24.00%	DYIALNEDLR	3.37	1,221.61
Control	6018	MHC class I antigen	gi|84095083	40,657.50	100.00%	7	9	85	0.83%	24.00%	FIAVGYVDDTQFVR	5.3	1,629.83
Control	6018	MHC class I antigen	gi|84095083	40,657.50	100.00%	7	9	85	0.83%	24.00%	IYTQAASSDSAQGSDVSLTVPK	5.88	2,225.09
Control	6018	MHC class I antigen	gi|84095083	40,657.50	100.00%	7	9	85	0.83%	24.00%	IYTQAASSDSAQGSDVSLTVPKV	5.11	2,324.16
Control	6018	MHC class I antigen	gi|84095083	40,657.50	100.00%	7	9	85	0.83%	24.00%	SWTAADTAAQITK	4.35	1,363.69
Control	6018	MHC class I antigen	gi|84095083	40,657.50	100.00%	7	9	85	0.83%	24.00%	VQHEGLQEPLTLR	4.05	1,519.82
Control	6018	MHC class I antigen	gi|84095083	40,657.50	100.00%	7	9	85	0.83%	24.00%	WAALVVPSGEEQR	3.61	1,441.74
Control	6018	DDRGK domain containing 1	gi|115496153,gi|94534940	35,649.00	99.80%	2	3	3	0.03%	9.58%	FIYITPEELAAVANFIR	3.97	1,967.06
Control	6018	DDRGK domain containing 1	gi|115496153,gi|94534940	35,649.00	99.80%	2	3	3	0.03%	9.58%	LRLEEEQKEEEER	2.55	1,716.84

Control	6018	RecName: Full=Serine palmitoyltransferase 1; AltName: Full=Serine-palmitoyl-CoA transferase 1; Short=SPT 1; Short=SPT1; AltName: Full=Long chain base biosynthesis protein 1; Short=L	gi|122139929,gi|75948211,gi|77736443	52,771.80	99.80%	2	3	4	0.04%	5.92%	LLKEQEIEDQKNPR	2.95	1,739.93
Control	6018	RecName: Full=Serine palmitoyltransferase 1; AltName: Full=Serine-palmitoyl-CoA transferase 1; Short=SPT 1; Short=SPT1; AltName: Full=Long chain base biosynthesis protein 1; Short=L	gi|122139929,gi|75948211,gi|77736443	52,771.80	99.80%	2	3	4	0.04%	5.92%	VVVTVEQTEEDLEK	3.62	1,617.82
Control	6018	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	3	3	3	0.03%	4.90%	ALLELQLEPEELYQTFQR	3.93	2,220.15
Control	6018	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	3	3	3	0.03%	4.90%	EGIPALDNFLDKL	2.67	1,444.77

Control	6018	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	3	3	3	0.03%	4.90%	VFSGLVSTGLK	2.52	1,107.64
Control	6018	RecName: Full=Synaptic glycoprotein SC2; AltName: Full=Trans-2,3-enoyl-CoA reductase; Short=TER	gi|122140918,gi|73586600,gi|77736441	36,056.10	100.00%	3	3	3	0.03%	10.40%	HYEVEILDAK	2.55	1,216.62
Control	6018	RecName: Full=Synaptic glycoprotein SC2; AltName: Full=Trans-2,3-enoyl-CoA reductase; Short=TER	gi|122140918,gi|73586600,gi|77736441	36,056.10	100.00%	3	3	3	0.03%	10.40%	LPVGTTATLYFR	3.45	1,338.74
Control	6018	RecName: Full=Synaptic glycoprotein SC2; AltName: Full=Trans-2,3-enoyl-CoA reductase; Short=TER	gi|122140918,gi|73586600,gi|77736441	36,056.10	100.00%	3	3	3	0.03%	10.40%	SLKDEDVLQK	2.9	1,174.63
Control	6018	RecName: Full=Galectin-9	gi|122145068,gi|59858325,gi|62751460,gi|75775171,gi|87044899	39,329.70	100.00%	3	4	5	0.05%	9.86%	LKNLPAINNLEVGGDIQLTHVQT	3.36	2,487.36
Control	6018	RecName: Full=Galectin-9	gi|122145068,gi|59858325,gi|62751460,gi|75775171,gi|87044899	39,329.70	100.00%	3	4	5	0.05%	9.86%	NLPAINNLEVGGDIQLTHVQT	5.15	2,246.18

Control	6018	RecName: Full=Galectin-9	gi|122145068,gi|59858325,gi|62751460,gi|75775171,gi|87044899	39,329.70	100.00%	3	4	5	0.05%	9.86%	SGSDIAFHLNPR	2.9	1,313.66
Control	6018	PREDICTED: similar to Calpain-5 (nCL-3) (htra-3) isoform 1	gi|76636134	72,988.00	100.00%	3	3	3	0.03%	8.12%	ANADDLQALHTLHLR	2.98	1,687.89
Control	6018	PREDICTED: similar to Calpain-5 (nCL-3) (htra-3) isoform 1	gi|76636134	72,988.00	100.00%	3	3	3	0.03%	8.12%	VLFEDPNFPATDDSLYYK	2.63	2,134.00
Control	6018	PREDICTED: similar to Calpain-5 (nCL-3) (htra-3) isoform 1	gi|76636134	72,988.00	100.00%	3	3	3	0.03%	8.12%	YVIIPTTFEPGHTGEFLLR	2.13	2,190.16
Control	6018	PREDICTED: similar to SMILE protein	gi|194667013	104,216.00	99.80%	2	2	3	0.03%	4.25%	DKISSSSFVEQPIFPAGK	3.61	1,937.00
Control	6018	PREDICTED: similar to SMILE protein	gi|194667013	104,216.00	99.80%	2	2	3	0.03%	4.25%	YFLQATHVQPDDIGAHMNVGR	4.59	2,385.14
Control	6018	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	4	4	5	0.05%	21.80%	GVDLQENNPASR	3.28	1,299.63
Control	6018	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	4	4	5	0.05%	21.80%	LVLLGESAVGK	2.98	1,085.66
Control	6018	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	4	4	5	0.05%	21.80%	QASPNIVIALAGNK	3.23	1,395.80
Control	6018	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	4	4	5	0.05%	21.80%	YHSLAPMYYR	2.31	1,316.61
Control	6018	Coiled-coil-helix-coiled-coil-helix domain containing 9	gi|73587249,gi|77736437	15,615.40	99.80%	2	2	2	0.02%	43.10%	QFLECAQSQGDLKLCEGFSEVLK	3.31	2,572.24

Control	6018	Coiled-coil-helix-coiled-coil-helix domain containing 9	gi|73587249,gi|77736437	15,615.40	99.80%	2	2	2	0.02%	43.10%	QPGLMAQMATTAAGVAVGSAVGHTLGHAITGGFSGGSSAEPSR	3.86	4,010.95
Control	6018	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	7	12	0.12%	32.70%	ELNVMFIETSAK	3.72	1,397.70
Control	6018	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	7	12	0.12%	32.70%	GSDVIIMLVGNK	3.19	1,261.68
Control	6018	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	7	12	0.12%	32.70%	GSDVIIMLVGNKTDLADKR	3.45	2,061.10
Control	6018	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	7	12	0.12%	32.70%	LQLWDTAGQER	2.62	1,316.66
Control	6018	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	7	12	0.12%	32.70%	LVFLGEQSVGK	2.35	1,176.66
Control	6018	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	7	12	0.12%	32.70%	RVAAALPGMESTQDR	3.3	1,617.80

Control	6018	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	7	12	0.12%	32.70%	VAAALPGMESTQDR	3.19	1,461.70
Control	6018	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	2	3	0.03%	24.70%	DLTDYLMK	2.07	1,014.48
Control	6018	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	2	3	0.03%	24.70%	GYSFTTTAER	3.39	1,132.53
Control	6018	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	2	3	0.03%	24.70%	HQGVMVGMGQKDCYVGDEAQSK	3.59	2,383.05
Control	6018	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	2	3	0.03%	24.70%	HQGVMVGMGQKDCYVGDEAQSKR	3.8	2,539.15
Control	6018	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	2	3	0.03%	24.70%	LDLAGRDLTDYLMK	2.18	1,639.84
Control	6018	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	2	3	0.03%	24.70%	SYELPDGQVITIGNER	3.46	1,790.89
Control	6018	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	2	3	0.03%	24.70%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	6.85	3,199.61

Control	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	gi|27806197,gi|3676399,gi|71153779,gi|73586683	29,157.00	100.00%	2	3	6	0.06%	15.70%	AAFDDAIAELDTLSEESYKDSTLIMQLLR	4.42	3,274.60
Control	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	gi|27806197,gi|3676399,gi|71153779,gi|73586683	29,157.00	100.00%	2	3	6	0.06%	15.70%	EAAENSLVAYK	2.08	1,194.60
Control	6018	Transducin (beta)-like 2	gi|112362303,gi|115495815	49,894.00	99.80%	2	2	2	0.02%	5.83%	APIVNIGIADTGK	3.12	1,268.72
Control	6018	Transducin (beta)-like 2	gi|112362303,gi|115495815	49,894.00	99.80%	2	2	2	0.02%	5.83%	LQQQLTQAQEALK	4.6	1,498.82
Control	6018	RecName: Full=Coiled-coil domain-containing protein 56	gi|108935963,gi|74268043,gi|77736311	11,689.70	99.80%	2	2	2	0.02%	18.90%	FLDELEDEAK	3.55	1,208.57
Control	6018	RecName: Full=Coiled-coil domain-containing protein 56	gi|108935963,gi|74268043,gi|77736311	11,689.70	99.80%	2	2	2	0.02%	18.90%	LTPAQLQFMR	2.2	1,220.65
Control	6018	proteasome activator 28 alpha subunit	gi|63139650,gi|73921836,gi|86821522,gi|91680535	28,675.80	100.00%	2	2	2	0.02%	9.64%	NAYAVLYDIILK	3.35	1,395.79
Control	6018	proteasome activator 28 alpha subunit	gi|63139650,gi|73921836,gi|86821522,gi|91680535	28,675.80	100.00%	2	2	2	0.02%	9.64%	QLVHELDEAEYR	2.33	1,501.73
Control	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	12	16	23	0.22%	14.50%	FNTSDVSAIEK	3.09	1,210.60
Control	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	12	16	23	0.22%	14.50%	GAALITAVGVR	2.9	1,027.63
Control	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	12	16	23	0.22%	14.50%	GAAMVTAVAYR	3.03	1,125.57

Control	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	12	16	23	0.22%	14.50%	GKFNTSDVSAIEK	3.18	1,395.71
Control	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	12	16	23	0.22%	14.50%	HIDLVEGDEGR	3.71	1,239.60
Control	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	12	16	23	0.22%	14.50%	IDKYLYAMR	2.15	1,188.61
Control	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	12	16	23	0.22%	14.50%	LSDETLLDIMNR	4.19	1,435.71
Control	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	12	16	23	0.22%	14.50%	LVDEFSLNSGK	2.98	1,208.62
Control	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	12	16	23	0.22%	14.50%	QIEETLAHFSLTK	3.23	1,516.80
Control	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	12	16	23	0.22%	14.50%	SANLVAATLGAILSR	4.06	1,456.85
Control	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	12	16	23	0.22%	14.50%	TTVGVDGSLYK	2.72	1,139.59
Control	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	12	16	23	0.22%	14.50%	YLSQIESDRLALLQVR	3.31	1,904.06
Control	6018	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	5	7	7	0.07%	10.80%	DIQGSLQDIFK	3.47	1,263.66
Control	6018	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	5	7	7	0.07%	10.80%	INENTGSVSVTR	4.03	1,276.65
Control	6018	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	5	7	7	0.07%	10.80%	MTAFDADDPATDNALLR	4.02	1,852.84
Control	6018	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	5	7	7	0.07%	10.80%	SIVVSPILIPENQR	2.36	1,564.91

Control	6018	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	5	7	7	0.07%	10.80%	TLEGPVPLEVIVIDQNDNRPIFR	2.09	2,634.43
Control	6018	alpha-actinin 1	gi|145286437,gi|77567675,gi|78369242	102,966.00	99.80%	2	2	4	0.04%	3.70%	IDQLEGDHQLIQEALIFDNK	6.12	2,339.19
Control	6018	alpha-actinin 1	gi|145286437,gi|77567675,gi|78369242	102,966.00	99.80%	2	2	4	0.04%	3.70%	LSNRPAFMPSEGR	3.2	1,477.72
Control	6018	PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa isoform 1	gi|194673284	40,877.60	99.80%	2	3	4	0.04%	7.69%	FLMSLVNQVPK	2.89	1,291.71
Control	6018	PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa isoform 1	gi|194673284	40,877.60	99.80%	2	3	4	0.04%	7.69%	IQDALSTVLQYAEDVLSGK	4.94	2,050.07
Control	6018	PREDICTED: similar to programmed cell death 8 isoform 2	gi|76658657	66,854.50	100.00%	4	4	5	0.05%	9.95%	ATSSALEGEPEPQVR	4.03	1,570.77
Control	6018	PREDICTED: similar to programmed cell death 8 isoform 2	gi|76658657	66,854.50	100.00%	4	4	5	0.05%	9.95%	IPSHVPFLLIGGGTAAFAAAR	4.22	2,066.15
Control	6018	PREDICTED: similar to programmed cell death 8 isoform 2	gi|76658657	66,854.50	100.00%	4	4	5	0.05%	9.95%	ISGLGLTPEEK	2.93	1,143.63
Control	6018	PREDICTED: similar to programmed cell death 8 isoform 2	gi|76658657	66,854.50	100.00%	4	4	5	0.05%	9.95%	TGGLEIDSDFGGFR	4.08	1,470.69

Control	6018	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	7	10	13	0.13%	18.80%	FAIQTDPNSNDGLVTVVKPIDFETNR	3.32	2,890.46
Control	6018	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	7	10	13	0.13%	18.80%	FLEAGIYEVPIIITDSGNPPK	5.46	2,273.21
Control	6018	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	7	10	13	0.13%	18.80%	MYVLTVAAENQVPLAK	2.31	1,762.94

Control	6018	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	7	10	13	0.13%	18.80%	QLLIDPEDDVRDNILK	2.42	1,896.01
Control	6018	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	7	10	13	0.13%	18.80%	SAAPHPGDIGDFINEGLK	4.61	1,837.91
Control	6018	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	7	10	13	0.13%	18.80%	YDEEGGGEEDQDYDLSQLQQPDTVEPDAIKPVGIR	6.83	3,905.78

Control	6018	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	7	10	13	0.13%	18.80%	YSVTGPGADQPPTGIFIINPISGQLSVTKPLDR	3.46	3,438.83
Control	6018	RecName: Full=Cytochrome c1, heme protein, mitochondrial; AltName: Full=Ubiquinol-cytochrome-c reductase complex cytochrome c1 subunit; Short=Cytochrome c-1; AltName: Full=Cytochrome b-c1 complex	gi|109940069,gi|114793904,gi|71042588,gi|75765182,gi|75765193,gi|82407279,gi|82407290,gi|83638779,gi|84000289	27,269.70	100.00%	4	5	6	0.06%	29.90%	ALAEEVEVQDGPNEDGEMFMRPGK	4.45	2,664.19

Control	6018	RecName: Full=Cytochrome c1, heme protein, mitochondrial; AltName: Full=Ubiquinol-cytochrome-c reductase complex cytochrome c1 subunit; Short=Cytochrome c-1; AltName: Full=Cytochrome b-c1 complex	gi|109940069,gi|114793904,gi|71042588,gi|75765182,gi|75765193,gi|82407279,gi|82407290,gi|83638779,gi|84000289	27,269.70	100.00%	4	5	6	0.06%	29.90%	GLLSSLDHTSIR	3.09	1,298.71
Control	6018	RecName: Full=Cytochrome c1, heme protein, mitochondrial; AltName: Full=Ubiquinol-cytochrome-c reductase complex cytochrome c1 subunit; Short=Cytochrome c-1; AltName: Full=Cytochrome b-c1 complex	gi|109940069,gi|114793904,gi|71042588,gi|75765182,gi|75765193,gi|82407279,gi|82407290,gi|83638779,gi|84000289	27,269.70	100.00%	4	5	6	0.06%	29.90%	LSDYFPKPYPNPEAAR	3.53	1,864.92

Control	6018	RecName: Full=Cytochrome c1, heme protein, mitochondrial; AltName: Full=Ubiquinol-cytochrome-c reductase complex cytochrome c1 subunit; Short=Cytochrome c-1; AltName: Full=Cytochrome b-c1 complex	gi|109940069,gi|114793904,gi|71042588,gi|75765182,gi|75765193,gi|82407279,gi|82407290,gi|83638779,gi|84000289	27,269.70	100.00%	4	5	6	0.06%	29.90%	MGLKMLLMMGLLLPLVYAMK	3.01	2,266.26
Control	6018	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	100.00%	3	3	14	0.14%	52.10%	ELAEAQEDTILK	3.71	1,359.70
Control	6018	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	100.00%	3	3	14	0.14%	52.10%	MVPPVQVSPLIK	2.12	1,323.77
Control	6018	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	100.00%	3	3	14	0.14%	52.10%	YSALFLGMAYGAK	4.03	1,407.70
Control	6018	PREDICTED: similar to ATP-binding cassette, sub-family B, member 7	gi|194680502	83,040.70	100.00%	3	3	3	0.03%	9.43%	ADNDAGNAAIDSLLNYETVK	3.33	2,094.00
Control	6018	PREDICTED: similar to ATP-binding cassette, sub-family B, member 7	gi|194680502	83,040.70	100.00%	3	3	3	0.03%	9.43%	AVGVVPQDAVLFHNTIYYNLLYGNISASPEEVYAVAK	6.18	4,025.07

Control	6018	PREDICTED: similar to ATP-binding cassette, sub-family B, member 7	gi|194680502	83,040.70	100.00%	3	3	3	0.03%	9.43%	QALIDMNTLFTLLK	2.76	1,636.90
Control	6018	DnaJ (Hsp40) homolog, subfamily C, member 19	gi|73587098,gi|77735867,gi|83305915	12,481.10	99.80%	2	2	2	0.02%	27.60%	EAALILGVSPTANK	4.23	1,383.78
Control	6018	DnaJ (Hsp40) homolog, subfamily C, member 19	gi|73587098,gi|77735867,gi|83305915	12,481.10	99.80%	2	2	2	0.02%	27.60%	IMLLNHPDKGGSPYIAAK	2.93	1,941.03
Control	6018	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	10	12	0.12%	23.50%	FLESGGQDGAGDDDDLEDLEEAEEPDLEEDDDQK	4.1	3,739.49
Control	6018	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	10	12	0.12%	23.50%	FLESGGQDGAGDDDDLEDLEEAEEPDLEEDDDQKAVKDEL	6.35	4,394.84
Control	6018	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	10	12	0.12%	23.50%	GNFDEALAAHK	3.2	1,172.57
Control	6018	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	10	12	0.12%	23.50%	ILEFFGLK	2.52	966.566
Control	6018	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	10	12	0.12%	23.50%	LITLEEEMTK	2.61	1,222.62
Control	6018	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	10	12	0.12%	23.50%	NFEEVAFDEKK	3.09	1,355.65
Control	6018	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	10	12	0.12%	23.50%	VDATEESDLAQQYGVR	2.78	1,780.83
Control	6018	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	10	12	0.12%	23.50%	YKPESDELTAEK	3.26	1,409.68
Control	6018	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	9	10	12	0.12%	23.50%	YQLDKDGVVLFK	3.43	1,424.78
Control	6018	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	5	7	0.07%	25.70%	DHADSNIVIMLVGNK	3.56	1,641.83
Control	6018	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	5	7	0.07%	25.70%	GAVGALLVYDIAK	3.69	1,289.75

Control	6018	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	5	7	0.07%	25.70%	HLTYENVER	2.27	1,160.57
Control	6018	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	5	7	0.07%	25.70%	NILTEIYR	2.39	1,021.57
Control	6018	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	5	7	0.07%	25.70%	VVLIGDSGVGK	3.07	1,043.61
Control	6018	SEPT11 protein	gi|126010811,gi|126723403,gi|162416046	48,974.60	100.00%	3	3	3	0.03%	9.88%	AAAQLLQSQAQQSGAQQTK	6.01	1,957.01
Control	6018	SEPT11 protein	gi|126010811,gi|126723403,gi|162416046	48,974.60	100.00%	3	3	3	0.03%	9.88%	FESDPATHNEPGVR	2.4	1,555.71
Control	6018	SEPT11 protein	gi|126010811,gi|126723403,gi|162416046	48,974.60	100.00%	3	3	3	0.03%	9.88%	VNIIPIIAK	1.91	980.6504
Control	6018	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	4	4	5	0.05%	15.00%	IPDEFDNDPILVQQLR	4.71	1,911.98
Control	6018	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	4	4	5	0.05%	15.00%	QNLFFSSLTSR	2.32	1,299.67
Control	6018	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	4	4	5	0.05%	15.00%	TVLEHYALEEDPLEAFK	4.33	2,004.00
Control	6018	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	4	4	5	0.05%	15.00%	VLLDLSAFLK	2.92	1,118.68
Control	6018	CSE1L protein	gi|146186877,gi|164448620,gi|193806599	110,362.80	99.80%	2	2	2	0.02%	4.53%	FLESVEGNQNYPLLLLTLLEK	4.81	2,433.33
Control	6018	CSE1L protein	gi|146186877,gi|164448620,gi|193806599	110,362.80	99.80%	2	2	2	0.02%	4.53%	SFSLLQEAIIPYIPTLITQLTQK	3.55	2,617.49

Control	6018	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	5	5	5	0.05%	6.71%	GLGYAQYLPR	3.49	1,137.61
Control	6018	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	5	5	5	0.05%	6.71%	VALLLLEK	2.16	898.5973
Control	6018	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	5	5	5	0.05%	6.71%	VGQISFDLPR	3.37	1,131.62
Control	6018	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	5	5	5	0.05%	6.71%	VSEEIFFGR	3.15	1,083.55
Control	6018	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	5	5	5	0.05%	6.71%	VTQSAYAQIVQFGMNEK	4.12	1,929.94
Control	6018	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	8	11	27	0.26%	49.30%	HLIIGVSSDR	2.88	1,096.61
Control	6018	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	8	11	27	0.26%	49.30%	IIGVGDKIR	2.83	970.6046
Control	6018	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	8	11	27	0.26%	49.30%	NASEMIDKLTLTFNR	3.71	1,768.89

Control	6018	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	8	11	27	0.26%	49.30%	NYQEYSLANIIYYSLK	4.13	1,981.99
Control	6018	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	8	11	27	0.26%	49.30%	RPPTFGDASVIALELLNSGYEFDEGSIIFNR	6.89	3,427.72
Control	6018	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	8	11	27	0.26%	49.30%	TEEKPIFSLDTISSAESMSIYDDIDADVLR	5.7	3,376.60
Control	6018	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	8	11	27	0.26%	49.30%	THSDQFLVTFK	3.5	1,322.67
Control	6018	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	8	11	27	0.26%	49.30%	VYGVGSLALYEK	4.83	1,298.70
Control	6018	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	3	4	6	0.06%	18.60%	QMEQISQFLQAAER	3.53	1,694.82

Control	6018	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	3	4	6	0.06%	18.60%	TLMNLGGLAVAR	3.14	1,231.68
Control	6018	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	3	4	6	0.06%	18.60%	YFSDNQLQEGK	2.77	1,328.61
Control	6018	PREDICTED: similar to Heparan sulfate 2-O-sulfotransferase 1 (2-O-sulfotransferase) (2OST), partial	gi|119889909	37,063.70	100.00%	3	3	4	0.04%	12.10%	EKDGDLYILAQNFFYEK	3.41	2,093.02
Control	6018	PREDICTED: similar to Heparan sulfate 2-O-sulfotransferase 1 (2-O-sulfotransferase) (2OST), partial	gi|119889909	37,063.70	100.00%	3	3	4	0.04%	12.10%	LVSYYYFLR	2.77	1,223.65
Control	6018	PREDICTED: similar to Heparan sulfate 2-O-sulfotransferase 1 (2-O-sulfotransferase) (2OST), partial	gi|119889909	37,063.70	100.00%	3	3	4	0.04%	12.10%	NNPVMSLQDQVR	4.19	1,416.69
Control	6018	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	4	4	5	0.05%	6.89%	LAADEENVDSNMR	4.01	1,608.68
Control	6018	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	4	4	5	0.05%	6.89%	SSVGTSLLLTLAR	3.22	1,317.77
Control	6018	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	4	4	5	0.05%	6.89%	VEYHLLSPYVSPR	2.76	1,559.82

Control	6018	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	4	4	5	0.05%	6.89%	VSASPLLYSLIEK	4.47	1,419.81
Control	6018	Heterogeneous nuclear ribonucleoprotein C (C1/C2)	gi|74356361,gi|77735745	32,410.20	99.80%	2	2	2	0.02%	9.18%	GFAFVQYVNER	3.45	1,329.66
Control	6018	Heterogeneous nuclear ribonucleoprotein C (C1/C2)	gi|74356361,gi|77735745	32,410.20	99.80%	2	2	2	0.02%	9.18%	MIAGQVLDINLAAEPK	4.33	1,698.91
Control	6018	Caveolin 2	gi|157279219,gi|38322700,gi|51512145,gi|56119130,gi|66774044	18,142.30	100.00%	3	3	6	0.06%	27.20%	ADVQLFMDDDSYSR	3.18	1,677.71
Control	6018	Caveolin 2	gi|157279219,gi|38322700,gi|51512145,gi|56119130,gi|66774044	18,142.30	100.00%	3	3	6	0.06%	27.20%	SFSSVSLQLSHD	3.77	1,306.63
Control	6018	Caveolin 2	gi|157279219,gi|38322700,gi|51512145,gi|56119130,gi|66774044	18,142.30	100.00%	3	3	6	0.06%	27.20%	VGFEDVIAEPVSTHSFDK	4.17	1,976.96
Control	6018	solute carrier family 29 (nucleoside transporters), member 1	gi|110331885,gi|73587285,gi|77735743	49,866.60	100.00%	3	3	3	0.03%	10.10%	DIQASASPLAPSPER	3.4	1,538.78
Control	6018	solute carrier family 29 (nucleoside transporters), member 1	gi|110331885,gi|73587285,gi|77735743	49,866.60	100.00%	3	3	3	0.03%	10.10%	LAFVPLLLLCNVQPR	4.06	1,696.00
Control	6018	solute carrier family 29 (nucleoside transporters), member 1	gi|110331885,gi|73587285,gi|77735743	49,866.60	100.00%	3	3	3	0.03%	10.10%	LEGPGEQETKLDLISK	2.65	1,756.93

Control	6018	calcium binding protein P22	gi|115497570,gi|122142989,gi|152941188,gi|74354201	22,425.20	99.80%	2	2	3	0.03%	13.80%	ASTLLRDEELEEIKK	3.01	1,773.96
Control	6018	calcium binding protein P22	gi|115497570,gi|122142989,gi|152941188,gi|74354201	22,425.20	99.80%	2	2	3	0.03%	13.80%	IPELAINPLGDR	3.7	1,307.73
Control	6018	Chromosome 9 open reading frame 46 ortholog	gi|74354529,gi|77735799	17,091.30	99.80%	2	2	4	0.04%	15.60%	GMITFESLEK	3.04	1,170.57
Control	6018	Chromosome 9 open reading frame 46 ortholog	gi|74354529,gi|77735799	17,091.30	99.80%	2	2	4	0.04%	15.60%	MKGEAENILETEK	3.61	1,507.73
Control	6018	STAT1 protein	gi|154426144	86,914.50	99.80%	2	2	2	0.02%	3.35%	ELSAVTFPDIIR	3.04	1,360.75
Control	6018	STAT1 protein	gi|154426144	86,914.50	99.80%	2	2	2	0.02%	3.35%	VMAAENIPENPLK	3.7	1,441.74
Control	6018	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	100.00%	3	4	5	0.05%	26.00%	DYLALNEDLR	3.37	1,221.61
Control	6018	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	100.00%	3	4	5	0.05%	26.00%	FITVGYVDDTQFVR	3.22	1,659.84
Control	6018	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	100.00%	3	4	5	0.05%	26.00%	NGEDQTQDMELVETRPSGDGTFQK	3.76	2,698.19
Control	6018	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	100.00%	3	4	5	0.05%	26.00%	SWTAADTAAQITK	4.35	1,363.69
Control	6018	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	100.00%	3	4	5	0.05%	26.00%	VQHEGLQEPLTLR	4.05	1,519.82
Control	6018	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	100.00%	3	4	5	0.05%	26.00%	YFLTAVSRPGLGEPR	3.29	1,662.90
Control	6018	LOC539976 protein	gi|133778097,gi|157074098	83,155.80	99.80%	2	2	2	0.02%	4.62%	AVGFSSGTENPHGVK	2.4	1,486.73
Control	6018	LOC539976 protein	gi|133778097,gi|157074098	83,155.80	99.80%	2	2	2	0.02%	4.62%	LYSEEQPQEAVPHLEAALR	3.37	2,180.10

Control	6018	v-ral simian leukemia viral oncogene homolog B	gi|146231722,gi|147900776,gi|148878477	23,421.00	99.80%	2	2	2	0.02%	13.60%	AEEDKIPLLVVGNK	3.8	1,524.86
Control	6018	v-ral simian leukemia viral oncogene homolog B	gi|146231722,gi|147900776,gi|148878477	23,421.00	99.80%	2	2	2	0.02%	13.60%	ANVDKVFFDLMR	4.93	1,470.74
Control	6018	v-ral simian leukemia viral oncogene homolog B	gi|146231722,gi|147900776,gi|148878477	23,421.00	99.80%	2	2	2	0.02%	13.60%	VFFDLMR	2.07	943.4707
Control	6018	v-ral simian leukemia viral oncogene homolog B	gi|146231722,gi|147900776,gi|148878477	23,421.00	99.80%	2	2	2	0.02%	13.60%	VKAEEDKIPLLVVGNK	2.05	1,752.03
Control	6018	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	5	5	5	0.05%	15.90%	DTILQLNLK	2.52	1,057.63

Control	6018	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	5	5	5	0.05%	15.90%	IATSGYLPTQQDVLR	3.77	1,661.89
Control	6018	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	5	5	5	0.05%	15.90%	LLLLGTGESGK	2.79	1,087.64

Control	6018	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	5	5	5	0.05%	15.90%	VPTTGIIEYPFDLENIIFR	5.19	2,237.19
Control	6018	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	5	5	5	0.05%	15.90%	VRVPTTGIIEYPFDLENIIFR	5.22	2,492.36
Control	6018	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	4	5	7	0.07%	26.40%	IALMPLLQAEK	2.87	1,242.71
Control	6018	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	4	5	7	0.07%	26.40%	LQIEDFEAR	2.91	1,120.56

Control	6018	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	4	5	7	0.07%	26.40%	VKQDMPPVGGYGPIDYK	3.84	1,879.93
Control	6018	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	4	5	7	0.07%	26.40%	VKQDMPPVGGYGPIDYKR	5.22	2,036.03
Control	6018	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	5	6	8	0.08%	21.80%	FFVVSSESR	3.07	1,057.53
Control	6018	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	5	6	8	0.08%	21.80%	RKPDEVLDDEDIGSAPLK	4.62	1,997.02
Control	6018	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	5	6	8	0.08%	21.80%	TELHIPNVDLK	2.94	1,278.71
Control	6018	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	5	6	8	0.08%	21.80%	VLKEDALPDLK	2.77	1,240.72
Control	6018	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	5	6	8	0.08%	21.80%	VLKEDALPDLKTEYEVDSEDR	5.67	2,464.21
Control	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	13	19	0.19%	42.90%	ALTVPELTQQMFDAK	3.39	1,707.86
Control	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	13	19	0.19%	42.90%	AVLVDLEPGTMDSVR	3.78	1,617.82
Control	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	13	19	0.19%	42.90%	EAESDCLQGFQLTHSLGGGTGSGMGTLLISK	3.11	3,213.49
Control	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	13	19	0.19%	42.90%	EVDEQMLNVQNK	2.76	1,462.68

Control	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	13	19	0.19%	42.90%	GHYTEGAELVDSVLDVVR	4.4	1,958.98
Control	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	13	19	0.19%	42.90%	GHYTEGAELVDSVLDVVRK	3.51	2,087.08
Control	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	13	19	0.19%	42.90%	IMNTFSVVPSPK	4.35	1,335.70
Control	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	13	19	0.19%	42.90%	LAVNMVPFPR	3.83	1,159.63
Control	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	13	19	0.19%	42.90%	LHFFMPGFAPLTSR	4.05	1,636.83
Control	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	13	19	0.19%	42.90%	NSSYFVEWIPNNVK	2.39	1,696.83
Control	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	13	19	0.19%	42.90%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	4.6	4,479.06
Control	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	13	19	0.19%	42.90%	YLTVAAVFR	2.73	1,039.59
Control	6018	RAN binding protein 6	gi|78174362,gi|83715972	47,285.80	99.80%	2	2	2	0.02%	6.16%	KQAEETYENIPGQSK	3.05	1,721.83
Control	6018	RAN binding protein 6	gi|78174362,gi|83715972	47,285.80	99.80%	2	2	2	0.02%	6.16%	SLVEIADTVPK	3.72	1,171.66
Control	6018	RecName: Full=Peptidyl-prolyl cis-trans isomerase B; Short=PPIase; Short=Rotamase; AltName: Full=Cyclophilin B; AltName: Full=S-cyclophilin; Short=SCYLP; Flags: Precursor	gi|215274238,gi|27806469,gi|529242,gi|59858297,gi|74268324	23,726.00	100.00%	3	3	3	0.03%	18.10%	IEVEKPFAIAKE	2.95	1,373.77

Control	6018	RecName: Full=Peptidyl-prolyl cis-trans isomerase B; Short=PPIase; Short=Rotamase; AltName: Full=Cyclophilin B; AltName: Full=S-cyclophilin; Short=SCYLP; Flags: Precursor	gi|215274238,gi|27806469,gi|529242,gi|59858297,gi|74268324	23,726.00	100.00%	3	3	3	0.03%	18.10%	TVDNFVALATGEK	2.67	1,364.71
Control	6018	RecName: Full=Peptidyl-prolyl cis-trans isomerase B; Short=PPIase; Short=Rotamase; AltName: Full=Cyclophilin B; AltName: Full=S-cyclophilin; Short=SCYLP; Flags: Precursor	gi|215274238,gi|27806469,gi|529242,gi|59858297,gi|74268324	23,726.00	100.00%	3	3	3	0.03%	18.10%	VIKDFMIQGGDFTR	4.41	1,642.83
Control	6018	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	99.90%	2	2	2	0.02%	7.01%	MALVLDALPR	3.31	1,114.63
Control	6018	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	99.90%	2	2	2	0.02%	7.01%	SILGTLTVEQIYQDRDQFAK	3.31	2,325.21

Control	6018	RecName: Full=GPI transamidase component PIG-S; AltName: Full=Phosphatidylinositol-glycan biosynthesis class S protein	gi|116248578,gi|74268100,gi|77735383	61,769.20	100.00%	3	3	3	0.03%	11.90%	APLPYSQISGLNSLK	3.84	1,587.87
Control	6018	RecName: Full=GPI transamidase component PIG-S; AltName: Full=Phosphatidylinositol-glycan biosynthesis class S protein	gi|116248578,gi|74268100,gi|77735383	61,769.20	100.00%	3	3	3	0.03%	11.90%	LMVPVTVVFTQESVPLDDQEKLPFTVVHER	4.22	3,468.81
Control	6018	RecName: Full=GPI transamidase component PIG-S; AltName: Full=Phosphatidylinositol-glycan biosynthesis class S protein	gi|116248578,gi|74268100,gi|77735383	61,769.20	100.00%	3	3	3	0.03%	11.90%	SVENLATATTTLTSLAQLLGK	3.14	2,132.18
Control	6018	PREDICTED: phosphoenolpyruvate carboxykinase 2 (mitochondrial) isoform 1	gi|194670361	70,632.70	100.00%	3	3	3	0.03%	5.78%	EVLAELEALEGR	2.37	1,328.71

Control	6018	PREDICTED: phosphoenolpyruvate carboxykinase 2 (mitochondrial) isoform 1	gi|194670361	70,632.70	100.00%	3	3	3	0.03%	5.78%	SYLTEQVNQDLPK	4.26	1,534.77
Control	6018	PREDICTED: phosphoenolpyruvate carboxykinase 2 (mitochondrial) isoform 1	gi|194670361	70,632.70	100.00%	3	3	3	0.03%	5.78%	VLSGDLGQLPAK	2.54	1,197.68
Control	6018	PREDICTED: similar to 1-acylglycerophosphocholine O-acyltransferase 1 (Lung-type acyl-CoA:lysophosphatidylcholine acyltransferase 1) (Lysophosphatidylcholine acyltransferase 1) (Acyltransferase-like 2)	gi|194676422	54,069.40	99.80%	2	2	2	0.02%	11.50%	MFGSQDGSVEEHALSSILK	3.11	2,050.98

Control	6018	PREDICTED: similar to 1-acylglycerophosphocholine O-acyltransferase 1 (Lung-type acyl-CoA:lysophosphatidylcholine acyltransferase 1) (Lysophosphatidylcholine acyltransferase 1) (Acyltransferase-like 2)	gi|194676422	54,069.40	99.80%	2	2	2	0.02%	11.50%	RVTLPEFAAQLGVPESESLEDLFSLFDEGGGEVDLR	4.13	3,978.96
Control	6018	PREDICTED: similar to Solute carrier family 12 member 7 (Electroneutral potassium-chloride cotransporter 4) (K-Cl cotransporter 4)	gi|194676429	128,599.80	99.80%	2	2	2	0.02%	3.11%	LANYTNLSQGVVEHEEAEDSR	3.73	2,361.10
Control	6018	PREDICTED: similar to Solute carrier family 12 member 7 (Electroneutral potassium-chloride cotransporter 4) (K-Cl cotransporter 4)	gi|194676429	128,599.80	99.80%	2	2	2	0.02%	3.11%	SQDAQLVLLNMPGPPK	3.44	1,723.91
Control	6018	YWHAG protein	gi|157279400,gi|157744500,gi|2852385,gi|71153781	28,235.10	99.80%	2	2	3	0.03%	17.40%	NVTELNEPLSNEER	4.13	1,643.79

Control	6018	YWHAG protein	gi|157279400,gi|157744500,gi|2852385,gi|71153781	28,235.10	99.80%	2	2	3	0.03%	17.40%	TAFDDAIAELDTLNEDSYKDSTLIMQLLR	4.43	3,317.61
Control	6018	Chain C, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591028,gi|110591031,gi|114687,gi|163036,gi|27807291,gi|55670489,gi|73586602	12,514.70	99.80%	2	2	2	0.02%	22.20%	QTSGGPVDAGPEYQQDLDRELFK	3.24	2,550.21
Control	6018	Chain C, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591028,gi|110591031,gi|114687,gi|163036,gi|27807291,gi|55670489,gi|73586602	12,514.70	99.80%	2	2	2	0.02%	22.20%	RQTSGGPVDAGPEYQQDLDRELFK	6.55	2,706.31
Control	6018	heterogeneous nuclear ribonucleoprotein A2/B1	gi|114051756,gi|122145945,gi|87578315	35,988.50	99.80%	2	3	3	0.03%	13.20%	GFGFVTFDDHDPVDKIVLQK	2.57	2,277.16
Control	6018	heterogeneous nuclear ribonucleoprotein A2/B1	gi|114051756,gi|122145945,gi|87578315	35,988.50	99.80%	2	3	3	0.03%	13.20%	NMGGPYGGGNYGPGGSGGSGGYGGR	5.4	2,205.90
Control	6018	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	7	8	8	0.08%	6.38%	ALEHFTDLYDIKR	4.69	1,620.84
Control	6018	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	7	8	8	0.08%	6.38%	KFDVNTSAVQVLIEHIGNLDR	6.65	2,368.26

Control	6018	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	7	8	8	0.08%	6.38%	LAELEEFINGPNNAHIQQVGDR	3.87	2,464.22
Control	6018	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	7	8	8	0.08%	6.38%	LLYNNVSNFGR	2.35	1,296.67
Control	6018	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	7	8	8	0.08%	6.38%	NNLAGAEELFAR	3.54	1,304.66
Control	6018	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	7	8	8	0.08%	6.38%	RPISADSAIMNPASK	3.89	1,573.80
Control	6018	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	7	8	8	0.08%	6.38%	TLQIFNIEMK	2.73	1,252.66

Control	6018	coiled-coil domain containing 47	gi|146231852,gi|73586661,gi|78369308,gi|97045772	55,725.10	99.80%	2	2	2	0.02%	5.59%	RQDLLNVLAR	3.41	1,197.71
Control	6018	coiled-coil domain containing 47	gi|146231852,gi|73586661,gi|78369308,gi|97045772	55,725.10	99.80%	2	2	2	0.02%	5.59%	TLLFTFNVPGSGNTYPK	3.59	1,855.96
Control	6018	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	3	4	7	0.07%	13.90%	FDAVIGYK	2.41	912.4826
Control	6018	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	3	4	7	0.07%	13.90%	NPSTSLGPTLEPEEVVNK	5.52	1,910.97
Control	6018	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	3	4	7	0.07%	13.90%	SVTGEIVLITGAGHGIGR	4.41	1,736.97
Control	6018	pre-B-cell leukemia transcription factor interacting protein 1	gi|110331795,gi|115497324,gi|151554897,gi|158706093	80,239.50	100.00%	3	3	3	0.03%	6.19%	ALESELQQLR	2.69	1,186.64
Control	6018	pre-B-cell leukemia transcription factor interacting protein 1	gi|110331795,gi|115497324,gi|151554897,gi|158706093	80,239.50	100.00%	3	3	3	0.03%	6.19%	EQGPTGQEPSPGFLEQK	4.14	1,828.87
Control	6018	pre-B-cell leukemia transcription factor interacting protein 1	gi|110331795,gi|115497324,gi|151554897,gi|158706093	80,239.50	100.00%	3	3	3	0.03%	6.19%	LLQAQLQAQKEELQSLMR	4.57	2,143.15
Control	6018	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	5	5	5	0.05%	28.80%	AELNEFLTR	2.77	1,092.57
Control	6018	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	5	5	5	0.05%	28.80%	DEILPTTPISEQK	2.58	1,470.77
Control	6018	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	5	5	5	0.05%	28.80%	FVDGLMIHSGDPVNYYVDTAVR	5.64	2,484.19
Control	6018	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	5	5	5	0.05%	28.80%	GGKPEPPAMPQPVPTA	2.52	1,589.80

Control	6018	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	5	5	5	0.05%	28.80%	IRELTAVVQK	2.94	1,156.70
Control	6018	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	10	14	0.14%	15.20%	ADDKLIAEEGVDSLNVK	4.95	1,815.93
Control	6018	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	10	14	0.14%	15.20%	FLQDTIEEMALK	4.1	1,453.72
Control	6018	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	10	14	0.14%	15.20%	IRETGERPSNEEIMR	1.93	1,832.89
Control	6018	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	10	14	0.14%	15.20%	KLEEGGPVYSPPAQAAVR	6.2	1,868.99
Control	6018	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	10	14	0.14%	15.20%	LLELQSIGTNNFLR	5.26	1,617.90
Control	6018	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	10	14	0.14%	15.20%	LLSLASALDDNKDGKVDIDDLVK	3.47	2,457.31
Control	6018	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	10	14	0.14%	15.20%	STLQTLPEIVAK	2.47	1,299.75
Control	6018	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	56	0.55%	37.80%	GYGFGLIK	2.02	854.4772
Control	6018	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	56	0.55%	37.80%	LTFDSSFSPNTGK	4.32	1,400.67

Control	6018	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	56	0.55%	37.80%	LTFDSSFSPNTGKK	3.83	1,528.76
Control	6018	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	56	0.55%	37.80%	LTLSALLDGK	3.22	1,030.61
Control	6018	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	56	0.55%	37.80%	SENGLEFTSSGSANTETTK	4.59	1,959.88
Control	6018	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	56	0.55%	37.80%	TDEFQLHTNVNDGTEFGGSIYQK	5.94	2,600.19
Control	6018	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	56	0.55%	37.80%	TKSENGLEFTSSGSANTETTK	4.64	2,189.02
Control	6018	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	56	0.55%	37.80%	VNNSSLIGLGYTQTLKPGIK	6	2,103.18
Control	6018	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	10	56	0.55%	37.80%	VTQSNFAVGYK	3.94	1,213.62
Control	6018	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	7	9	25	0.24%	29.60%	GFGFGLVK	2.01	824.4666
Control	6018	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	7	9	25	0.24%	29.60%	LTFDTTFSPNTGK	3.64	1,428.70
Control	6018	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	7	9	25	0.24%	29.60%	LTFDTTFSPNTGKK	3.68	1,556.80
Control	6018	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	7	9	25	0.24%	29.60%	LTLSALVDGK	3.59	1,016.60
Control	6018	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	7	9	25	0.24%	29.60%	TGDFQLHTNVNDGTEFGGSIYQK	4.59	2,528.17
Control	6018	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	7	9	25	0.24%	29.60%	VNNSSLIGVGYTQTLRPGVK	5.16	2,103.16

Control	6018	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	7	9	25	0.24%	29.60%	YQLDPTASISAK	3.46	1,293.67
Control	6018	Trx-like protein	gi|109726696,gi|115494922,gi|122145628,gi|126920889,gi|146231808	31,563.90	100.00%	4	4	4	0.04%	8.63%	KLLPESSQPLK	2.72	1,239.73
Control	6018	Trx-like protein	gi|109726696,gi|115494922,gi|122145628,gi|126920889,gi|146231808	31,563.90	100.00%	4	4	4	0.04%	8.63%	KLLPESSQPLKK	3.31	1,367.83
Control	6018	Trx-like protein	gi|109726696,gi|115494922,gi|122145628,gi|126920889,gi|146231808	31,563.90	100.00%	4	4	4	0.04%	8.63%	LLPESSQPLKK	2.04	1,239.73
Control	6018	Trx-like protein	gi|109726696,gi|115494922,gi|122145628,gi|126920889,gi|146231808	31,563.90	100.00%	4	4	4	0.04%	8.63%	VDVTEQPGLSGR	4.78	1,257.64
Control	6018	PREDICTED: similar to Vezatin isoform 2	gi|119891996	88,604.30	99.80%	2	2	2	0.02%	2.94%	NDTEEENNKTSTADNEISSR	3.65	2,253.97
Control	6018	PREDICTED: similar to Vezatin isoform 2	gi|119891996	88,604.30	99.80%	2	2	2	0.02%	2.94%	VGKNDTEEENNKTSTADNEISSR	2.68	2,538.16
Control	6018	Ribosomal protein L26	gi|148744293,gi|28189348,gi|28189641,gi|62751887,gi|74268218,gi|76613859	17,240.40	99.80%	2	3	3	0.03%	17.20%	MKFNPFVTSDR	3.49	1,357.66
Control	6018	Ribosomal protein L26	gi|148744293,gi|28189348,gi|28189641,gi|62751887,gi|74268218,gi|76613859	17,240.40	99.80%	2	3	3	0.03%	17.20%	SMPIRKDDEVQVVR	3.13	1,687.88
Control	6018	endothelial cell-specific molecule 2	gi|114053335,gi|86438024	20,621.00	99.80%	2	3	7	0.07%	13.20%	ESEDPQKPGSSGLSESGSTANGEK	4.6	2,378.06

Control	6018	endothelial cell-specific molecule 2	gi|114053335,gi|86438024	20,621.00	99.80%	2	3	7	0.07%	13.20%	NKESEDPQKPGSSGLSESGSTANGEK	3.71	2,620.20
Control	6018	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	7	9	11	0.11%	8.31%	ANLINNIFELAGLGK	4.38	1,586.89
Control	6018	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	7	9	11	0.11%	8.31%	DEQYTALSNMPK	3.21	1,412.64
Control	6018	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	7	9	11	0.11%	8.31%	GFPLVTVQR	2.91	1,016.59
Control	6018	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	7	9	11	0.11%	8.31%	GLGEHELDEDEEDYESSAK	6.17	2,151.88
Control	6018	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	7	9	11	0.11%	8.31%	IFGELSSYEDFLDAR	4.79	1,761.83
Control	6018	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	7	9	11	0.11%	8.31%	IKRDEQYTALSNMPK	3.99	1,809.92
Control	6018	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	7	9	11	0.11%	8.31%	KYFAATQFEPLAAR	3.38	1,612.85
Control	6018	CYB5B protein	gi|158455068,gi|76640228	26,782.70	99.80%	2	2	4	0.04%	19.40%	EQGVETSVTYYR	2.54	1,431.68
Control	6018	CYB5B protein	gi|158455068,gi|76640228	26,782.70	99.80%	2	2	4	0.04%	19.40%	FLDEHPGGEEVLMEQAGGDATESFEDVGHSSDAR	4.88	3,634.55

Control	6018	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	4	4	5	0.05%	18.50%	EQNGDSLVHAALVAESAAIGSAEANAFSVLQHVLGAGPHVK	3.45	4,065.08
Control	6018	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	4	4	5	0.05%	18.50%	MALIGLGVSHPVLK	4	1,450.85
Control	6018	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	4	4	5	0.05%	18.50%	QVAEQFLNIR	2.95	1,217.66
Control	6018	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	4	4	5	0.05%	18.50%	TIAQGNLSNPDVQAAK	5.15	1,626.84
Control	6018	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	gi|111308529,gi|128825,gi|163414,gi|27807355	79,425.10	100.00%	4	4	4	0.04%	8.94%	ALSEIAGMTLPYDTLDQVR	3.07	2,109.05

Control	6018	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	gi|111308529,gi|128825,gi|163414,gi|27807355	79,425.10	100.00%	4	4	4	0.04%	8.94%	NDGAAILAAVSNIAQK	4.23	1,555.84
Control	6018	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	gi|111308529,gi|128825,gi|163414,gi|27807355	79,425.10	100.00%	4	4	4	0.04%	8.94%	NRLEEVSPNLVR	3.77	1,425.78
Control	6018	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	gi|111308529,gi|128825,gi|163414,gi|27807355	79,425.10	100.00%	4	4	4	0.04%	8.94%	YDDVEGANYFQQASELSK	3.27	2,063.92
Control	6018	Chain A, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793901,gi|71042575,gi|71042585,gi|75765179,gi|75765190,gi|82407287	49,194.40	100.00%	5	6	6	0.06%	16.80%	ADLTEYLSR	2.61	1,067.54
Control	6018	Chain A, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793901,gi|71042575,gi|71042585,gi|75765179,gi|75765190,gi|82407287	49,194.40	100.00%	5	6	6	0.06%	16.80%	DVILQELQENDTSMR	4.09	1,806.85

Control	6018	Chain A, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793901,gi|71042575,gi|71042585,gi|75765179,gi|75765190,gi|82407287	49,194.40	100.00%	5	6	6	0.06%	16.80%	EVESMGAHLNAYSTR	3.18	1,680.76
Control	6018	Chain A, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793901,gi|71042575,gi|71042585,gi|75765179,gi|75765190,gi|82407287	49,194.40	100.00%	5	6	6	0.06%	16.80%	MVLAAAGGLEHR	2.96	1,240.65
Control	6018	Chain A, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793901,gi|71042575,gi|71042585,gi|75765179,gi|75765190,gi|82407287	49,194.40	100.00%	5	6	6	0.06%	16.80%	TATYAQALQSVPETQVSQLDNGLR	3.58	2,590.31
Control	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	10	12	13	0.13%	34.40%	AQQVAVQEQEIAR	4.22	1,469.77
Control	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	10	12	13	0.13%	34.40%	DIHDDQDYLHSLGK	3.3	1,655.77
Control	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	10	12	13	0.13%	34.40%	ISLNTLTLNVK	2.84	1,215.73
Control	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	10	12	13	0.13%	34.40%	ITLVSSGSGAMGAAK	4.33	1,365.70
Control	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	10	12	13	0.13%	34.40%	KAEAFQLYQEAAQLDMLLEK	3.96	2,355.19

Control	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	10	12	13	0.13%	34.40%	LPQVAEEISGPLTSANK	4.99	1,753.93
Control	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	10	12	13	0.13%	34.40%	SQLIMQAEAEAEAVR	4.29	1,661.82
Control	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	10	12	13	0.13%	34.40%	TEAEIAHIALETLEGHQR	4.04	2,018.03
Control	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	10	12	13	0.13%	34.40%	VSAQYLSEIEMAK	3.51	1,484.73
Control	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	10	12	13	0.13%	34.40%	VTGEVLDILSR	2.37	1,201.68
Control	6018	PREDICTED: similar to ribosomal protein S24	gi|119914811,gi|194677142,gi|58760477,gi|70778760,gi|74268388,gi|91207637	15,283.40	100.00%	3	3	5	0.05%	29.50%	KQMVIDVLHPGK	3.68	1,380.77
Control	6018	PREDICTED: similar to ribosomal protein S24	gi|119914811,gi|194677142,gi|58760477,gi|70778760,gi|74268388,gi|91207637	15,283.40	100.00%	3	3	5	0.05%	29.50%	TTGFGMIYDSLDYAK	3.99	1,697.77
Control	6018	PREDICTED: similar to ribosomal protein S24	gi|119914811,gi|194677142,gi|58760477,gi|70778760,gi|74268388,gi|91207637	15,283.40	100.00%	3	3	5	0.05%	29.50%	TTPDVIFVFGFR	2.37	1,398.74
Control	6018	similar to 40S ribosomal protein S18	gi|28189422,gi|28189549,gi|28189799,gi|74268023,gi|75812924,gi|91207636	15,380.70	100.00%	3	4	6	0.06%	25.20%	IAFAITAIK	2.75	947.5925
Control	6018	similar to 40S ribosomal protein S18	gi|28189422,gi|28189549,gi|28189799,gi|74268023,gi|75812924,gi|91207636	15,380.70	100.00%	3	4	6	0.06%	25.20%	RAGELTEDEVER	4.27	1,403.68

Control	6018	similar to 40S ribosomal protein S18	gi|28189422,gi|28189549,gi|28189799,gi|74268023,gi|75812924,gi|91207636	15,380.70	100.00%	3	4	6	0.06%	25.20%	YSQVLANGLDNK	3.76	1,321.67
Control	6018	glutathione peroxidase 8	gi|114052907,gi|122143886,gi|84708688	23,965.80	99.80%	2	3	3	0.03%	11.00%	ILGSEAEPAFR	3.1	1,189.62
Control	6018	glutathione peroxidase 8	gi|114052907,gi|122143886,gi|84708688	23,965.80	99.80%	2	3	3	0.03%	11.00%	NNFGVTFPIFHK	2.77	1,420.74
Control	6018	Tumor protein p53 inducible protein 11	gi|111304979,gi|115496424	20,907.40	99.80%	2	2	2	0.02%	13.80%	ISQVLGNEIK	3.09	1,100.63
Control	6018	Tumor protein p53 inducible protein 11	gi|111304979,gi|115496424	20,907.40	99.80%	2	2	2	0.02%	13.80%	KILGVGGEDDDGEVHR	4.51	1,695.83
Control	6018	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	7	8	18	0.18%	28.50%	GFVLTFK	2.03	811.4713
Control	6018	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	7	8	18	0.18%	28.50%	GVGMVADPDNPLVLDILTGSSTSYSFFPDKPITQYPHAVGK	5.32	4,350.16
Control	6018	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	7	8	18	0.18%	28.50%	LPDVYGVFQFK	3.95	1,312.69
Control	6018	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	7	8	18	0.18%	28.50%	TADDPSLSLIK	3.31	1,159.62
Control	6018	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	7	8	18	0.18%	28.50%	TAVIDHHNYDVSDLGQHTLIVADTENLLK	5.41	3,231.63
Control	6018	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	7	8	18	0.18%	28.50%	TLVLLDNLNLR	3.61	1,283.77

Control	6018	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	7	8	18	0.18%	28.50%	YSQTGNYELAVALSR	4.09	1,671.83
Control	6018	reticulon 4 isoform 2	gi|164259354,gi|92096636	40,940.20	100.00%	3	3	6	0.06%	11.10%	GPLPAAPLAAPER	3.4	1,259.71
Control	6018	reticulon 4 isoform 2	gi|164259354,gi|92096636	40,940.20	100.00%	3	3	6	0.06%	11.10%	HQAQIDHYLGLANK	4.26	1,607.83
Control	6018	reticulon 4 isoform 2	gi|164259354,gi|92096636	40,940.20	100.00%	3	3	6	0.06%	11.10%	RGSSGSVVVDLLYWR	2.3	1,693.90
Control	6018	ADP-ribosylation factor-like 8B	gi|114051548,gi|86438183,gi|93204537	21,493.90	100.00%	2	2	2	0.02%	21.50%	GVNAIVYMIDAADREK	4.3	1,780.89
Control	6018	ADP-ribosylation factor-like 8B	gi|114051548,gi|86438183,gi|93204537	21,493.90	100.00%	2	2	2	0.02%	21.50%	NELHNLLDKPQLQGIPVLVLGNKR	2.61	2,708.56
Control	6018	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	6	8	10	0.10%	20.00%	ALASILLQDHIR	2.1	1,349.79
Control	6018	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	6	8	10	0.10%	20.00%	IYQGEDLPHPK	3.41	1,296.66
Control	6018	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	6	8	10	0.10%	20.00%	LAMDEIFQKPFQTLMFLVR	3.86	2,343.22
Control	6018	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	6	8	10	0.10%	20.00%	LKDIASEFKEQLQTLILHVLNPANLMEK	3.93	3,251.77
Control	6018	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	6	8	10	0.10%	20.00%	SMLQATAEANNLAAAASAK	5.33	1,848.91
Control	6018	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	6	8	10	0.10%	20.00%	VAVVLMDTQGAFDSQSTVK	4.02	2,012.00
Control	6018	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	5	6	6	0.06%	12.10%	IRIDSLSAQLSQLQK	4.2	1,699.97
Control	6018	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	5	6	6	0.06%	12.10%	LQEKEDLQELNDR	4.83	1,629.81
Control	6018	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	5	6	6	0.06%	12.10%	LQTLKEELDFQK	3.26	1,491.81
Control	6018	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	5	6	6	0.06%	12.10%	MQQQLDEYQELLDIK	4.43	1,909.92
Control	6018	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	5	6	6	0.06%	12.10%	TALINSTGEEVAMR	3.64	1,507.74

Control	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	12	21	0.21%	36.80%	AVAISLPK	2.08	798.5084
Control	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	12	21	0.21%	36.80%	AVLSAEQLRDDEVHAGLGELLR	5.45	2,391.26
Control	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	12	21	0.21%	36.80%	DQAVENILLSPVVVASSLGLVSLGGK	4.49	2,565.45
Control	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	12	21	0.21%	36.80%	DTQSGSLLFIGR	2.42	1,293.68

Control	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	12	21	0.21%	36.80%	GVVEVTHDLQK	3.45	1,224.66
Control	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	12	21	0.21%	36.80%	HLAGLGLTEAIDKNK	5.37	1,579.88
Control	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	12	21	0.21%	36.80%	KAVAISLPK	3.27	926.6034
Control	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	12	21	0.21%	36.80%	LFYADHPFIFLVR	3.4	1,637.88

Control	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	12	21	0.21%	36.80%	LSSLIIIMPHHVEPLER	2.57	2,000.10
Control	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	12	21	0.21%	36.80%	LYGPSSVSFAEDFVR	4.41	1,673.82
Control	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	12	21	0.21%	36.80%	SAGLAFSLYQAMAK	4.41	1,473.74
Control	6018	PREDICTED: hypothetical protein	gi|194667311	68,113.30	99.80%	2	3	3	0.03%	4.64%	ELESQISELQEDLESER	4.22	2,033.95
Control	6018	PREDICTED: hypothetical protein	gi|194667311	68,113.30	99.80%	2	3	3	0.03%	4.64%	XXXXXXXXXXX	3.62	1,240.02
Control	6018	PREDICTED: transmembrane emp24 protein transport domain containing 4	gi|194666384	37,465.50	100.00%	3	3	4	0.04%	13.10%	DKLTELQLR	3.32	1,115.64

Control	6018	PREDICTED: transmembrane emp24 protein transport domain containing 4	gi|194666384	37,465.50	100.00%	3	3	4	0.04%	13.10%	QKEVFLPSTPGLGMHVEVKDPEGK	2.58	2,638.36
Control	6018	PREDICTED: transmembrane emp24 protein transport domain containing 4	gi|194666384	37,465.50	100.00%	3	3	4	0.04%	13.10%	QLLDQVEQIQK	4.1	1,341.74
Control	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	10	12	17	0.17%	14.70%	AVVLAANHFGR	2.59	1,154.64
Control	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	10	12	17	0.17%	14.70%	FFTGQITAAGK	3.18	1,140.60
Control	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	10	12	17	0.17%	14.70%	GITHIGYTDLPSR	4.41	1,429.74
Control	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	10	12	17	0.17%	14.70%	ILIVGGGVAGLASAGAAK	4.76	1,524.91
Control	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	10	12	17	0.17%	14.70%	MATQASTLYSNNITK	5.03	1,658.81
Control	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	10	12	17	0.17%	14.70%	SLGAEPLEVDLK	2.49	1,270.69
Control	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	10	12	17	0.17%	14.70%	SLGVGYAAVDNPIFYKPNTAMLLGDAK	3.49	2,841.45
Control	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	10	12	17	0.17%	14.70%	TSGTLISFIYPAQNPDLLNK	4.52	2,192.16

Control	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	10	12	17	0.17%	14.70%	VALSPAGVQALVK	3.23	1,252.76
Control	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	10	12	17	0.17%	14.70%	VTIAQGYDALSSMANIAGYK	5.17	2,089.03
Control	6018	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	14	29	0.28%	42.00%	DLLVTGAYEITDQSGGAGGLR	4.78	2,093.05
Control	6018	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	14	29	0.28%	42.00%	IPDQLVILDMK	4.38	1,284.72
Control	6018	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	14	29	0.28%	42.00%	IPDQLVILDMKHGVEAK	3.92	1,922.04
Control	6018	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	14	29	0.28%	42.00%	ITDSAGHILYSK	4.3	1,304.68
Control	6018	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	14	29	0.28%	42.00%	ITDSAGHILYSKEDATK	3.94	1,848.93
Control	6018	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	14	29	0.28%	42.00%	LKPLEVELR	3.41	1,096.67
Control	6018	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	14	29	0.28%	42.00%	NYEEIAKVEK	3	1,222.63

Control	6018	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	14	29	0.28%	42.00%	RLEDLSESIVNDFAYMK	3.72	2,045.99
Control	6018	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	9	14	29	0.28%	42.00%	RLEDLSESIVNDFAYMKK	4.76	2,174.08
Control	6018	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	100.00%	3	3	3	0.03%	8.61%	LITVNTPDLVLFVGEALVGNEAVDQLVK	3.8	2,966.65
Control	6018	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	100.00%	3	3	3	0.03%	8.61%	NQGFDVVLVDTAGR	4.38	1,490.76
Control	6018	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	100.00%	3	3	3	0.03%	8.61%	VMGTFSTVTSTVK	3.09	1,373.70
Control	6018	Stromal interaction molecule 1	gi|154426132,gi|61555683,gi|75057528,gi|78369570	77,134.40	100.00%	4	4	4	0.04%	12.00%	ALDTVLFGPPLLTR	3.62	1,512.88
Control	6018	Stromal interaction molecule 1	gi|154426132,gi|61555683,gi|75057528,gi|78369570	77,134.40	100.00%	4	4	4	0.04%	12.00%	DLTHSDSESSLHMSDR	2.96	1,832.77
Control	6018	Stromal interaction molecule 1	gi|154426132,gi|61555683,gi|75057528,gi|78369570	77,134.40	100.00%	4	4	4	0.04%	12.00%	KAAAEEDNGSIGEETDSSPGR	4.16	2,119.94
Control	6018	Stromal interaction molecule 1	gi|154426132,gi|61555683,gi|75057528,gi|78369570	77,134.40	100.00%	4	4	4	0.04%	12.00%	LMDDDANGDVDVEESDEFLREDLNYHDPTVK	4.35	3,611.56
Control	6018	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	6	6	0.06%	22.20%	FSDLDSASVDSDMYDLPK	3.38	2,020.87
Control	6018	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	6	6	0.06%	22.20%	FSDLDSASVDSDMYDLPKKEDALLYQSK	3.95	3,196.49
Control	6018	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	6	6	0.06%	22.20%	GYNDDYYEESYLTTR	3.66	1,888.79
Control	6018	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	6	6	0.06%	22.20%	LSPPSSSASSFSYR	1.62	1,472.70

Control	6018	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	6	6	0.06%	22.20%	RLSPPSSSASSFSYR	3.23	1,628.80
Control	6018	PREDICTED: nestin	gi|76612380	175,609.70	99.80%	2	2	2	0.02%	2.97%	ALEEQNELLSAELGGLR	3.1	1,841.96
Control	6018	PREDICTED: nestin	gi|76612380	175,609.70	99.80%	2	2	2	0.02%	2.97%	RPGPLLSVLSPTPLSSPLPGTLETPVPTFLK	4.58	3,211.83
Control	6018	NADH dehydrogenase (ubiquinone) 42 kDa subunit	gi|228,gi|45430053,gi|464255,gi|74268236,gi|95768472	41,642.50	99.80%	2	2	2	0.02%	5.15%	FLNYFANIR	3.35	1,157.61
Control	6018	NADH dehydrogenase (ubiquinone) 42 kDa subunit	gi|228,gi|45430053,gi|464255,gi|74268236,gi|95768472	41,642.50	99.80%	2	2	2	0.02%	5.15%	IPQAIAQVSK	2.77	1,054.63
Control	6018	Lu-ECAM-1	gi|2623763,gi|2623765,gi|2623767,gi|30794326	100,991.10	100.00%	3	3	3	0.03%	4.75%	QESYDQADVIVANPYLK	4.05	1,952.96
Control	6018	Lu-ECAM-1	gi|2623763,gi|2623765,gi|2623767,gi|30794326	100,991.10	100.00%	3	3	3	0.03%	4.75%	SGSITQQAIQLESK	4.22	1,489.79
Control	6018	Lu-ECAM-1	gi|2623763,gi|2623765,gi|2623767,gi|30794326	100,991.10	100.00%	3	3	3	0.03%	4.75%	TSDFKEDKLNIR	3.45	1,465.76
Control	6018	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	4	4	7	0.07%	21.30%	ATIGADFLTK	2.47	1,036.57
Control	6018	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	4	4	7	0.07%	21.30%	DPENFPFVVLGNK	4.62	1,475.75
Control	6018	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	4	4	7	0.07%	21.30%	FQSLGVAFYR	2.91	1,187.62
Control	6018	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	4	4	7	0.07%	21.30%	VIILGDSGVGK	2.77	1,057.63
Control	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	7	8	11	0.11%	14.50%	ARFEELNADLFR	3.67	1,480.75

Control	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	7	8	11	0.11%	14.50%	DAGTIAGLNVLR	3.51	1,199.67
Control	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	7	8	11	0.11%	14.50%	IINEPTAAAIAYGLDK	3.81	1,659.90
Control	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	7	8	11	0.11%	14.50%	IINEPTAAAIAYGLDKK	3.32	1,787.99
Control	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	7	8	11	0.11%	14.50%	LLQDFFNGK	2.52	1,081.57
Control	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	7	8	11	0.11%	14.50%	NQVAMNPTNTVFDAK	4.65	1,665.79
Control	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	7	8	11	0.11%	14.50%	STAGDTHLGGEDFDNR	3.01	1,691.73
Control	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	7	8	11	0.11%	14.50%	TTPSYVAFTDTER	3.12	1,487.70
Control	6018	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	11	55	0.54%	33.60%	AAYFGIYDTAK	3.74	1,219.60
Control	6018	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	11	55	0.54%	33.60%	DFLAGGIAAAISK	5.33	1,233.68
Control	6018	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	11	55	0.54%	33.60%	EQGVLSFWR	2.51	1,121.57
Control	6018	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	11	55	0.54%	33.60%	GLYQGFNVSVQGIIIYR	3.59	1,927.04
Control	6018	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	11	55	0.54%	33.60%	GMGGAFVLVLYDELK	4.74	1,627.84
Control	6018	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	11	55	0.54%	33.60%	GMGGAFVLVLYDELKK	4.7	1,755.94
Control	6018	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	11	55	0.54%	33.60%	LLLQVQHASK	3.02	1,136.68

Control	6018	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	11	55	0.54%	33.60%	QIFLGGVDKR	2.35	1,132.65
Control	6018	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	11	55	0.54%	33.60%	YFPTQALNFAFK	3.65	1,446.74
Control	6018	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	11	55	0.54%	33.60%	YFPTQALNFAFKDK	4.14	1,689.86
Control	6018	PREDICTED: insulin-like growth factor 1 receptor	gi|119913553	135,693.80	100.00%	2	2	2	0.02%	3.24%	ELGQGSFGMVYEGVAK	4.2	1,687.80
Control	6018	PREDICTED: insulin-like growth factor 1 receptor	gi|119913553	135,693.80	100.00%	2	2	2	0.02%	3.24%	GNNIASELENFMGLIEVVTGYVK	5.26	2,513.26
Control	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	16	17	17	0.17%	11.00%	APLNVQFSSPGPGDAVK	5.28	1,683.87
Control	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	16	17	17	0.17%	11.00%	DLDIIDNYDYSHTVK	4.12	1,810.85
Control	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	16	17	17	0.17%	11.00%	EAFTNKPNVFTVVTR	2.95	1,722.92

Control	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	16	17	17	0.17%	11.00%	GAGIGGLGITVEGPSESK	4.75	1,628.85
Control	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	16	17	17	0.17%	11.00%	GFQDGVYAFEYYPSTQGK	3.73	2,056.93
Control	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	16	17	17	0.17%	11.00%	GLVEPVNVVDNGDGTHTVTYTPSQEGPYMVSVK	6.24	3,505.68
Control	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	16	17	17	0.17%	11.00%	GQHVTGSPFQFTVGPLGEGGAHK	4.55	2,308.15
Control	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	16	17	17	0.17%	11.00%	IFAQDGDGQPIDIQMK	4.33	1,791.86
Control	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	16	17	17	0.17%	11.00%	IVGPGLGSGVR	2.66	1,011.59
Control	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	16	17	17	0.17%	11.00%	LIALLEVLSQK	2.97	1,226.77

Control	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	16	17	17	0.17%	11.00%	SPFEVQVGPEAGMQK	4.75	1,619.77
Control	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	16	17	17	0.17%	11.00%	SPFTVGVAAPLDLSR	3.38	1,529.83
Control	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	16	17	17	0.17%	11.00%	VLFASQEIPTSPFR	3.74	1,591.85
Control	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	16	17	17	0.17%	11.00%	VTASGPGLSTYGVPASLPVEFAIDAR	4.05	2,575.34
Control	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	16	17	17	0.17%	11.00%	YMIGVTYGGDDIPLSPYR	4.12	2,032.97
Control	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	16	17	17	0.17%	11.00%	YTPTQQGNMQVLVTYGGDPIPK	4.13	2,423.19
Control	6018	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	99.80%	2	2	2	0.02%	5.90%	ADVGFAMGIAGTDVAK	4.36	1,538.75

Control	6018	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	99.80%	2	2	2	0.02%	5.90%	EAGHGTQKEEIPEEELAEDVEEIDHAER	3.09	3,189.45
Control	6018	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	99.80%	2	2	2	0.02%	5.90%	EASDIILTDDNFTSIVK	4	1,880.95
Control	6018	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	99.80%	2	2	2	0.02%	5.90%	GIIDSTVSEQR	2.94	1,204.62
Control	6018	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	99.90%	2	2	2	0.02%	2.06%	IIGNLLYYR	2.91	1,124.65
Control	6018	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	99.90%	2	2	2	0.02%	2.06%	VNLLAALTNIDLALEQGSAPALFK	5.43	2,482.39
Control	6018	RecName: Full=Vesicle transport protein GOT1B; AltName: Full=Golgi transport 1 homolog B	gi|109939723,gi|114053223,gi|82571709	15,408.60	100.00%	3	3	3	0.03%	20.30%	RVPVLGSLLNLPGIR	3.73	1,604.00
Control	6018	RecName: Full=Vesicle transport protein GOT1B; AltName: Full=Golgi transport 1 homolog B	gi|109939723,gi|114053223,gi|82571709	15,408.60	100.00%	3	3	3	0.03%	20.30%	SFVDKVGESNNMV	3.54	1,441.66

Control	6018	RecName: Full=Vesicle transport protein GOT1B; AltName: Full=Golgi transport 1 homolog B	gi|109939723,gi|114053223,gi|82571709	15,408.60	100.00%	3	3	3	0.03%	20.30%	VPVLGSLLNLPGIR	3.9	1,447.90
Control	6018	UNC84B protein	gi|151553917,gi|156121283	81,429.80	100.00%	4	5	6	0.06%	6.04%	IRPTAVTLEHVPK	3.71	1,460.86
Control	6018	UNC84B protein	gi|151553917,gi|156121283	81,429.80	100.00%	4	5	6	0.06%	6.04%	LEGQLAGLR	2.79	956.5525
Control	6018	UNC84B protein	gi|151553917,gi|156121283	81,429.80	100.00%	4	5	6	0.06%	6.04%	LEGQLAGLRQELAALTLK	3.51	1,924.12
Control	6018	UNC84B protein	gi|151553917,gi|156121283	81,429.80	100.00%	4	5	6	0.06%	6.04%	SEHQQDSEDLFKK	3.78	1,590.74
Control	6018	heat shock protein beta-1	gi|71037405,gi|74354863,gi|85542053	22,375.10	100.00%	5	5	5	0.05%	44.30%	KYTLPPGVDPTLVSSSLSPEGTLTVEAPLPK	4.07	3,193.72
Control	6018	heat shock protein beta-1	gi|71037405,gi|74354863,gi|85542053	22,375.10	100.00%	5	5	5	0.05%	44.30%	LFDQAFGLPR	3.39	1,163.62
Control	6018	heat shock protein beta-1	gi|71037405,gi|74354863,gi|85542053	22,375.10	100.00%	5	5	5	0.05%	44.30%	QLSSGVSEIQQTADR	4.53	1,618.80
Control	6018	heat shock protein beta-1	gi|71037405,gi|74354863,gi|85542053	22,375.10	100.00%	5	5	5	0.05%	44.30%	SATQSAEITIPVTFQAR	2.62	1,819.95
Control	6018	heat shock protein beta-1	gi|71037405,gi|74354863,gi|85542053	22,375.10	100.00%	5	5	5	0.05%	44.30%	VSLDVNHFAPEELTVK	2.67	1,797.94
Control	6018	ribosomal protein L4	gi|61553010,gi|62460480,gi|73917531,gi|74267758	47,395.70	100.00%	3	4	5	0.05%	11.40%	APIRPDIVNFVHTNLR	2.43	1,862.04
Control	6018	ribosomal protein L4	gi|61553010,gi|62460480,gi|73917531,gi|74267758	47,395.70	100.00%	3	4	5	0.05%	11.40%	IEEVPELPLVVEDKVEGYKK	1.9	2,313.26
Control	6018	ribosomal protein L4	gi|61553010,gi|62460480,gi|73917531,gi|74267758	47,395.70	100.00%	3	4	5	0.05%	11.40%	NIPGITLLNVSK	2.44	1,268.76
Control	6018	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	4	4	4	0.04%	5.25%	LLGVEGSTLR	2.61	1,044.60

Control	6018	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	4	4	4	0.04%	5.25%	LLQSNPVLEAFGNAK	4.65	1,600.87
Control	6018	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	4	4	4	0.04%	5.25%	MSLLELVEILK	3.43	1,303.75
Control	6018	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	4	4	4	0.04%	5.25%	VLQALGSEPIQYAVPVVK	4.01	1,911.10
Control	6018	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	6	6	6	0.06%	8.43%	EDGSFSFYSLPSGGYTVIPFYR	3.19	2,489.17
Control	6018	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	6	6	6	0.06%	8.43%	GQPLGPAGVQVSLR	3.13	1,378.78
Control	6018	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	6	6	6	0.06%	8.43%	SQYDFVLPQVSFTAAGYHK	2.87	2,158.06
Control	6018	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	6	6	6	0.06%	8.43%	SSIDSEPALVLGPLK	3.13	1,525.85
Control	6018	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	6	6	6	0.06%	8.43%	VLNGPEGEGVPDAVVTLNSQIK	3.34	2,236.18
Control	6018	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	6	6	6	0.06%	8.43%	VQVMVPEAETR	3	1,274.64
Control	6018	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	4	7	12	0.12%	39.40%	ADALQAGASQFETSAAK	5.38	1,665.81
Control	6018	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	4	7	12	0.12%	39.40%	LQQTQNQVDEVVDIMR	5.39	1,931.95
Control	6018	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	4	7	12	0.12%	39.40%	LSELDDRADALQAGASQFETSAAK	5.97	2,494.21

Control	6018	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	4	7	12	0.12%	39.40%	RLQQTQNQVDEVVDIMR	3.93	2,072.06
Control	6018	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	7	9	15	0.15%	33.60%	DKLSELQLR	2.93	1,101.63
Control	6018	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	7	9	15	0.15%	33.60%	EEYQPATPGLGMFVEVKDPEDK	3.06	2,495.17
Control	6018	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	7	9	15	0.15%	33.60%	EEYQPATPGLGMFVEVKDPEDKVILAR	2.98	3,047.54
Control	6018	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	7	9	15	0.15%	33.60%	FSLFAGGMLR	3.21	1,114.57
Control	6018	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	7	9	15	0.15%	33.60%	QLVEQVEQIQK	4.36	1,341.74
Control	6018	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	7	9	15	0.15%	33.60%	QREEYQPATPGLGMFVEVKDPEDK	3.45	2,779.32
Control	6018	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	7	9	15	0.15%	33.60%	VHLDIQVGEHANDYAEIAAK	3.12	2,193.09
Control	6018	KRT4 protein	gi|134024768	58,029.30	100.00%	3	3	10	0.10%	5.65%	LALDIEIATYR	3.59	1,277.71
Control	6018	KRT4 protein	gi|134024768	58,029.30	100.00%	3	3	10	0.10%	5.65%	NEISELNR	3.49	974.4901
Control	6018	KRT4 protein	gi|134024768	58,029.30	100.00%	3	3	10	0.10%	5.65%	NLDLDSIIAEVR	3.35	1,357.73

Control	6018	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	5	11	0.11%	36.10%	EFADSLGIPFLETSAK	3.59	1,724.87
Control	6018	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	5	11	0.11%	36.10%	FADDTYTESYISTIGVDFK	2.84	2,172.00
Control	6018	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	5	11	0.11%	36.10%	LLLIGDSGVGK	3.4	1,071.64
Control	6018	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	5	11	0.11%	36.10%	LQIWDTAGQER	2.62	1,316.66
Control	6018	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	5	11	0.11%	36.10%	NATNVEQSFMTMAAEIK	2.75	1,900.88
Control	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	13	19	26	0.25%	31.90%	ALYETELADAR	3.63	1,251.62
Control	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	13	19	26	0.25%	31.90%	DQMQQQLNDYEQLLDVK	3.95	2,123.99
Control	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	13	19	26	0.25%	31.90%	FKAEHDQLLLNYAK	4.48	1,689.90
Control	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	13	19	26	0.25%	31.90%	IESLSSQLSNLQK	3.87	1,446.78
Control	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	13	19	26	0.25%	31.90%	IQELEDLLAK	3.02	1,171.66
Control	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	13	19	26	0.25%	31.90%	LAQALHEMREQHDAQVK	2.27	2,020.00
Control	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	13	19	26	0.25%	31.90%	LREYEAALNSK	3.83	1,293.68
Control	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	13	19	26	0.25%	31.90%	LSSEMNTSTVNSAR	4.42	1,496.70
Control	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	13	19	26	0.25%	31.90%	LYKEELEQTYHAK	3.69	1,651.83
Control	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	13	19	26	0.25%	31.90%	MRIESLSSQLSNLQK	3.37	1,749.92
Control	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	13	19	26	0.25%	31.90%	NMYEEEINETR	3.4	1,443.61
Control	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	13	19	26	0.25%	31.90%	SLESDLEDLKDQIAQLEASLAAAK	5.68	2,558.32
Control	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	13	19	26	0.25%	31.90%	TTIPEEEEEEEAEVAVEEELFHQQGAPR	4.26	3,425.55

Control	6018	RecName: Full=40S ribosomal protein S20	gi|108860955,gi|61822677,gi|73587131,gi|77735823	13,355.00	100.00%	2	4	4	0.04%	12.60%	DTGKTPVEPEVAIHR	4.05	1,648.87
Control	6018	RecName: Full=40S ribosomal protein S20	gi|108860955,gi|61822677,gi|73587131,gi|77735823	13,355.00	100.00%	2	4	4	0.04%	12.60%	TPVEPEVAIHR	4.26	1,247.67
Control	6018	SACM1L protein	gi|151554372,gi|156120909,gi|167016544	67,077.30	99.80%	2	2	2	0.02%	4.43%	LSNTSPEFQEMSLLER	3.58	1,896.90
Control	6018	SACM1L protein	gi|151554372,gi|156120909,gi|167016544	67,077.30	99.80%	2	2	2	0.02%	4.43%	TNVIQSLLAR	2.9	1,114.66
Control	6018	Interleukin enhancer binding factor 2, 45kDa	gi|83405442,gi|84000347	43,068.60	99.80%	2	2	2	0.02%	8.72%	ILPTLEAVAALGNK	3.86	1,409.84
Control	6018	Interleukin enhancer binding factor 2, 45kDa	gi|83405442,gi|84000347	43,068.60	99.80%	2	2	2	0.02%	8.72%	NQDLAPNSAEQASILSLVTK	2.7	2,099.10
Control	6018	CALM3 protein	gi|111308539,gi|114053089,gi|115305083,gi|157831834,gi|157879669,gi|194671098,gi|28189857,gi|49037473,gi|86822265	19,973.60	99.80%	2	3	5	0.05%	18.10%	EAFSLFDKDGDGTITTK	4.71	1,844.89
Control	6018	CALM3 protein	gi|111308539,gi|114053089,gi|115305083,gi|157831834,gi|157879669,gi|194671098,gi|28189857,gi|49037473,gi|86822265	19,973.60	99.80%	2	3	5	0.05%	18.10%	VFDKDGNGYISAAELR	4.76	1,754.87

Control	6018	RecName: Full=Cytochrome c oxidase polypeptide 7A2, mitochondrial; AltName: Full=Cytochrome c oxidase polypeptide VIIa-liver/heart; Short=Cytochrome c oxidase subunit VIIa-L; Short=VIIC; Flags: Precursor	gi|117120,gi|28461241,gi|488158,gi|74354141	9,305.40	99.80%	2	3	5	0.05%	27.70%	GGIADALLYR	3.24	1,048.58
Control	6018	RecName: Full=Cytochrome c oxidase polypeptide 7A2, mitochondrial; AltName: Full=Cytochrome c oxidase polypeptide VIIa-liver/heart; Short=Cytochrome c oxidase subunit VIIa-L; Short=VIIC; Flags: Precursor	gi|117120,gi|28461241,gi|488158,gi|74354141	9,305.40	99.80%	2	3	5	0.05%	27.70%	LFQEDNGIPVHLK	3	1,509.81
Control	6018	SLC25A24 protein	gi|148745486,gi|149642721,gi|167016553	53,268.40	100.00%	3	4	6	0.06%	13.20%	GYVPNLLGIIPYAGIDLAVYELLK	5.9	2,604.47
Control	6018	SLC25A24 protein	gi|148745486,gi|149642721,gi|167016553	53,268.40	100.00%	3	4	6	0.06%	13.20%	HSTGIDIGDSLTIPDEFTEDEKK	4.65	2,547.21
Control	6018	SLC25A24 protein	gi|148745486,gi|149642721,gi|167016553	53,268.40	100.00%	3	4	6	0.06%	13.20%	VLPAVGISYVVYENMK	2.48	1,797.95

Control	6018	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	3	5	5	0.05%	8.09%	ATTPVIMVGPGTGVAPFIGFIQER	4.31	2,474.31
Control	6018	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	3	5	5	0.05%	8.09%	GMAADPEEYDLADLSSLPEIEK	3.43	2,409.10
Control	6018	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	3	5	5	0.05%	8.09%	YAVFALGNK	2.36	982.5356
Control	6018	TXNDC10 protein	gi|151554048,gi|156121223	51,713.50	100.00%	3	4	5	0.05%	9.69%	FQNYLTMDGFLLYELGDTGK	3.52	2,341.11
Control	6018	TXNDC10 protein	gi|151554048,gi|156121223	51,713.50	100.00%	3	4	5	0.05%	9.69%	TKDDIIEFAHR	3.66	1,344.69
Control	6018	TXNDC10 protein	gi|151554048,gi|156121223	51,713.50	100.00%	3	4	5	0.05%	9.69%	VFFVYIGGESPLK	3.44	1,455.79
Control	6018	RecName: Full=Histone H2A.V; AltName: Full=H2A.F/Z	gi|109940032,gi|163150,gi|27807373,gi|410,gi|81674301,gi|81674755,gi|83288407,gi|84000371	13,535.20	100.00%	3	6	8	0.08%	41.40%	ATIAGGGVIPHIHK	4.28	1,370.79
Control	6018	RecName: Full=Histone H2A.V; AltName: Full=H2A.F/Z	gi|109940032,gi|163150,gi|27807373,gi|410,gi|81674301,gi|81674755,gi|83288407,gi|84000371	13,535.20	100.00%	3	6	8	0.08%	41.40%	GDEELDSLIK	3.46	1,118.56

Control	6018	RecName: Full=Histone H2A.V; AltName: Full=H2A.F/Z	gi|109940032,gi|163150,gi|27807373,gi|410,gi|81674301,gi|81674755,gi|83288407,gi|84000371	13,535.20	100.00%	3	6	8	0.08%	41.40%	VGATAAVYSAAILEYLTAEVLELAGNASK	5.26	2,895.54
Control	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	11	14	0.14%	24.80%	ALEEAMEQKAELER	4.38	1,662.80
Control	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	11	14	0.14%	24.80%	ANLQIDQLNTDLNLER	4.75	1,869.97
Control	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	11	14	0.14%	24.80%	ELEDATETADAMNR	3.67	1,581.67
Control	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	11	14	0.14%	24.80%	IAQLEEELEEEQGNTELVNDR	5.39	2,458.16
Control	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	11	14	0.14%	24.80%	IAQLEEQLDNETKER	3.13	1,815.91
Control	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	11	14	0.14%	24.80%	LKDVLLQVDDERR	2.47	1,598.89
Control	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	11	14	0.14%	24.80%	LQQELDDLLVDLDHQR	3.18	1,949.99
Control	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	11	14	0.14%	24.80%	NAEQYKDQADKASTR	3.5	1,724.82
Control	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	11	14	0.14%	24.80%	QAQQERDELADEIANSSGK	5.35	2,088.98
Control	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	11	14	0.14%	24.80%	RQLEEAEEEAQR	3.15	1,487.71

Control	6018	RecName: Full=T-complex protein 1 subunit delta; Short=TCP-1-delta; AltName: Full=CCT-delta	gi|115305839,gi|83406133,gi|84000361	58,190.00	99.80%	2	2	2	0.02%	5.35%	ALIAGGGAPEIELALR	3.79	1,550.89
Control	6018	RecName: Full=T-complex protein 1 subunit delta; Short=TCP-1-delta; AltName: Full=CCT-delta	gi|115305839,gi|83406133,gi|84000361	58,190.00	99.80%	2	2	2	0.02%	5.35%	VIDPATATSVDLR	3.44	1,357.73
Control	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	16	22	42	0.41%	39.40%	AASFLLALEPELEAR	3.91	1,629.88
Control	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	16	22	42	0.41%	39.40%	ENLVEQHIQDIVVHYTFNK	4.13	2,326.18
Control	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	16	22	42	0.41%	39.40%	IDHILDAL	2.28	909.5042
Control	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	16	22	42	0.41%	39.40%	ISVIVEAVYTHVLQPYPTQITQSEK	3.42	2,843.52
Control	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	16	22	42	0.41%	39.40%	LAHLGVQVK	2.69	964.5939
Control	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	16	22	42	0.41%	39.40%	LAHLGVQVKGEDEEENNLEVR	3.56	2,378.19
Control	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	16	22	42	0.41%	39.40%	LPVALDPGAK	1.97	980.5777
Control	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	16	22	42	0.41%	39.40%	LVDHVFDEQVIDSLTVK	5.37	1,957.03
Control	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	16	22	42	0.41%	39.40%	NIQVDSPYEISR	3.9	1,420.71
Control	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	16	22	42	0.41%	39.40%	QFVVFEGNHYFYSPYPTK	4.05	2,223.05
Control	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	16	22	42	0.41%	39.40%	SEDLLDYGPFR	4.12	1,311.62
Control	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	16	22	42	0.41%	39.40%	THYIVGYNLPSYEYLYNLGDQYALK	5	2,997.47

Control	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	16	22	42	0.41%	39.40%	TVDLSSHLAK	3.11	1,070.58
Control	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	16	22	42	0.41%	39.40%	VHSENNSPFLTITSMTR	4.62	1,949.94
Control	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	16	22	42	0.41%	39.40%	VTAEVVLAHAGSGSSPR	4.38	1,637.86
Control	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	16	22	42	0.41%	39.40%	YDYQRQPDSGVSSVR	3.58	1,756.82
Control	6018	acyl-Coenzyme A dehydrogenase, very long chain isoform 1 precursor	gi|146231822,gi|160332360,gi|27806205,gi|74267810,gi|930358	70,632.20	99.80%	2	2	2	0.02%	3.97%	DIINEQFLLQR	3.37	1,388.75
Control	6018	acyl-Coenzyme A dehydrogenase, very long chain isoform 1 precursor	gi|146231822,gi|160332360,gi|27806205,gi|74267810,gi|930358	70,632.20	99.80%	2	2	2	0.02%	3.97%	VPAENVLGEVGGGFK	4.7	1,472.77
Control	6018	RecName: Full=60S ribosomal protein L8	gi|108860941,gi|154426156,gi|74267654,gi|77736197	28,006.80	99.90%	2	3	3	0.03%	17.90%	AQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	3.95	3,169.57
Control	6018	RecName: Full=60S ribosomal protein L8	gi|108860941,gi|154426156,gi|74267654,gi|77736197	28,006.80	99.90%	2	3	3	0.03%	17.90%	ASGNYATVISHNPETK	4.2	1,688.82
Control	6018	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	4	5	7	0.07%	5.70%	ALTLGALTLPLAR	2.55	1,309.82
Control	6018	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	4	5	7	0.07%	5.70%	GEGSGTLGSLSLPLSELLVADR	3.96	2,171.16

Control	6018	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	4	5	7	0.07%	5.70%	LHVLEAQDLIAK	3.18	1,349.78
Control	6018	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	4	5	7	0.07%	5.70%	LLVPLVPDLQDVAQLR	2.85	1,789.06
Control	6018	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	7	7	0.07%	12.90%	LKVTEGGEPYR	3.03	1,248.66
Control	6018	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	7	7	0.07%	12.90%	LSFQHDPETSVLILR	3.42	1,754.94
Control	6018	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	7	7	0.07%	12.90%	MLDYLQGSGETPQTDVR	5.03	1,925.89
Control	6018	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	7	7	0.07%	12.90%	QYASLTGTQALPPLFSLGYHQSR	3.47	2,535.30
Control	6018	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	7	7	0.07%	12.90%	VVIIGAGKPATVVLQTK	3.95	1,694.06
Control	6018	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	7	7	0.07%	12.90%	YHGPQTLYLPVTLSSIPVFQR	3.69	2,416.30
Control	6018	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	7	7	0.07%	12.90%	YRVPDVLVADPPTAGLSVSGR	3.4	2,169.17
Control	6018	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	3	3	3	0.03%	4.37%	DVIDKQHTEQEASYGR	3.55	1,875.88
Control	6018	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	3	3	3	0.03%	4.37%	LNQPQPDFTK	2.61	1,187.61
Control	6018	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	3	3	3	0.03%	4.37%	SFHSFYQLLQGGSDQMLR	4.74	2,130.01
Control	6018	Chromosome 20 open reading frame 3 ortholog	gi|74268319,gi|78369434	46,074.40	100.00%	3	4	5	0.05%	10.70%	EPPLFLGVLQPNTK	2.44	1,552.87
Control	6018	Chromosome 20 open reading frame 3 ortholog	gi|74268319,gi|78369434	46,074.40	100.00%	3	4	5	0.05%	10.70%	GGADVFVENLPGFPDNIR	2.86	1,916.95

Control	6018	Chromosome 20 open reading frame 3 ortholog	gi|74268319,gi|78369434	46,074.40	100.00%	3	4	5	0.05%	10.70%	LLLSSETPIEGR	3.05	1,314.73
Control	6018	PREDICTED: similar to Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A	gi|119896006	130,855.40	100.00%	4	4	4	0.04%	4.72%	FYTDLNGYQIQPR	2.3	1,614.79
Control	6018	PREDICTED: similar to Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A	gi|119896006	130,855.40	100.00%	4	4	4	0.04%	4.72%	IQFGTLSDYFDALEK	3.53	1,746.86

Control	6018	PREDICTED: similar to Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A	gi|119896006	130,855.40	100.00%	4	4	4	0.04%	4.72%	LLAENNEIISNIR	4.08	1,498.82
Control	6018	PREDICTED: similar to Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A	gi|119896006	130,855.40	100.00%	4	4	4	0.04%	4.72%	TTVVLAPLGDDFR	3.18	1,403.75
Control	6018	RecName: Full=Mitochondrial fission factor	gi|122140919,gi|148744119,gi|73586594,gi|77735489	29,683.40	99.80%	2	2	2	0.02%	14.80%	RLQLLEEENKER	4.01	1,556.84
Control	6018	RecName: Full=Mitochondrial fission factor	gi|122140919,gi|148744119,gi|73586594,gi|77735489	29,683.40	99.80%	2	2	2	0.02%	14.80%	VLTLSERPLDFLDLERPAPTPQNEEIR	3.43	3,148.66

Control	6018	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	5	13	0.13%	20.10%	DYPLPDVAHVK	2.57	1,253.65
Control	6018	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	5	13	0.13%	20.10%	FKESFAEMNR	3.8	1,274.58

Control	6018	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	5	13	0.13%	20.10%	SEDYALPSYVDR	2.94	1,414.65
Control	6018	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	5	13	0.13%	20.10%	SEDYALPSYVDRR	1.78	1,570.75
Control	6018	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	6	9	21	0.21%	12.30%	APVPTGEVYFADSFDR	4.19	1,770.83
Control	6018	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	6	9	21	0.21%	12.30%	IPNPDFFEDLEPFK	3.21	1,707.83
Control	6018	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	6	9	21	0.21%	12.30%	KIPNPDFFEDLEPFK	5.2	1,835.92
Control	6018	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	6	9	21	0.21%	12.30%	TDAPQPDVKEDEEEKEEEK	2.88	2,245.00
Control	6018	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	6	9	21	0.21%	12.30%	TPELNLDQFHDK	3.96	1,456.71

Control	6018	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	6	9	21	0.21%	12.30%	TPELNLDQFHDKTPYTIMFGPDK	5.2	2,723.30
Control	6018	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	11	18	0.18%	29.10%	AKMDAQQEPNIQLDHLNLLK	4.1	2,335.21
Control	6018	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	11	18	0.18%	29.10%	DLELLIQTATR	2.81	1,272.72
Control	6018	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	11	18	0.18%	29.10%	ELQQAVLQMEQR	3.95	1,488.75
Control	6018	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	11	18	0.18%	29.10%	KQQQQSHNNPAPGPEGQLK	4.34	2,086.04
Control	6018	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	11	18	0.18%	29.10%	LVTLEEFLASTQR	3.22	1,506.82
Control	6018	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	11	18	0.18%	29.10%	TFFILHDINSDGVLDEQELEALFTK	3.72	2,894.45
Control	6018	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	11	18	0.18%	29.10%	VNVPGSQAQLK	2.92	1,140.64
Control	6018	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	11	18	0.18%	29.10%	YLESLGEEQRK	3.13	1,351.69
Control	6018	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	11	18	0.18%	29.10%	YLQEVINVLETDGHFR	2.9	1,932.98
Control	6018	nicalin	gi|115494944,gi|94534903	63,091.10	100.00%	3	3	4	0.04%	8.72%	AAQLVDKDGTFLSTLEHYLSR	5.73	2,364.22
Control	6018	nicalin	gi|115494944,gi|94534903	63,091.10	100.00%	3	3	4	0.04%	8.72%	ELETVAAHQFPEVR	3.6	1,625.83
Control	6018	nicalin	gi|115494944,gi|94534903	63,091.10	100.00%	3	3	4	0.04%	8.72%	MQQYDLQGQPYGTR	3.81	1,700.77
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	DLQFVEVTDVK	3.33	1,292.67
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	EINLAPDSSSVVVSGLMVATK	4.3	2,133.11
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	GATYNIIVEAVK	2.97	1,277.71

Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	GDSPASSKPVSINYR	4.02	1,577.79
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	GFNCESKPEPEETCFDKYTGNTYR	2.83	2,815.20
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	KKTDELPQLVTLPHPNLHGPEILDVPSTVQK	3.37	3,443.89
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	NLQPGSEYAVSLVAVK	4.14	1,674.91
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	NSITLTNLNPGTEYVVSIVALNSK	4.37	2,547.37
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	NTFAEVTGLSPGVTYHFK	3.44	1,967.99
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	QYNVGPAASQYPLR	3.8	1,563.79
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	RPGAEPGNEGSTAHSYNQYSQR	5.74	2,406.08
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	SSPVVIDASTAIDAPSNLR	5.25	1,913.00
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	STTPDITGYR	2.41	1,110.54
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	SYTITGLQPGTDYK	4.23	1,543.76

Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	TEIDKPSQMQVTDVQDNSISVR	4.6	2,506.21
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	TETITGFQVDAIPANGQTPIQR	3.32	2,357.21
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	TKTETITGFQVDAIPANGQTPIQR	3.58	2,586.35
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	TPFITNPGYDTGNGIQLPGTSGQQPSLGQQMIFEEHGFRR	3.48	4,392.11
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	VDVIPVNLPGEHGQR	2.4	1,629.87
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	VEYELSEEGDEPQYLDLPSTATSVNIPDLLPGRK	4.14	3,774.86
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	VPGTSASATLTGLTR	4.33	1,431.78
Control	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	28	39	0.38%	17.50%	VTWAPPSSIELTNLLVR	2.33	1,896.06
Control	6018	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	4	5	9	0.09%	22.70%	KLPPLPLTLALGAFLNHR	2.22	1,971.19
Control	6018	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	4	5	9	0.09%	22.70%	MQDTSVSFGYQLDLPK	4.32	1,844.87
Control	6018	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	4	5	9	0.09%	22.70%	QLSPTEAFPVLVGDMDNSGSLNAQVIHQLGPGLR	3.76	3,576.81

Control	6018	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	4	5	9	0.09%	22.70%	RPGEEGAVMSLAGK	4.14	1,417.71
Control	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	6	6	6	0.06%	8.29%	ADVGFAMGIAGTDVAK	4.36	1,538.75
Control	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	6	6	6	0.06%	8.29%	EASDIILTDDNFTSIVK	4	1,880.95
Control	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	6	6	6	0.06%	8.29%	GIIDSTVGDQR	3.31	1,160.59
Control	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	6	6	6	0.06%	8.29%	TNPVEGLSGNPADLEK	4.26	1,640.81
Control	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	6	6	6	0.06%	8.29%	TPLLDEQEEEIFEK	4.6	1,719.83
Control	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	6	6	6	0.06%	8.29%	TQDGVALEIQPLNSQEGIDSEEKEKK	3.84	2,885.44

Control	6018	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	5	8	27	0.26%	57.70%	AGLQFPVGR	3.56	944.5313
Control	6018	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	5	8	27	0.26%	57.70%	HLQLAIR	2.63	850.5258
Control	6018	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	5	8	27	0.26%	57.70%	NDEELNKLLGK	3.68	1,272.68
Control	6018	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	5	8	27	0.26%	57.70%	VGAGAPVYLAAVLEYLTAEILELAGNAAR	6.19	2,915.59
Control	6018	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	5	8	27	0.26%	57.70%	VTIAQGGVLPNIQAVLLPK	5.48	1,931.17
Control	6018	RecName: Full=Nucleophosmin; Short=NPM	gi|116248556,gi|74353960,gi|78369456	32,685.20	99.80%	2	3	3	0.03%	11.60%	MSVQPTVSLGGFEITPPVVLR	4.41	2,243.21
Control	6018	RecName: Full=Nucleophosmin; Short=NPM	gi|116248556,gi|74353960,gi|78369456	32,685.20	99.80%	2	3	3	0.03%	11.60%	VDNDENEHQLSLR	4.16	1,568.73
Control	6018	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	100.00%	3	3	4	0.04%	8.47%	EIPVLVTQISSTNHPVK	4.34	1,862.04
Control	6018	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	100.00%	3	3	4	0.04%	8.47%	GSGHPAYAEVEPVGEK	4.01	1,626.78

Control	6018	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	100.00%	3	3	4	0.04%	8.47%	VGLSDAFVVVHR	4.71	1,298.72
Control	6018	RecName: Full=OCIA domain-containing protein 2	gi|122140146,gi|74353966,gi|77735471	16,827.50	99.80%	2	2	2	0.02%	14.30%	FHSFEGQLR	2.34	1,120.55
Control	6018	RecName: Full=OCIA domain-containing protein 2	gi|122140146,gi|74353966,gi|77735471	16,827.50	99.80%	2	2	2	0.02%	14.30%	VALAGILGFGLGK	4.18	1,215.75
Control	6018	PREDICTED: low density lipoprotein receptor (familial hypercholesterolemia) isoform 2	gi|76621801	92,850.80	99.80%	2	2	3	0.03%	3.20%	NVVALDTEVASNR	3.69	1,387.72
Control	6018	PREDICTED: low density lipoprotein receptor (familial hypercholesterolemia) isoform 2	gi|76621801	92,850.80	99.80%	2	2	3	0.03%	3.20%	SINSINFDNPVYQK	4.22	1,638.81
Control	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	18	27	0.26%	35.80%	ASLDRPFTSLESAFYSIVGLSSLGAQVPDVK	4.54	3,254.69

Control	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	18	27	0.26%	35.80%	ASLDRPFTSLESAFYSIVGLSSLGAQVPDVKK	4.97	3,382.79
Control	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	18	27	0.26%	35.80%	DLLLAAVSEDSSVAQIYHAVAALSGFGLPLASQEALGALTAR	3.87	4,196.22

Control	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	18	27	0.26%	35.80%	ISTEVGITNVDLSTVDKDQSIAPK	4.98	2,530.33
Control	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	18	27	0.26%	35.80%	KNFESLSEAFSVASAAALSENR	3.64	2,399.18

Control	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	18	27	0.26%	35.80%	LMDHVGTEPSIKEDQVIQLMNAIFSK	3.31	2,959.49
Control	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	18	27	0.26%	35.80%	LQVTNVLSQPLTQATVK	4.55	1,840.05

Control	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	18	27	0.26%	35.80%	LSKEETVLATVQALQTASYLSQQADLR	5.25	2,963.57
Control	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	18	27	0.26%	35.80%	NFESLSEAFSVASAAAALSENR	4.48	2,271.09

Control	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	18	27	0.26%	35.80%	SIVEEIEDLVAR	4.33	1,372.73
Control	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	18	27	0.26%	35.80%	TGQEVVFVAEPDSK	3.9	1,505.75

Control	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	18	27	0.26%	35.80%	YIANTVELR	3.27	1,078.59
Control	6018	RecName: Full=60S acidic ribosomal protein P2	gi|1173072,gi|27807523,gi|600177,gi|82571755	11,684.40	100.00%	2	2	2	0.02%	46.10%	ILDSVGIEADDDRLNK	4.06	1,772.90
Control	6018	RecName: Full=60S acidic ribosomal protein P2	gi|1173072,gi|27807523,gi|600177,gi|82571755	11,684.40	100.00%	2	2	2	0.02%	46.10%	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKKEEK	3.45	3,288.71
Control	6018	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	4	5	6	0.06%	11.70%	GLLPQLLGVAPEK	2.53	1,334.80

Control	6018	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	4	5	6	0.06%	11.70%	IAPLEEGTLPFNLAEAQR	4.25	1,969.04
Control	6018	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	4	5	6	0.06%	11.70%	ITLPAPNPDHVGGYK	2.11	1,578.83
Control	6018	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	4	5	6	0.06%	11.70%	LAVATFAGIENK	3.52	1,233.68

Control	6018	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	4	5	6	0.06%	11.70%	LTVNDFVR	2	963.5258
Control	6018	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	4	5	6	0.06%	11.70%	YLNIFGESQPNPK	3.82	1,506.76
Control	6018	STT3B protein	gi|146186621,gi|148235371	93,202.50	100.00%	3	3	3	0.03%	5.96%	ENPPVEDSSDEDDKRNPGNLYDK	2.31	2,633.16
Control	6018	STT3B protein	gi|146186621,gi|148235371	93,202.50	100.00%	3	3	3	0.03%	5.96%	FGEMQLDFR	2.42	1,158.53
Control	6018	STT3B protein	gi|146186621,gi|148235371	93,202.50	100.00%	3	3	3	0.03%	5.96%	HVTEQEKTEEGLGPNIK	3.17	1,908.97
Control	6018	Synaptojanin 2 binding protein	gi|74354054,gi|78369420	15,792.00	99.80%	2	4	7	0.07%	19.30%	LQEGDKILSVNGQDLK	5.21	1,756.94
Control	6018	Synaptojanin 2 binding protein	gi|74354054,gi|78369420	15,792.00	99.80%	2	4	7	0.07%	19.30%	NLLHQDAVDLFR	3.5	1,440.76
Control	6018	ADPGK protein	gi|126010731,gi|126722892,gi|205686178	54,066.80	99.80%	2	2	2	0.02%	9.66%	FFSDKETFHDIAQVASEFPEAQHYVGGNAALIGQK	3.18	3,851.87

Control	6018	ADPGK protein	gi|126010731,gi|126722892,gi|205686178	54,066.80	99.80%	2	2	2	0.02%	9.66%	NDLEEAFVHFMGK	2.06	1,552.71
Control	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	15	17	32	0.31%	17.30%	DYAKDDPLEFK	3.03	1,340.64
Control	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	15	17	32	0.31%	17.30%	ENPETEEDVGPVVQHIYELR	3.44	2,353.13
Control	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	15	17	32	0.31%	17.30%	FDLQIQSSNLFDK	4	1,554.78
Control	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	15	17	32	0.31%	17.30%	FDLQIQSSNLFDKVSPVVSYK	4.12	2,414.26
Control	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	15	17	32	0.31%	17.30%	FGSAIAPLGDLDQDGFNDIAIAAPYGGEDK	3.79	3,037.44
Control	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	15	17	32	0.31%	17.30%	FGSAIAPLGDLDQDGFNDIAIAAPYGGEDKK	5.4	3,165.54
Control	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	15	17	32	0.31%	17.30%	FSVHQQSEMDTSVK	3.3	1,638.74
Control	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	15	17	32	0.31%	17.30%	GATDIDKNGYPDLIVGAFGVDR	5.03	2,293.15
Control	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	15	17	32	0.31%	17.30%	GIVYIFNGRPTGLNAVPSQILEGK	4.25	2,543.40
Control	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	15	17	32	0.31%	17.30%	IYIGDDNPLTLIVK	4.22	1,573.88
Control	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	15	17	32	0.31%	17.30%	MFLLVGAPK	3.86	991.5647
Control	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	15	17	32	0.31%	17.30%	NGYPDLIVGAFGVDR	3.27	1,592.81
Control	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	15	17	32	0.31%	17.30%	PTGLNAVPSQILEGK	4.09	1,523.84
Control	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	15	17	32	0.31%	17.30%	SSASFNVIEFPYK	3.83	1,488.74
Control	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	15	17	32	0.31%	17.30%	YKENPETEEDVGPVVQHIYELR	4.29	2,644.29
Control	6018	poly(A) binding protein, cytoplasmic 1	gi|41386798,gi|47117093,gi|74268035,gi|8979741	70,653.30	100.00%	3	3	3	0.03%	6.60%	ALDTMNFDVIK	2.81	1,282.64
Control	6018	poly(A) binding protein, cytoplasmic 1	gi|41386798,gi|47117093,gi|74268035,gi|8979741	70,653.30	100.00%	3	3	3	0.03%	6.60%	IVATKPLYVALAQR	2.43	1,542.94

Control	6018	poly(A) binding protein, cytoplasmic 1	gi|41386798,gi|47117093,gi|74268035,gi|8979741	70,653.30	100.00%	3	3	3	0.03%	6.60%	SLGYAYVNFQQPADAER	2.73	1,928.91
Control	6018	RecName: Full=Monocarboxylate transporter 1; Short=MCT 1; AltName: Full=Solute carrier family 16 member 1	gi|122139973,gi|77567740,gi|82617542	54,281.70	100.00%	3	4	5	0.05%	3.79%	GASDANTDLIGGNPK	4.65	1,429.69
Control	6018	RecName: Full=Monocarboxylate transporter 1; Short=MCT 1; AltName: Full=Solute carrier family 16 member 1	gi|122139973,gi|77567740,gi|82617542	54,281.70	100.00%	3	4	5	0.05%	3.79%	GASDANTDLIGGNPKEEK	3.97	1,815.87
Control	6018	RecName: Full=Monocarboxylate transporter 1; Short=MCT 1; AltName: Full=Solute carrier family 16 member 1	gi|122139973,gi|77567740,gi|82617542	54,281.70	100.00%	3	4	5	0.05%	3.79%	GASDANTDLIGGNPKEEKK	2.82	1,943.97
Control	6018	RecName: Full=L-lactate dehydrogenase B chain; Short=LDH-B	gi|118572666,gi|148744825,gi|154425698,gi|27806561,gi|59858383,gi|74353944,gi|8979739	36,679.70	99.80%	2	2	3	0.03%	7.49%	IVADKDYSVTANSK	4.53	1,510.77

Control	6018	RecName: Full=L-lactate dehydrogenase B chain; Short=LDH-B	gi|118572666,gi|148744825,gi|154425698,gi|27806561,gi|59858383,gi|74353944,gi|8979739	36,679.70	99.80%	2	2	3	0.03%	7.49%	LKDEEVAQLKK	3.02	1,300.75
Control	6018	PREDICTED: similar to programmed cell death 6 interacting protein isoform 1	gi|119914274	96,862.00	99.80%	2	2	2	0.02%	2.74%	LLDEEEATDNDLR	2.88	1,532.71
Control	6018	PREDICTED: similar to programmed cell death 6 interacting protein isoform 1	gi|119914274	96,862.00	99.80%	2	2	2	0.02%	2.74%	NIQVSHQEFSK	3.47	1,316.66
Control	6018	Sec61 alpha 1 subunit (S. cerevisiae)	gi|154426140,gi|59857767,gi|75060961,gi|94966817	52,208.90	100.00%	3	6	15	0.15%	15.10%	GMEFEGAIIALFHLLATR	4.47	2,005.06
Control	6018	Sec61 alpha 1 subunit (S. cerevisiae)	gi|154426140,gi|59857767,gi|75060961,gi|94966817	52,208.90	100.00%	3	6	15	0.15%	15.10%	GTLMELGISPIVTSGLIMQLLAGAK	4.5	2,529.40
Control	6018	Sec61 alpha 1 subunit (S. cerevisiae)	gi|154426140,gi|59857767,gi|75060961,gi|94966817	52,208.90	100.00%	3	6	15	0.15%	15.10%	LFYTSNIPIILQSALVSNLYVISQMLSAR	4.89	3,270.78
Control	6018	Actin related protein 2/3 complex, subunit 4, 20kDa	gi|109939945,gi|115495705,gi|119361249,gi|149243014,gi|149243029,gi|149243036,gi|149243043,gi|149243050,gi|149243057,gi|149243064,gi|56966197	19,649.40	99.80%	2	2	3	0.03%	11.30%	AENFFILR	2.46	1,009.55

Control	6018	Actin related protein 2/3 complex, subunit 4, 20kDa	gi|109939945,gi|115495705,gi|119361249,gi|149243014,gi|149243029,gi|149243036,gi|149243043,gi|149243050,gi|149243057,gi|149243064,gi|56966197	19,649.40	99.80%	2	2	3	0.03%	11.30%	ELLLQPVTISR	3.58	1,268.76
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	AVDSLVPIGR	3.01	1,026.59
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	EAYPGDVFYLHSR	3.55	1,553.74
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	EVAAFAQFGSDLDAATQQLLSR	4.3	2,338.17
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	FENAFLSHVISQHQALLSK	4.65	2,169.15
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	GIRPAINVGLSVSR	2.83	1,438.85

Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	GMSLNLEPDNVGVVVFGNDK	6.37	2,120.03
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	GYLDKLEPSK	2.78	1,149.62
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	HALIIYDDLSK	3.2	1,287.69
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	ILGADTSVDLEETGR	4.56	1,575.79
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	ITKFENAFLSHVISQHQALLSK	3.68	2,511.37
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	LELAQYR	2.35	892.4887

Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	LKEIVTNFLAGFEA	3.91	1,551.84
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	NVQAEEMVEFSSGLK	3.68	1,683.79
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	QGQYSPMAIEEQVAVIYAGVR	3.57	2,325.15
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	TGAIVDVPVGEELLGR	4.73	1,624.89
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	TGTAEVSSILEER	3.58	1,391.70
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	TSIAIDTIINQK	3.23	1,316.74

Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	VGLKAPGIIPR	3.46	1,120.72
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	VLSIGDGIAR	2.84	1,000.58
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	VVDALGNAIDGK	4.04	1,171.63
Control	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	21	24	44	0.43%	53.70%	VVDALGNAIDGKGPIGSK	4.93	1,710.94
Control	6018	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	5	8	14	0.14%	29.90%	IMVANIEEVLQR	4.89	1,430.77
Control	6018	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	5	8	14	0.14%	29.90%	KLAFAYLEDLHSEFDEQHGK	4.47	2,377.15
Control	6018	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	5	8	14	0.14%	29.90%	NLGSINTELQDVQR	5.15	1,586.81
Control	6018	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	5	8	14	0.14%	29.90%	VADGLPLAASMQEDEQSGR	4.93	1,989.92

Control	6018	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	5	8	14	0.14%	29.90%	VADGLPLAASMQEDEQSGRDLQQYQSQAK	4.35	3,179.49
Control	6018	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	5	5	8	0.08%	27.70%	INVNEIFYDLVR	4.99	1,494.80
Control	6018	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	5	5	8	0.08%	27.70%	LVVLGSGGVGK	2.8	985.6042
Control	6018	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	5	5	8	0.08%	27.70%	SKINVNEIFYDLVR	3.61	1,709.92
Control	6018	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	5	5	8	0.08%	27.70%	VKDTDDVPMILVGNK	4.36	1,659.86
Control	6018	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	5	5	8	0.08%	27.70%	YDPTIEDSYRK	2.69	1,386.65
Control	6018	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	7	8	8	0.08%	14.60%	EEAAAAAPAPAADDQGVLK	4.07	1,794.89
Control	6018	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	7	8	8	0.08%	14.60%	KREEAAAAAPAPAADDQGVLK	4	2,079.08
Control	6018	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	7	8	8	0.08%	14.60%	LQEMLSVGLGFLR	2.88	1,478.80
Control	6018	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	7	8	8	0.08%	14.60%	NKGDSHLNVQVSNFK	2.84	1,686.86
Control	6018	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	7	8	8	0.08%	14.60%	TELGLDLGLEPK	3.35	1,284.70
Control	6018	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	7	8	8	0.08%	14.60%	TIEVAEEEVVR	2.88	1,273.66
Control	6018	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	7	8	8	0.08%	14.60%	TISTSDPADALIK	2.73	1,331.71

Control	6018	RecName: Full=Aconitate hydratase, mitochondrial; Short=Aconitase; AltName: Full=Citrate hydro-lyase; Flags: Precursor	gi|110282935,gi|1364216,gi|27806769,gi|74268076,gi|90970312	85,342.00	99.80%	2	2	2	0.02%	3.72%	IVYGHLDDPANQEIER	5.11	1,868.91
Control	6018	RecName: Full=Aconitate hydratase, mitochondrial; Short=Aconitase; AltName: Full=Citrate hydro-lyase; Flags: Precursor	gi|110282935,gi|1364216,gi|27806769,gi|74268076,gi|90970312	85,342.00	99.80%	2	2	2	0.02%	3.72%	SQFTITPGSEQIR	3.58	1,463.75
Control	6018	RecName: Full=ATP synthase subunit g, mitochondrial; Short=ATPase subunit g	gi|2493093,gi|74354012,gi|7579922,gi|94400870	11,604.00	100.00%	3	4	7	0.07%	37.50%	APALVNAAVTYSKPR	5.36	1,557.87
Control	6018	RecName: Full=ATP synthase subunit g, mitochondrial; Short=ATPase subunit g	gi|2493093,gi|74354012,gi|7579922,gi|94400870	11,604.00	100.00%	3	4	7	0.07%	37.50%	NLAEKAPALVNAAVTYSKPR	4.78	2,113.18
Control	6018	RecName: Full=ATP synthase subunit g, mitochondrial; Short=ATPase subunit g	gi|2493093,gi|74354012,gi|7579922,gi|94400870	11,604.00	100.00%	3	4	7	0.07%	37.50%	VELVPPTPAEIPTAIQSLK	2.57	2,003.14

Control	6018	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	99.80%	2	2	2	0.02%	15.60%	DTILQLNLK	2.52	1,057.63
Control	6018	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	99.80%	2	2	2	0.02%	15.60%	LLLLGTGESGK	2.79	1,087.64
Control	6018	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	99.80%	2	2	2	0.02%	15.60%	VADPAYLPTQQDVLR	3.56	1,685.89
Control	6018	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	99.80%	2	2	2	0.02%	15.60%	VRVPTTGIIEYPFDLQSVIFR	5.6	2,450.34
Control	6018	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	100.00%	4	4	4	0.04%	8.23%	LPVPASAPIPFFHR	3.65	1,548.87
Control	6018	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	100.00%	4	4	4	0.04%	8.23%	NAELEAIPNSGMDHTHR	2.79	1,907.87
Control	6018	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	100.00%	4	4	4	0.04%	8.23%	NLPFTPILASVNR	3.27	1,441.82
Control	6018	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	100.00%	4	4	4	0.04%	8.23%	VLMEFVENSR	3.29	1,239.60
Control	6018	RecName: Full=60S ribosomal protein L7a	gi|108860939,gi|146231828,gi|83638795,gi|94966839	30,008.40	99.80%	2	2	3	0.03%	10.20%	LKVPPAINQFTQALDR	5.19	1,811.02

Control	6018	RecName: Full=60S ribosomal protein L7a	gi|108860939,gi|146231828,gi|83638795,gi|94966839	30,008.40	99.80%	2	2	3	0.03%	10.20%	NFGIGQDIQPK	2.87	1,216.63
Control	6018	RecName: Full=Transgelin; AltName: Full=Smooth muscle protein 22-alpha; Short=SM22-alpha; AltName: Full=25 kDa F-actin-binding protein	gi|109940320,gi|114051586,gi|86823808	22,580.80	100.00%	4	4	4	0.04%	30.30%	EFTESQLQEGK	2.75	1,295.61
Control	6018	RecName: Full=Transgelin; AltName: Full=Smooth muscle protein 22-alpha; Short=SM22-alpha; AltName: Full=25 kDa F-actin-binding protein	gi|109940320,gi|114051586,gi|86823808	22,580.80	100.00%	4	4	4	0.04%	30.30%	LVNSLYPDGSKPVKVPENPPSMVFK	3.37	2,758.45
Control	6018	RecName: Full=Transgelin; AltName: Full=Smooth muscle protein 22-alpha; Short=SM22-alpha; AltName: Full=25 kDa F-actin-binding protein	gi|109940320,gi|114051586,gi|86823808	22,580.80	100.00%	4	4	4	0.04%	30.30%	TDMFQTVDLFEGK	3.12	1,546.71

Control	6018	RecName: Full=Transgelin; AltName: Full=Smooth muscle protein 22-alpha; Short=SM22-alpha; AltName: Full=25 kDa F-actin-binding protein	gi|109940320,gi|114051586,gi|86823808	22,580.80	100.00%	4	4	4	0.04%	30.30%	TLMALGSLAVTK	3.68	1,220.69
Control	6018	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	5	6	6	0.06%	16.50%	GFKDQIYDIFQK	3.52	1,501.77
Control	6018	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	5	6	6	0.06%	16.50%	GIYAYGFEKPSAIQQR	4.54	1,827.94

Control	6018	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	5	6	6	0.06%	16.50%	GYDVIAQAQSGTGK	3.88	1,394.69
Control	6018	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	5	6	6	0.06%	16.50%	LQMEAPHIIVGTPGR	3.41	1,634.87
Control	6018	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	5	6	6	0.06%	16.50%	VLITTDLLAR	2.41	1,114.68
Control	6018	CDGSH iron sulfur domain 2	gi|115545422,gi|122131734,gi|122692399	15,260.70	99.80%	2	2	2	0.02%	9.63%	LPVPESITGFAR	2.91	1,286.71
Control	6018	CDGSH iron sulfur domain 2	gi|115545422,gi|122131734,gi|122692399	15,260.70	99.80%	2	2	2	0.02%	9.63%	RLPVPESITGFAR	3.95	1,442.81

Control	6018	RecName: Full=Mitochondrial Rho GTPase 1; Short=MIRO-1; AltName: Full=Ras homolog gene family member T1	gi|108860795,gi|114051724,gi|88682961	72,061.70	100.00%	2	3	3	0.03%	4.44%	ILLVGEPR	2.57	896.5565
Control	6018	RecName: Full=Mitochondrial Rho GTPase 1; Short=MIRO-1; AltName: Full=Ras homolog gene family member T1	gi|108860795,gi|114051724,gi|88682961	72,061.70	100.00%	2	3	3	0.03%	4.44%	ISDQDNDGTLNDAELNFFQR	4.49	2,312.04
Control	6018	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	13	14	0.14%	27.20%	DVYVQLYLQHLTAR	4.42	1,718.92
Control	6018	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	13	14	0.14%	27.20%	GPPDFSSDEEREPTPVLGSGAAVAGR	5.42	2,598.24
Control	6018	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	13	14	0.14%	27.20%	HAAPILPITEFSDIPR	3.22	1,776.96
Control	6018	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	13	14	0.14%	27.20%	LKSELVANNVTLPAGEQR	5.39	1,939.06
Control	6018	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	13	14	0.14%	27.20%	LKSELVANNVTLPAGEQRK	4.04	2,067.16
Control	6018	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	13	14	0.14%	27.20%	SELVANNVTLPAGEQR	3.36	1,697.88
Control	6018	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	13	14	0.14%	27.20%	SSTPLPTISSSVENTR	3.38	1,675.85
Control	6018	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	13	14	0.14%	27.20%	YGVNPGPIVGTTR	3.12	1,330.71
Control	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	7	8	8	0.08%	4.92%	AVSSAIAQLLGEVAQGNENYAGIAAR	3.89	2,573.33

Control	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	7	8	8	0.08%	4.92%	GVGAAATAVTQALNELLQHVR	3.61	2,119.16
Control	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	7	8	8	0.08%	4.92%	ILAQATSDLVNAIK	4.11	1,456.84
Control	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	7	8	8	0.08%	4.92%	LAQAAQSSVATITR	3.85	1,416.78
Control	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	7	8	8	0.08%	4.92%	LLAALLEDEGGSGRPLLQAAK	2.51	2,122.19
Control	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	7	8	8	0.08%	4.92%	TLSHPQQMALLDQTK	3.98	1,726.88
Control	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	7	8	8	0.08%	4.92%	VLGEAMTGISQNAK	4.15	1,434.73
Control	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	11	12	14	0.14%	23.60%	FGLYLPK	2.84	837.487
Control	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	11	12	14	0.14%	23.60%	FTLGSVAGAVGATAVYPIDLVK	4.03	2,149.19
Control	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	11	12	14	0.14%	23.60%	GLIPQLIGVAPEK	2.53	1,334.80
Control	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	11	12	14	0.14%	23.60%	HLNYTEFTQFLQELQLEHAR	5.2	2,517.25
Control	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	11	12	14	0.14%	23.60%	IAPLAEGALPYNLAELQR	4.5	1,939.06
Control	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	11	12	14	0.14%	23.60%	IVQLLAGVADQTK	2.64	1,355.79
Control	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	11	12	14	0.14%	23.60%	LATATFAGIENK	3.05	1,235.66
Control	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	11	12	14	0.14%	23.60%	LTLADIER	2.38	930.5256
Control	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	11	12	14	0.14%	23.60%	LTVNDFVR	2	963.5258
Control	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	11	12	14	0.14%	23.60%	NIFLQYASTEVDGEHYMTPEDFVQR	3.92	3,005.36
Control	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	11	12	14	0.14%	23.60%	YLGLYNDPNSNPK	3.58	1,494.72

Control	6018	RecName: Full=Electron transfer flavoprotein subunit alpha, mitochondrial; Short=Alpha-ETF; Flags: Precursor	gi|110808222,gi|115496196,gi|86823828	34,944.00	99.80%	2	2	2	0.02%	8.71%	GLLPEELTPLILATQK	4.62	1,736.02
Control	6018	RecName: Full=Electron transfer flavoprotein subunit alpha, mitochondrial; Short=Alpha-ETF; Flags: Precursor	gi|110808222,gi|115496196,gi|86823828	34,944.00	99.80%	2	2	2	0.02%	8.71%	LDVAPISDIIAIK	2.66	1,367.81
Control	6018	RecName: Full=Cytochrome b5	gi|117806,gi|1372997,gi|157830773,gi|27806667,gi|298,gi|79160196	15,311.60	100.00%	2	2	3	0.03%	24.60%	EQAGGDATENFEDVGHSTDAR	3.3	2,205.93
Control	6018	RecName: Full=Cytochrome b5	gi|117806,gi|1372997,gi|157830773,gi|27806667,gi|298,gi|79160196	15,311.60	100.00%	2	2	3	0.03%	24.60%	TFIIGELHPDDR	3.77	1,412.72
Control	6018	IKK interacting protein	gi|126010633,gi|126165284,gi|193806036	39,199.60	100.00%	4	4	6	0.06%	16.90%	LEPLVNDLTLR	2.64	1,282.74
Control	6018	IKK interacting protein	gi|126010633,gi|126165284,gi|193806036	39,199.60	100.00%	4	4	6	0.06%	16.90%	METSEFQGLQSK	4.14	1,400.64
Control	6018	IKK interacting protein	gi|126010633,gi|126165284,gi|193806036	39,199.60	100.00%	4	4	6	0.06%	16.90%	MSGLVTDVTSLTDSVQELENKIEK	3.27	2,652.33
Control	6018	IKK interacting protein	gi|126010633,gi|126165284,gi|193806036	39,199.60	100.00%	4	4	6	0.06%	16.90%	NIGDLLSSIDR	3.79	1,289.67
Control	6018	ALDH3A2 protein	gi|151557095,gi|156120617	54,059.30	100.00%	4	4	4	0.04%	10.30%	EKDILAAIGADLSK	2.51	1,443.81
Control	6018	ALDH3A2 protein	gi|151557095,gi|156120617	54,059.30	100.00%	4	4	4	0.04%	10.30%	HLTPVTLELGGK	2.75	1,264.73

Control	6018	ALDH3A2 protein	gi|151557095,gi|156120617	54,059.30	100.00%	4	4	4	0.04%	10.30%	IAFGGEMDEATR	2.98	1,312.58
Control	6018	ALDH3A2 protein	gi|151557095,gi|156120617	54,059.30	100.00%	4	4	4	0.04%	10.30%	NADEAIQFINER	3.76	1,419.69
Control	6018	defender against cell death 1	gi|59858361,gi|73918963,gi|74354770,gi|77736467,gi|83286811	12,477.50	99.80%	2	2	5	0.05%	19.50%	ADFQGISPER	2.73	1,119.54
Control	6018	defender against cell death 1	gi|59858361,gi|73918963,gi|74354770,gi|77736467,gi|83286811	12,477.50	99.80%	2	2	5	0.05%	19.50%	FLEEYLSATPQR	3.42	1,453.73
Control	6018	heterogeneous nuclear ribonucleoprotein A1	gi|114052384,gi|172046785,gi|86823844	34,178.40	99.80%	2	2	2	0.02%	8.12%	IEVIEIMTDR	2.7	1,234.64
Control	6018	heterogeneous nuclear ribonucleoprotein A1	gi|114052384,gi|172046785,gi|86823844	34,178.40	99.80%	2	2	2	0.02%	8.12%	SSGPYGGGGQYFAKPR	3.41	1,628.78
Control	6018	Chain A, Adenylate Kinase Isoenzyme-2	gi|157829916,gi|157834545,gi|224029	16,091.20	99.80%	2	2	2	0.02%	19.50%	APNVPAAEPVPESPK	2.56	1,502.79
Control	6018	Chain A, Adenylate Kinase Isoenzyme-2	gi|157829916,gi|157834545,gi|224029	16,091.20	99.80%	2	2	2	0.02%	19.50%	APNVPAAEPVPESPKGVRAVLLGPPGAGK	2.78	2,775.55
Control	6018	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	8	8	9	0.09%	12.50%	DFFTTGSPGETAFR	3.37	1,532.70
Control	6018	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	8	8	9	0.09%	12.50%	EFDLTKEEDLAALR	3.26	1,649.84
Control	6018	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	8	8	9	0.09%	12.50%	ESVEQQADSFK	3.1	1,267.58
Control	6018	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	8	8	9	0.09%	12.50%	EVLEDFAEDSEK	3.08	1,410.63

Control	6018	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	8	8	9	0.09%	12.50%	GNSSESIEAIRDYEEEFFQNSK	4.84	2,579.15
Control	6018	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	8	8	9	0.09%	12.50%	IDQLQEELLHTQLK	3.41	1,707.93
Control	6018	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	8	8	9	0.09%	12.50%	MLAITANTLR	2.84	1,119.62
Control	6018	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	8	8	9	0.09%	12.50%	SLIDMYSEVLDVLSDYDASYNTQDHLPR	3.81	3,275.51
Control	6018	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	7	10	13	0.13%	20.00%	ELQALTDAMYTNLR	4.37	1,654.81
Control	6018	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	7	10	13	0.13%	20.00%	EVVADLALPMADGR	4.16	1,472.74
Control	6018	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	7	10	13	0.13%	20.00%	GELETVLLGAEQPISQMTTLPQK	3.44	2,483.31
Control	6018	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	7	10	13	0.13%	20.00%	LLLFPFLSPQK	2.75	1,302.78
Control	6018	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	7	10	13	0.13%	20.00%	LLLFPFLSPQKDPEIYTDPEVFK	5.32	2,736.45
Control	6018	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	7	10	13	0.13%	20.00%	LTAAPFITR	2.45	989.5779
Control	6018	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	7	10	13	0.13%	20.00%	VLDSMPVLDSVLSESLR	4.8	1,875.97

Control	6018	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	4	4	4	0.04%	8.77%	AFITNIPFDVK	2.61	1,264.69
Control	6018	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	4	4	4	0.04%	8.77%	GNFGGSFAGSFGGAGGHAPGVAR	2.63	2,034.95
Control	6018	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	4	4	4	0.04%	8.77%	INEILSNALK	2.71	1,114.65
Control	6018	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	4	4	4	0.04%	8.77%	MEEESGAPGVPSGNGAPGPK	2.59	1,883.84
Control	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	7	0.07%	45.70%	AILVDLEPGTMDSVR	4.42	1,631.83
Control	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	7	0.07%	45.70%	ALTVPELTQQVFDAK	3.93	1,659.90
Control	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	7	0.07%	45.70%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	3.11	3,213.49
Control	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	7	0.07%	45.70%	EVDEQMLNVQNK	2.76	1,462.68
Control	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	7	0.07%	45.70%	GHYTEGAELVDSVLDVVR	4.4	1,958.98
Control	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	7	0.07%	45.70%	GHYTEGAELVDSVLDVVRK	3.51	2,087.08
Control	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	7	0.07%	45.70%	IMNTFSVVPSPK	4.35	1,335.70
Control	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	7	0.07%	45.70%	ISVYYNEATGGK	3.22	1,301.64

Control	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	7	0.07%	45.70%	LAVNMVPFPR	3.83	1,159.63
Control	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	7	0.07%	45.70%	LHFFMPGFAPLTSR	4.05	1,636.83
Control	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	7	0.07%	45.70%	NSSYFVEWIPNNVK	2.39	1,696.83
Control	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	7	0.07%	45.70%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	4.6	4,479.06
Control	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	4	7	0.07%	45.70%	YLTVAAVFR	2.73	1,039.59
Control	6018	melanoma cell adhesion molecule	gi|2323281	9,468.30	99.80%	2	4	7	0.07%	22.10%	SDKLPEEMGLLQGSSGDK	4.73	1,906.91
Control	6018	melanoma cell adhesion molecule	gi|2323281	9,468.30	99.80%	2	4	7	0.07%	22.10%	SDKLPEEMGLLQGSSGDKR	3.45	2,063.01
Control	6018	RecName: Full=Ornithine aminotransferase, mitochondrial; AltName: Full=Ornithine--oxo-acid aminotransferase; Flags: Precursor	gi|122140925,gi|73586966,gi|77735431	48,058.30	99.90%	2	2	2	0.02%	5.24%	GLLNAIVIR	2.86	968.6252
Control	6018	RecName: Full=Ornithine aminotransferase, mitochondrial; AltName: Full=Ornithine--oxo-acid aminotransferase; Flags: Precursor	gi|122140925,gi|73586966,gi|77735431	48,058.30	99.90%	2	2	2	0.02%	5.24%	TVQGPPSSDYIFER	3.72	1,595.77

Control	6018	RecName: Full=Transmembrane protein 111	gi|115311872,gi|73587331,gi|78050079	29,903.00	100.00%	2	2	2	0.02%	11.90%	LTQEQVSDSQVLIR	3.81	1,615.87
Control	6018	RecName: Full=Transmembrane protein 111	gi|115311872,gi|73587331,gi|78050079	29,903.00	100.00%	2	2	2	0.02%	11.90%	SIYSLILGQDNAADQSR	3.06	1,850.92
Control	6018	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	99.80%	2	2	93	0.91%	17.20%	LLGNVLVVVLAR	4.41	1,265.83
Control	6018	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	99.80%	2	2	93	0.91%	17.20%	VKVDEVGGEALGR	4.31	1,328.72
Control	6018	vesicle-associated membrane protein 5	gi|114050717,gi|122135927,gi|86826577	12,760.30	99.80%	2	2	4	0.04%	24.10%	QADEVTEIMLNNFDK	3.19	1,782.82
Control	6018	vesicle-associated membrane protein 5	gi|114050717,gi|122135927,gi|86826577	12,760.30	99.80%	2	2	4	0.04%	24.10%	SDQLLDMSSAFSK	4.29	1,444.66
Control	6018	Ribosomal protein L6	gi|126717393,gi|58760432,gi|61553343,gi|61553350,gi|67461090,gi|72534798	32,672.90	100.00%	4	4	4	0.04%	19.20%	ASITPGTILIILTGR	3.34	1,525.93
Control	6018	Ribosomal protein L6	gi|126717393,gi|58760432,gi|61553343,gi|61553350,gi|67461090,gi|72534798	32,672.90	100.00%	4	4	4	0.04%	19.20%	AVPQLQGYLR	2.85	1,144.65
Control	6018	Ribosomal protein L6	gi|126717393,gi|58760432,gi|61553343,gi|61553350,gi|67461090,gi|72534798	32,672.90	100.00%	4	4	4	0.04%	19.20%	QLGSGLLLVTGPLSLNR	4.3	1,738.02
Control	6018	Ribosomal protein L6	gi|126717393,gi|58760432,gi|61553343,gi|61553350,gi|67461090,gi|72534798	32,672.90	100.00%	4	4	4	0.04%	19.20%	SVFALTNGIYPHK	2.92	1,446.77

Control	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	11	13	0.13%	6.80%	AFGPGLQGGSAGSPAR	4.18	1,429.72
Control	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	11	13	0.13%	6.80%	ANLPQSFQVDTSK	3.53	1,434.72
Control	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	11	13	0.13%	6.80%	AYGPGIEPTGNMVK	3.22	1,449.70
Control	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	11	13	0.13%	6.80%	DVDIIDHHDNTYTVK	2.89	1,784.85
Control	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	11	13	0.13%	6.80%	FADQHVPGSPFSVK	2.69	1,515.76
Control	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	11	13	0.13%	6.80%	GAGTGGLGLAVEGPSEAK	3.98	1,570.81
Control	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	11	13	0.13%	6.80%	GLVEPVDVVDNADGTQTVNYVPSR	2.69	2,544.26
Control	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	11	13	0.13%	6.80%	IANLQTDLSDGLR	3.27	1,415.75

Control	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	11	13	0.13%	6.80%	LIALLEVLSQK	2.97	1,226.77
Control	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	11	13	0.13%	6.80%	VTAQGPGLEPSGNIANK	4.51	1,652.86
Control	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	11	13	0.13%	6.80%	YTPVQQGPVGINVTYGGDAIPK	4.39	2,274.18
Control	6018	NRAS protein	gi|146186548,gi|148226664	21,211.30	99.90%	2	2	2	0.02%	18.50%	SALTIQLIQNHFVDEYDPTIEDSYRK	2.94	3,095.53
Control	6018	NRAS protein	gi|146186548,gi|148226664	21,211.30	99.90%	2	2	2	0.02%	18.50%	SFADINLYR	2.69	1,098.56
Control	6018	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	7	9	16	0.16%	41.20%	ANQVTDESLESTR	3.93	1,449.68
Control	6018	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	7	9	16	0.16%	41.20%	ANQVTDESLESTRR	3.14	1,605.78
Control	6018	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	7	9	16	0.16%	41.20%	ILGLAIESQDAGIK	4.45	1,427.81
Control	6018	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	7	9	16	0.16%	41.20%	ITNDAREDEMEDNLTQVGSILGNLK	2.98	2,791.34
Control	6018	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	7	9	16	0.16%	41.20%	TITMLDEQGEQLK	3.83	1,521.75
Control	6018	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	7	9	16	0.16%	41.20%	TITMLDEQGEQLKR	2.37	1,677.85
Control	6018	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	7	9	16	0.16%	41.20%	VTNGQPQQATAGAASGGYIK	4.65	1,918.96

Control	6018	LBR protein	gi|151557087,gi|154152031	71,240.40	99.80%	2	3	3	0.03%	6.28%	APQDELSPASSGNAIYDFFIGR	4.97	2,355.13
Control	6018	LBR protein	gi|151557087,gi|154152031	71,240.40	99.80%	2	3	3	0.03%	6.28%	FHLSQESSYIPTQYSLR	2.91	2,056.01
Control	6018	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	gi|124828540,gi|126158903,gi|145566947	55,991.00	100.00%	3	3	3	0.03%	9.25%	ETVDSFLDLTR	2.87	1,295.65
Control	6018	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	gi|124828540,gi|126158903,gi|145566947	55,991.00	100.00%	3	3	3	0.03%	9.25%	NLFPSNLVVAAFR	2.81	1,447.81
Control	6018	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	gi|124828540,gi|126158903,gi|145566947	55,991.00	100.00%	3	3	3	0.03%	9.25%	SEEETSPLVTHPNPTGPAASTPESK	3.45	2,563.22
Control	6018	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	3	6	24	0.23%	5.51%	ESTLHLVLR	1.66	1,067.62
Control	6018	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	3	6	24	0.23%	5.51%	IQDKEGIPPDQQR	3.95	1,523.78
Control	6018	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	3	6	24	0.23%	5.51%	TITLEVEPSDTIENVK	4.2	1,787.93
Control	6018	TPA: predicted NADPH oxidase-5	gi|151427572,gi|155372001	86,454.40	99.80%	2	3	5	0.05%	3.71%	AIGLQMALDLLAK	3.79	1,372.79
Control	6018	TPA: predicted NADPH oxidase-5	gi|151427572,gi|155372001	86,454.40	99.80%	2	3	5	0.05%	3.71%	MAALHIVEVNLLPSK	4.58	1,650.92

Control	6018	RecName: Full=Small nuclear ribonucleoprotein Sm D1; Short=Sm-D1; AltName: Full=snRNP core protein D1	gi|109894869,gi|73586929,gi|78050059	13,263.90	99.80%	2	4	6	0.06%	27.70%	NREPVQLETLSIR	3.6	1,554.86
Control	6018	RecName: Full=Small nuclear ribonucleoprotein Sm D1; Short=Sm-D1; AltName: Full=snRNP core protein D1	gi|109894869,gi|73586929,gi|78050059	13,263.90	99.80%	2	4	6	0.06%	27.70%	YFILPDSLPLDTLLVDVEPK	4.71	2,287.25
Control	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	23	0.22%	16.10%	AKDIVPGDIVEIAVGDKVPADIR	3.1	2,390.33
Control	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	23	0.22%	16.10%	DIVPGDIVEIAVGDKVPADIR	3.52	2,191.20
Control	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	23	0.22%	16.10%	EEMNLEDSANFIK	3.13	1,555.69

Control	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	23	0.22%	16.10%	EFTLEFSR	1.9	1,028.50
Control	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	23	0.22%	16.10%	ISLPVILMDETLK	3.17	1,487.84
Control	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	23	0.22%	16.10%	KSEIGIAMGSGTAVAK	4.68	1,535.81
Control	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	23	0.22%	16.10%	LDEFGEQLSK	3.07	1,165.57
Control	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	23	0.22%	16.10%	MNVFDTELK	2.92	1,112.53
Control	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	23	0.22%	16.10%	NAENAIEALKEYEPEMGK	3.46	2,051.96

Control	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	23	0.22%	16.10%	NMLFSGTNIAAGK	3.99	1,339.67
Control	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	23	0.22%	16.10%	SEIGIAMGSGTAVAK	5.1	1,407.72
Control	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	23	0.22%	16.10%	TASEMVLADDNFSTIVAAVEEGR	4.32	2,441.15
Control	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	23	0.22%	16.10%	VDQSILTGESVSVIK	4.46	1,574.86
Control	6018	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	100.00%	4	6	6	0.06%	7.75%	DEEDDDEDMYSDNINAATEEK	5.77	2,463.91

Control	6018	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	100.00%	4	6	6	0.06%	7.75%	HSLEGNPRDEEDDDEDMYSDNINAATEEK	6.42	3,354.35
Control	6018	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	100.00%	4	6	6	0.06%	7.75%	IVTLDSLEDTK	2.58	1,233.66
Control	6018	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	100.00%	4	6	6	0.06%	7.75%	NLSLPFIFHEK	2.61	1,344.73
Control	6018	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	100.00%	4	4	5	0.05%	9.80%	FATLYSTQHR	3.2	1,223.62
Control	6018	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	100.00%	4	4	5	0.05%	9.80%	FFYAGTPPAGPAAAHVR	2.11	1,800.92
Control	6018	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	100.00%	4	4	5	0.05%	9.80%	ILEVVNQVQDEER	4.32	1,570.81
Control	6018	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	100.00%	4	4	5	0.05%	9.80%	IPVYSAFR	2.23	952.525
Control	6018	100 kDa coactivator	gi|30523262,gi|45429977,gi|60415927,gi|75517981	101,972.50	99.80%	2	2	2	0.02%	5.71%	DVQIILESCHNQNILGTILHPNGNITELLLKEGFAR	3.16	4,013.13
Control	6018	100 kDa coactivator	gi|30523262,gi|45429977,gi|60415927,gi|75517981	101,972.50	99.80%	2	2	2	0.02%	5.71%	EADGSETPEPFAAEAK	3.76	1,648.73

Control	6018	PREDICTED: similar to karyopherin beta 1 isoform 2	gi|76644624	97,210.30	100.00%	3	3	3	0.03%	5.25%	AAVENLPTFLVELSR	4.26	1,658.91
Control	6018	PREDICTED: similar to karyopherin beta 1 isoform 2	gi|76644624	97,210.30	100.00%	3	3	3	0.03%	5.25%	LAATNALLNSLEFTK	4.12	1,605.88
Control	6018	PREDICTED: similar to karyopherin beta 1 isoform 2	gi|76644624	97,210.30	100.00%	3	3	3	0.03%	5.25%	LLETTDRPDGHQNNLR	1.63	1,878.94
Control	6018	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	100.00%	4	5	5	0.05%	12.80%	DRQYLLFFHK	3.51	1,366.73
Control	6018	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	100.00%	4	5	5	0.05%	12.80%	LEDLKEQLAPLEK	4.57	1,525.85
Control	6018	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	100.00%	4	5	5	0.05%	12.80%	LRDPLQVHLPLR	3.48	1,456.87
Control	6018	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	100.00%	4	5	5	0.05%	12.80%	VAIYSPDGVR	2.57	1,076.57
Control	6018	sorting and assembly machinery component 50 homolog	gi|114051051,gi|87578317,gi|95769210	52,025.30	99.90%	2	2	3	0.03%	5.33%	ETSYGLSFFKPQPGNFDR	3.58	2,090.00
Control	6018	sorting and assembly machinery component 50 homolog	gi|114051051,gi|87578317,gi|95769210	52,025.30	99.90%	2	2	3	0.03%	5.33%	LPNLLGR	1.98	782.4884

Control	6018	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	6	0.06%	7.79%	FADIVSILDK	3.39	1,120.63
Control	6018	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	6	0.06%	7.79%	IAYSLLGLK	2.14	977.6031
Control	6018	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	6	0.06%	7.79%	IDTIAPDEITGSSDFEAR	3.85	1,936.91
Control	6018	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	6	0.06%	7.79%	TYVDPHTYEDPNQAVLK	2.57	1,989.96
Control	6018	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	6	0.06%	7.79%	VIGAGEFGEVYK	3.19	1,268.65
Control	6018	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	6	0.06%	7.79%	YSEPPLGLTR	2.45	1,132.60
Control	6018	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	4	5	9	0.09%	19.10%	FYGPEGPYGVFAGR	3.46	1,516.72
Control	6018	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	4	5	9	0.09%	19.10%	GDQPAASDSDDDEPPPLPR	3.89	1,978.86
Control	6018	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	4	5	9	0.09%	19.10%	IVRGDQPAASDSDDDEPPPLPR	5.6	2,347.12
Control	6018	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	4	5	9	0.09%	19.10%	KFYGPEGPYGVFAGR	4.91	1,644.82
Control	6018	similar to ribosomal protein L27	gi|28189717,gi|47117099,gi|74268027,gi|77404275	15,780.40	100.00%	3	3	3	0.03%	30.10%	NIDDGTSDRPYSHALVAGIDR	3.71	2,272.10

Control	6018	similar to ribosomal protein L27	gi|28189717,gi|47117099,gi|74268027,gi|77404275	15,780.40	100.00%	3	3	3	0.03%	30.10%	VYNYNHLMPTR	1.65	1,423.68
Control	6018	similar to ribosomal protein L27	gi|28189717,gi|47117099,gi|74268027,gi|77404275	15,780.40	100.00%	3	3	3	0.03%	30.10%	YSVDIPLDK	2.73	1,049.55
Control	6018	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.07%	14.70%	GVMLAVDAVIAELKK	2.48	1,572.90
Control	6018	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.07%	14.70%	IMQSSSEVGYDAMLGDFVNMVEK	3.22	2,566.15
Control	6018	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.07%	14.70%	ISSVQSIVPALEIANAHR	3.83	1,905.06
Control	6018	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.07%	14.70%	LVQDVANNTNEEAGDGTTTATVLAR	6.25	2,560.25
Control	6018	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.07%	14.70%	TLNDELEIIEGMK	2.21	1,504.76
Control	6018	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.07%	14.70%	VGLQVVAVK	2.94	912.5877
Control	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	10	14	24	0.23%	45.30%	DILLRPELEELRNEHSAR	1.91	2,190.16
Control	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	10	14	24	0.23%	45.30%	FALPSPEHILGLPVGQHIYLSAR	5.03	2,515.38

Control	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	10	14	24	0.23%	45.30%	GPNGLLVYQGK	3.99	1,145.63
Control	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	10	14	24	0.23%	45.30%	IDGNLVIRPYTPVSSDDDKGFVDLVIK	4.54	2,975.57
Control	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	10	14	24	0.23%	45.30%	IGDTIEFR	2.74	950.4943
Control	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	10	14	24	0.23%	45.30%	LIDKEVISHDTR	3.4	1,425.77
Control	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	10	14	24	0.23%	45.30%	LIDKEVISHDTRR	2.47	1,581.87
Control	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	10	14	24	0.23%	45.30%	STPAITLENPDIK	3.26	1,398.75
Control	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	10	14	24	0.23%	45.30%	STPAITLENPDIKYPLR	4.94	1,928.05
Control	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	10	14	24	0.23%	45.30%	SVGMIAGGTGITPMLQVIR	6.31	1,917.03
Control	6018	endothelial cell adhesion molecule	gi|118151218,gi|119919027,gi|86823868	41,779.80	100.00%	3	4	5	0.05%	14.90%	ALEEPANDIKEDAIAPR	4.53	1,851.94
Control	6018	endothelial cell adhesion molecule	gi|118151218,gi|119919027,gi|86823868	41,779.80	100.00%	3	4	5	0.05%	14.90%	LGALTPTPSLSSQVLPSPR	2.91	1,921.08
Control	6018	endothelial cell adhesion molecule	gi|118151218,gi|119919027,gi|86823868	41,779.80	100.00%	3	4	5	0.05%	14.90%	SPPSSQVFFAPVLDAIHGSLSLK	3.69	2,397.28
Control	6018	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	7	7	7	0.07%	2.87%	FAPGDFQGFALVNPQR	2.6	1,763.89
Control	6018	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	7	7	7	0.07%	2.87%	GTLEPVQRPDVVLVGAGHR	3.72	2,000.10
Control	6018	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	7	7	7	0.07%	2.87%	IPGDQVVSVVFIK	4.06	1,400.81

Control	6018	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	7	7	7	0.07%	2.87%	IQVVVLPGATTPPVR	3.58	1,546.93
Control	6018	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	7	7	7	0.07%	2.87%	LDVEFKPLAPDGVLLFSGGK	4.43	2,102.15
Control	6018	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	7	7	7	0.07%	2.87%	LRSPVISIDPPSSTVQQGQDASFK	4.88	2,557.33
Control	6018	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	7	7	7	0.07%	2.87%	VVPYFTQTPYSFLPLPTIK	3.43	2,211.21
Control	6018	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	7	7	9	0.09%	15.90%	ALEEANADLEVK	3.24	1,301.66
Control	6018	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	7	7	9	0.09%	15.90%	ASLENSLEETKGR	3.17	1,433.72
Control	6018	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	7	7	9	0.09%	15.90%	LASYLDKVR	2.97	1,064.61
Control	6018	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	7	7	9	0.09%	15.90%	LEQEIATYR	3.56	1,122.58
Control	6018	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	7	7	9	0.09%	15.90%	LLEGEDAHLSSSQFSSGSQSSR	3.44	2,309.06
Control	6018	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	7	7	9	0.09%	15.90%	TRLEQEIATYR	3.68	1,379.73
Control	6018	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	7	7	9	0.09%	15.90%	VLDELTLAR	3.32	1,029.59
Control	6018	PTBP1 protein	gi|158454983	47,010.90	100.00%	3	3	3	0.03%	13.70%	IIVENLFYPVTLDVLHQIFSK	3.89	2,488.39
Control	6018	PTBP1 protein	gi|158454983	47,010.90	100.00%	3	3	3	0.03%	13.70%	KLPGDVTEGEVISLGLPFGK	3.08	2,056.13

Control	6018	PTBP1 protein	gi|158454983	47,010.90	100.00%	3	3	3	0.03%	13.70%	NNQFQALLQYADPVSAQHAK	3.65	2,243.12
Control	6018	Transmembrane protein 49	gi|111307060,gi|115496266,gi|122133514	46,165.40	100.00%	3	3	5	0.05%	13.50%	EQYNGNFTDPSSVNEK	4.08	1,828.80
Control	6018	Transmembrane protein 49	gi|111307060,gi|115496266,gi|122133514	46,165.40	100.00%	3	3	5	0.05%	13.50%	LAVQNLVQK	2.45	1,012.62
Control	6018	Transmembrane protein 49	gi|111307060,gi|115496266,gi|122133514	46,165.40	100.00%	3	3	5	0.05%	13.50%	LSGAEPDDEEYQEFEEMLEHAETAQDFASR	5.12	3,489.46
Control	6018	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	3	4	23	0.22%	5.32%	LRSEIDNVKK	3.35	1,201.69
Control	6018	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	3	4	23	0.22%	5.32%	NKYEDEINKR	3.12	1,308.65
Control	6018	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	3	4	23	0.22%	5.32%	SLDLDSIIAEVK	4.57	1,302.72
Control	6018	MHC class I antigen	gi|72536919	40,523.80	99.80%	2	3	12	0.12%	20.90%	GFMQFGYDGR	3.46	1,193.50
Control	6018	MHC class I antigen	gi|72536919	40,523.80	99.80%	2	3	12	0.12%	20.90%	NGEDQTQDMELVETRPSGDGTFQK	3.76	2,698.19
Control	6018	MHC class I antigen	gi|72536919	40,523.80	99.80%	2	3	12	0.12%	20.90%	SWTAADTAAQITK	4.35	1,363.69
Control	6018	MHC class I antigen	gi|72536919	40,523.80	99.80%	2	3	12	0.12%	20.90%	VQHEGLQEPLTLR	4.05	1,519.82
Control	6018	MHC class I antigen	gi|72536919	40,523.80	99.80%	2	3	12	0.12%	20.90%	YFSTAVSRPGLGEPR	2.42	1,636.84
Control	6018	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	5	5	6	0.06%	8.60%	ALVQTEDHLLLFLQQLAGR	3.38	2,165.21
Control	6018	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	5	5	6	0.06%	8.60%	HLLVGLPSGAILSLPK	4.29	1,614.99
Control	6018	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	5	5	6	0.06%	8.60%	NFPQAALVSFATTGEK	4.77	1,680.86
Control	6018	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	5	5	6	0.06%	8.60%	QLHELAPSIFFYLVDADQGR	3.38	2,319.18

Control	6018	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	5	5	6	0.06%	8.60%	RPVLQSLLLPIMDQDYAK	3.2	2,116.15
Control	6018	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	99.80%	2	2	3	0.03%	9.35%	AQIQEQNPSIEVVYYNK	5.29	2,023.01
Control	6018	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	99.80%	2	2	3	0.03%	9.35%	NLLLSGAQLEASR	4.23	1,371.76
Control	6018	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	100.00%	3	4	7	0.07%	11.10%	LNQAVEFDVLPAFDALGQLTK	5.22	2,289.21
Control	6018	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	100.00%	3	4	7	0.07%	11.10%	PVILDPADPTGNVAGK	3.84	1,563.84
Control	6018	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	100.00%	3	4	7	0.07%	11.10%	QLAKPRPVILDPADPTGNVAGK	2.64	2,257.27
Control	6018	KIAA1715	gi|111304578,gi|115496264	48,163.90	99.90%	2	2	2	0.02%	6.06%	IVEYLVGDGPQNR	2.68	1,459.75
Control	6018	KIAA1715	gi|111304578,gi|115496264	48,163.90	99.90%	2	2	2	0.02%	6.06%	TVTPALSSNVLPR	2.98	1,354.77
Control	6018	RecName: Full=Chloride intracellular channel protein 4; AltName: Full=Intracellular chloride ion channel protein p64H1	gi|109877271,gi|122692293,gi|73587123	28,710.60	99.80%	2	3	3	0.03%	14.20%	HPESNTAGMDIFAK	2.62	1,533.70

Control	6018	RecName: Full=Chloride intracellular channel protein 4; AltName: Full=Intracellular chloride ion channel protein p64H1	gi|109877271,gi|122692293,gi|73587123	28,710.60	99.80%	2	3	3	0.03%	14.20%	LDEYLNSPLPDEIDENSMEDIK	3.44	2,595.17
Control	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	12	18	66	0.64%	38.90%	AVFPSIVGRPR	2.87	1,198.71
Control	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	12	18	66	0.64%	38.90%	DLTDYLMK	2.07	1,014.48
Control	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	12	18	66	0.64%	38.90%	DLYANTVLSGGTTMYPGIADR	5.35	2,231.07
Control	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	12	18	66	0.64%	38.90%	EITALAPSTMK	2.81	1,161.62
Control	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	12	18	66	0.64%	38.90%	GYSFTTTAER	3.39	1,132.53
Control	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	12	18	66	0.64%	38.90%	KDLYANTVLSGGTTMYPGIADR	5.27	2,359.16
Control	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	12	18	66	0.64%	38.90%	LDLAGRDLTDYLMK	2.18	1,639.84
Control	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	12	18	66	0.64%	38.90%	QEYDESGPSIVHR	3.47	1,516.70
Control	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	12	18	66	0.64%	38.90%	QEYDESGPSIVHRK	2.76	1,644.80
Control	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	12	18	66	0.64%	38.90%	SYELPDGQVITIGNER	3.46	1,790.89
Control	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	12	18	66	0.64%	38.90%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	6.85	3,199.61
Control	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	12	18	66	0.64%	38.90%	VAPEEHPVLLTEAPLNPK	4.73	1,954.06

Control	6018	RecName: Full=Peptidyl-tRNA hydrolase 2, mitochondrial; Short=PTH 2; AltName: Full=Bcl-2 inhibitor of transcription; Flags: Precursor	gi|109892883,gi|116292141,gi|60650282,gi|73587109,gi|77735985	19,272.70	99.80%	2	2	2	0.02%	16.20%	APDEETLVELLTHAK	4.41	1,665.87
Control	6018	RecName: Full=Peptidyl-tRNA hydrolase 2, mitochondrial; Short=PTH 2; AltName: Full=Bcl-2 inhibitor of transcription; Flags: Precursor	gi|109892883,gi|116292141,gi|60650282,gi|73587109,gi|77735985	19,272.70	99.80%	2	2	2	0.02%	16.20%	VLGLTVSLIQDAGR	4.25	1,441.84
Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	DLFSEAHSEFLK	4.43	1,422.69
Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	EATNPPVIQEEKPK	3.48	1,579.83
Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	ELSDFISYLK	2.13	1,214.63
Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	ELSDFISYLKR	2.66	1,370.73
Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	FLEDYFDGNLK	2.92	1,360.64
Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	FLEDYFDGNLKR	3.11	1,516.74
Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	FVMQEEFSR	3.2	1,188.54
Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	GFPTIYFSPANKK	2.43	1,469.78

Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	IFRDGEESGAYDGPR	4.32	1,668.76
Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	KTFSHELSDFGLESTTGEIPVVAVR	3.48	2,719.39
Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	LRKDPNIVIAK	3.08	1,266.79
Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	MDATANDVPSPYEVR	4.4	1,680.75
Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	QAGPASVPLKSEEEFEK	2.78	1,845.92
Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	SEPIPESNDGPVK	2.44	1,368.66
Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	TADGIVSHLK	2.64	1,040.57
Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	TADGIVSHLKK	2.13	1,168.67
Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	TFSHELSDFGLESTTGEIPVVAVR	3.85	2,591.30
Control	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	18	21	32	0.31%	37.20%	YGVSGYPTLK	3.07	1,084.57
Control	6018	MCAM protein	gi|158455045,gi|158519851	48,983.20	100.00%	2	3	5	0.05%	4.55%	EMEEERTDDNGVLVLDPAQK	4.53	2,304.07
Control	6018	MCAM protein	gi|158455045,gi|158519851	48,983.20	100.00%	2	3	5	0.05%	4.55%	TDDNGVLVLDPAQK	2.81	1,484.76
Control	6018	PECAM1 protein	gi|111308531	82,597.50	100.00%	5	7	22	0.21%	6.37%	APVHFTIEK	2.42	1,041.57
Control	6018	PECAM1 protein	gi|111308531	82,597.50	100.00%	5	7	22	0.21%	6.37%	FHIIPEGK	2.86	940.5252
Control	6018	PECAM1 protein	gi|111308531	82,597.50	100.00%	5	7	22	0.21%	6.37%	GTETVYSEIR	2.63	1,154.57
Control	6018	PECAM1 protein	gi|111308531	82,597.50	100.00%	5	7	22	0.21%	6.37%	PAVPLLNSNNEK	2.39	1,295.70
Control	6018	PECAM1 protein	gi|111308531	82,597.50	100.00%	5	7	22	0.21%	6.37%	QMPVEMSRPAVPLLNSNNEK	2.96	2,270.13
Control	6018	RecName: Full=FAS-associated factor 2; AltName: Full=UBX domain-containing protein 8	gi|109896151,gi|116004259,gi|88683021	52,646.60	100.00%	2	2	2	0.02%	4.72%	FQIEANFPR	2.74	1,121.57

Control	6018	RecName: Full=FAS-associated factor 2; AltName: Full=UBX domain-containing protein 8	gi|109896151,gi|116004259,gi|88683021	52,646.60	100.00%	2	2	2	0.02%	4.72%	QQQDEAYLASLR	3.39	1,421.70
Control	6018	RecName: Full=40S ribosomal protein S16	gi|108860953,gi|74354274,gi|75812950	16,427.90	99.90%	2	2	2	0.02%	15.10%	EIKDILIQYDR	3.2	1,405.77
Control	6018	RecName: Full=40S ribosomal protein S16	gi|108860953,gi|74354274,gi|75812950	16,427.90	99.90%	2	2	2	0.02%	15.10%	GPLQSVQVFGR	3.42	1,187.65
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	DGQVINETSQHHDDLE	3.71	1,836.80
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	DNLAEDIMR	2.56	1,092.50
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	EEAESTLQSFR	2.78	1,296.61
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	EEAESTLQSFRQDVDNASLAR	4.03	2,366.12
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	EKLQEEMLQREEAESTLQSFR	5.58	2,597.25
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	EMEENFSVEAANYQDTIGR	4.54	2,202.96
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	ETNLDSLPLVDTHSK	4.58	1,668.84
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	ETNLDSLPLVDTHSKR	3.39	1,824.95
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	EYQDLLNVK	2.25	1,121.58
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	FADLSEAANR	4.55	1,093.53
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	FADLSEAANRNNDALR	2.63	1,776.86
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	FANYIDKVR	2.86	1,125.61
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	ILLAELEQLK	4.39	1,169.71
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	ILLAELEQLKGQGK	2.07	1,539.91
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	ISLPLPNFSSLNLR	5.21	1,570.90

Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	KLHDEEIQELQAQIQEQHVQIDMDVSKPDLTAALR	6.68	4,085.06
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	KVESLQEEIAFLK	5.23	1,533.85
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	KVESLQEEIAFLKK	4.49	1,661.95
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	LHDEEIQELQAQIQEQHVQIDMDVSKPDLTAALR	5.43	3,956.97
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	LLQDSVDFSLADAINTEFK	4.92	2,126.07
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	LQDEIQNMKEEMAR	3.84	1,750.81
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	LQEEMLQREEAESTLQSFR	4.78	2,340.11
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	LQEEMLQREEAESTLQSFRQDVDNASLAR	3.86	3,393.63
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	MALDIEIATYR	4.64	1,311.66
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	NLQEAEEWYK	3.09	1,309.61
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	RMFGGPGTASRPSSTR	1.9	1,680.82
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	TLYTSSPGGVYATR	4.25	1,472.74
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	TNEKVELQELNDR	4.83	1,587.80
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	TNEKVELQELNDRFANYIDK	3.76	2,439.22
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	TVETRDGQVINETSQHHDLE	4.27	2,423.11
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	VELQELNDR	3.18	1,115.57
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	VESLQEEIAFLK	3.73	1,405.76
Control	6018	vimentin	gi|110347570	53,710.80	100.00%	33	47	126	1.23%	66.10%	VEVERDNLAEDIMR	4.22	1,688.83

Control	6018	PREDICTED: similar to Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) (GDI-1) isoform 1	gi|119938319,gi|121107,gi|28603774,gi|714,gi|7245833,gi|73587159	23,403.80	99.80%	2	2	2	0.02%	16.20%	SIQEIQELDKDDESLRK	2.99	2,046.04
Control	6018	PREDICTED: similar to Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) (GDI-1) isoform 1	gi|119938319,gi|121107,gi|28603774,gi|714,gi|7245833,gi|73587159	23,403.80	99.80%	2	2	2	0.02%	16.20%	VAVSADPNVPNVVVTR	4.38	1,636.90
Control	6018	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	7	9	16	0.16%	22.20%	DKLDGNELDLSLSDLNEVPVK	6.79	2,313.18
Control	6018	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	7	9	16	0.16%	22.20%	DKLDGNELDLSLSDLNEVPVKELAALPK	5.92	3,035.62
Control	6018	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	7	9	16	0.16%	22.20%	LDGNELDLSLSDLNEVPVK	4.77	2,070.06
Control	6018	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	7	9	16	0.16%	22.20%	LDGNELDLSLSDLNEVPVKELAALPK	3.35	2,792.49
Control	6018	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	7	9	16	0.16%	22.20%	LVNLQHLDLLNNR	3.27	1,561.88
Control	6018	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	7	9	16	0.16%	22.20%	LVTLPVSFAQLK	3.35	1,315.80
Control	6018	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	7	9	16	0.16%	22.20%	WLDLKDNPLDPVLAK	3.28	1,736.96

Control	6018	RecName: Full=CDGSH iron sulfur domain-containing protein 1; AltName: Full=MitoNEET	gi|110825757,gi|73587067,gi|77404223	11,964.80	99.80%	2	3	5	0.05%	26.40%	HNEETGDNVGPLIIK	4.99	1,635.83
Control	6018	RecName: Full=CDGSH iron sulfur domain-containing protein 1; AltName: Full=MitoNEET	gi|110825757,gi|73587067,gi|77404223	11,964.80	99.80%	2	3	5	0.05%	26.40%	VVHAFDMEDLGDK	3.78	1,491.68
Control	6018	17,000 dalton myosin light chain	gi|578,gi|74268209	16,942.80	99.80%	2	2	2	0.02%	19.20%	ALGQNPTNAEVLK	2.88	1,354.73
Control	6018	17,000 dalton myosin light chain	gi|578,gi|74268209	16,942.80	99.80%	2	2	2	0.02%	19.20%	VLDFEHFLPMLQTVAK	2.77	1,904.00
Control	6018	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	7	7	9	0.09%	14.70%	DAGQISGLNVLR	2.75	1,242.68

Control	6018	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	7	7	9	0.09%	14.70%	ETGVDLTKDNMALQR	2.47	1,706.84
Control	6018	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	7	7	9	0.09%	14.70%	MKETAENYLGHTAK	3.62	1,608.77

Control	6018	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	7	7	9	0.09%	14.70%	NAVITVPAYFNDSQR	2.46	1,694.85
Control	6018	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	7	7	9	0.09%	14.70%	QAVTNPNNTFYATK	3.7	1,568.77

Control	6018	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	7	7	9	0.09%	14.70%	STNGDTFLGGEDFDQALLR	4.33	2,055.96
Control	6018	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	7	7	9	0.09%	14.70%	VQQTVQDLFGR	3.27	1,290.68
Control	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	10	11	0.11%	42.70%	AVFPSIVGRPR	2.87	1,198.71
Control	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	10	11	0.11%	42.70%	DLTDYLMK	2.07	1,014.48
Control	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	10	11	0.11%	42.70%	DLYANNVLSGGTTMYPGIADR	5	2,244.06
Control	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	10	11	0.11%	42.70%	EITALAPSTMK	2.81	1,161.62

Control	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	10	11	0.11%	42.70%	GYSFVTTAER	3.36	1,130.55
Control	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	10	11	0.11%	42.70%	KDLYANNVLSGGTTMYPGIADR	4.88	2,372.16
Control	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	10	11	0.11%	42.70%	LDLAGRDLTDYLMK	2.18	1,639.84
Control	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	10	11	0.11%	42.70%	QEYDEAGPSIVHR	2.57	1,500.71
Control	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	10	11	0.11%	42.70%	SYELPDGQVITIGNER	3.46	1,790.89
Control	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	10	11	0.11%	42.70%	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	5.82	3,212.60
Control	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	10	11	0.11%	42.70%	VAPEEHPTLLTEAPLNPK	4.23	1,956.04
Control	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	10	11	0.11%	42.70%	YPIEHGIITNWDDMEK	3.43	1,976.91
Control	6018	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	5	7	11	0.11%	38.60%	GAAGALMVYDITR	3.87	1,353.68
Control	6018	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	5	7	11	0.11%	38.60%	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	4.4	3,150.56
Control	6018	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	5	7	11	0.11%	38.60%	LQIWDTAGQER	2.62	1,316.66
Control	6018	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	5	7	11	0.11%	38.60%	NLTNPNTVIILIGNK	4.71	1,623.94
Control	6018	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	5	7	11	0.11%	38.60%	TGENVEDAFLEAAK	2.98	1,493.71
Control	6018	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	5	6	8	0.08%	34.40%	EHGLIFMETSAK	3.17	1,378.67
Control	6018	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	5	6	8	0.08%	34.40%	FQPVHDLTIGVEFGAR	5.19	1,785.93
Control	6018	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	5	6	8	0.08%	34.40%	GAAGALLVYDITR	3.63	1,319.73

Control	6018	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	5	6	8	0.08%	34.40%	LQIWDTAGQESFR	4.48	1,550.76
Control	6018	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	5	6	8	0.08%	34.40%	YIIIGDTGVGK	3.06	1,135.64
Control	6018	RecName: Full=Phosphoglycerate kinase 1	gi|108860885,gi|74353972,gi|77735551	44,520.20	99.80%	2	2	2	0.02%	8.39%	VDFNVPMKNNQITNNQR	4.16	2,048.00
Control	6018	RecName: Full=Phosphoglycerate kinase 1	gi|108860885,gi|74353972,gi|77735551	44,520.20	99.80%	2	2	2	0.02%	8.39%	VLNNMEIGTSLFDEEGSK	3.97	1,998.93
Control	6018	Chain R, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Reduced State	gi|149241523,gi|149241540,gi|149241553,gi|149241570,gi|149241583,gi|149241600,gi|149241613,gi|42564216,gi|50872151,gi|60391934,gi|81674705	16,717.40	100.00%	4	5	13	0.13%	36.20%	EIYPYVIQELRPTLNELGISTPEELGLDKV	5.59	3,428.82
Control	6018	Chain R, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Reduced State	gi|149241523,gi|149241540,gi|149241553,gi|149241570,gi|149241583,gi|149241600,gi|149241613,gi|42564216,gi|50872151,gi|60391934,gi|81674705	16,717.40	100.00%	4	5	13	0.13%	36.20%	GMNTLVGYDLVPEPK	3.81	1,648.83
Control	6018	Chain R, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Reduced State	gi|149241523,gi|149241540,gi|149241553,gi|149241570,gi|149241583,gi|149241600,gi|149241613,gi|42564216,gi|50872151,gi|60391934,gi|81674705	16,717.40	100.00%	4	5	13	0.13%	36.20%	LNDFASAVR	3.06	992.5159

Control	6018	Chain R, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Reduced State	gi|149241523,gi|149241540,gi|149241553,gi|149241570,gi|149241583,gi|149241600,gi|149241613,gi|42564216,gi|50872151,gi|60391934,gi|81674705	16,717.40	100.00%	4	5	13	0.13%	36.20%	RLNDFASAVR	3.08	1,148.62
Control	6018	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	5	5	5	0.05%	14.80%	GTVGFSGAELENLVNQAALK	3.5	2,018.06
Control	6018	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	5	5	5	0.05%	14.80%	GVEEAKQELQEVVEFLK	4.02	1,975.04
Control	6018	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	5	5	5	0.05%	14.80%	IKFDQSVDPEIIAR	3.13	1,630.88
Control	6018	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	5	5	5	0.05%	14.80%	QTINQLLAEMDGFKPNEGVIIIGATNFPEALDNALIRPGR	2.88	4,352.27
Control	6018	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	5	5	5	0.05%	14.80%	TTTGLDSAVDPVQMK	4.03	1,578.77
Control	6018	RecName: Full=Vesicle-associated membrane protein 8; Short=VAMP-8	gi|122140420,gi|74353894,gi|77735533	11,339.40	99.80%	2	2	4	0.04%	14.00%	NKTEDLEATSEHFK	4.76	1,648.78
Control	6018	RecName: Full=Vesicle-associated membrane protein 8; Short=VAMP-8	gi|122140420,gi|74353894,gi|77735533	11,339.40	99.80%	2	2	4	0.04%	14.00%	TEDLEATSEHFK	2.82	1,406.64

Control	6018	RecName: Full=Annexin A1; AltName: Full=Annexin-1; AltName: Full=Annexin I; AltName: Full=Lipocortin I; AltName: Full=Calpactin II; AltName: Full=Chromobindin-9; AltName: Full=p35; AltName: Full=Phospholipase A2	gi|118597373,gi|264182,gi|61553085,gi|73587269,gi|73853762,gi|74	38,881.20	99.80%	2	2	2	0.02%	12.40%	GDRSEELAVNDDLADSDAR	4.84	2,047.92
Control	6018	RecName: Full=Annexin A1; AltName: Full=Annexin-1; AltName: Full=Annexin I; AltName: Full=Lipocortin I; AltName: Full=Calpactin II; AltName: Full=Chromobindin-9; AltName: Full=p35; AltName: Full=Phospholipase A2	gi|118597373,gi|264182,gi|61553085,gi|73587269,gi|73853762,gi|74	38,881.20	99.80%	2	2	2	0.02%	12.40%	GGPGSAVSPYPTFNPSSDVEALHK	3.55	2,414.16
Control	6018	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	7	7	0.07%	12.10%	IPQAVVDVSSHLQK	2.35	1,520.84
Control	6018	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	7	7	0.07%	12.10%	LELPLIMLSGLPDTVFEITELQSLK	4.28	2,815.54
Control	6018	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	7	7	0.07%	12.10%	NLEELYLVGSLSHDISR	2.9	1,945.00
Control	6018	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	7	7	0.07%	12.10%	QETGIDDIPDVK	3.05	1,329.65
Control	6018	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	7	7	0.07%	12.10%	SNTTQSGPEGSLVNSQSLK	4.92	1,933.95

Control	6018	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	7	7	0.07%	12.10%	YLDLSYNDIR	2.62	1,271.63
Control	6018	PREDICTED: similar to MYB binding protein 1a	gi|119911777	151,796.60	99.80%	2	2	2	0.02%	1.92%	DLAALELLNTLFR	2.76	1,488.84
Control	6018	PREDICTED: similar to MYB binding protein 1a	gi|119911777	151,796.60	99.80%	2	2	2	0.02%	1.92%	NVAPLTAFTTQQR	3.56	1,446.77
Control	6018	RecName: Full=Transitional endoplasmic reticulum ATPase; Short=TER ATPase; AltName: Full=15S Mg(2+)-ATPase p97 subunit; AltName: Full=Valosin-containing protein; Short=VCP	gi|122140828,gi|73586667,gi|77735541	89,314.70	100.00%	3	3	3	0.03%	5.21%	GILLYGPPGTGK	2.66	1,172.67
Control	6018	RecName: Full=Transitional endoplasmic reticulum ATPase; Short=TER ATPase; AltName: Full=15S Mg(2+)-ATPase p97 subunit; AltName: Full=Valosin-containing protein; Short=VCP	gi|122140828,gi|73586667,gi|77735541	89,314.70	100.00%	3	3	3	0.03%	5.21%	LDQLIYIPLPDEK	3.03	1,556.86

Control	6018	RecName: Full=Transitional endoplasmic reticulum ATPase; Short=TER ATPase; AltName: Full=15S Mg(2+)-ATPase p97 subunit; AltName: Full=Valosin-containing protein; Short=VCP	gi|122140828,gi|73586667,gi|77735541	89,314.70	100.00%	3	3	3	0.03%	5.21%	NAPAIIFIDELDAIAPK	2.98	1,811.00
Control	6018	PREDICTED: similar to Thioredoxin domain-containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein ERp46) isoform 1	gi|119915902	45,792.10	99.80%	2	2	4	0.04%	4.55%	FFKPGQEAVK	2.38	1,150.63
Control	6018	PREDICTED: similar to Thioredoxin domain-containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein ERp46) isoform 1	gi|119915902	45,792.10	99.80%	2	2	4	0.04%	4.55%	GYPTLLLFR	2.43	1,079.62

Control	6018	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	4	5	20	0.20%	25.60%	FFDEESYSLLR	3.64	1,405.66
Control	6018	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	4	5	20	0.20%	25.60%	FFDEESYSLLRK	2.63	1,533.76

Control	6018	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	4	5	20	0.20%	25.60%	NNEDVSVIPPLFTVSVDHR	4.16	2,138.09
Control	6018	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	4	5	20	0.20%	25.60%	VQNMALYADVSGK	4.79	1,411.69

Control	6018	RecName: Full=Serine hydroxymethyltransferase, mitochondrial; Short=SHMT; Short=Serine methylase; AltName: Full=Glycine hydroxymethyltransferase; Flags: Precursor	gi|108935997,gi|74268173,gi|77735519	55,589.20	100.00%	3	3	3	0.03%	7.74%	LIIAGTSAYAR	3.29	1,135.65
Control	6018	RecName: Full=Serine hydroxymethyltransferase, mitochondrial; Short=SHMT; Short=Serine methylase; AltName: Full=Glycine hydroxymethyltransferase; Flags: Precursor	gi|108935997,gi|74268173,gi|77735519	55,589.20	100.00%	3	3	3	0.03%	7.74%	SFLLKDPETSHQLADLR	2.38	1,970.03

Control	6018	RecName: Full=Serine hydroxymethyltransferase, mitochondrial; Short=SHMT; Short=Serine methylase; AltName: Full=Glycine hydroxymethyltransferase; Flags: Precursor	gi|108935997,gi|74268173,gi|77735519	55,589.20	100.00%	3	3	3	0.03%	7.74%	VLELVSITANK	3.42	1,186.70
Control	6018	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	8	9	10	0.10%	20.90%	ASPAPGSGHPDGPGTHLEMNSLDR	2.59	2,416.10
Control	6018	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	8	9	10	0.10%	20.90%	LDNKKECLEDVTAVCILEGFQNQQSMLLADK	4.31	3,511.71
Control	6018	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	8	9	10	0.10%	20.90%	LRPESALAQAQK	3.18	1,311.74
Control	6018	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	8	9	10	0.10%	20.90%	NVDLSTFYQNR	4.2	1,356.65

Control	6018	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	8	9	10	0.10%	20.90%	SDEDKDKEGEALEVK	3.89	1,691.80
Control	6018	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	8	9	10	0.10%	20.90%	SYFSSFTDDIISQPMLK	2.45	1,994.94
Control	6018	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	8	9	10	0.10%	20.90%	YGLKPPTL	2.2	888.5191
Control	6018	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	8	9	10	0.10%	20.90%	YMAEALLLR	2.37	1,095.59
Control	6018	RecName: Full=Probable saccharopine dehydrogenase	gi|122140337,gi|74354153,gi|77735529	47,302.40	99.80%	2	2	2	0.02%	9.09%	GVYIIGSSGFDSIPADLGVIYTR	3.21	2,400.24
Control	6018	RecName: Full=Probable saccharopine dehydrogenase	gi|122140337,gi|74354153,gi|77735529	47,302.40	99.80%	2	2	2	0.02%	9.09%	LRNESDMKPVPIVGPK	3	1,795.97
Control	6018	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	4	4	9	0.09%	7.62%	IPLNDIFR	2.92	987.5623

Control	6018	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	4	4	9	0.09%	7.62%	VALKIPLNDIFR	3.46	1,398.85
Control	6018	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	4	4	9	0.09%	7.62%	VQPFSVTEGK	1.97	1,091.57
Control	6018	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	4	4	9	0.09%	7.62%	YLDFVFAVK	2.6	1,101.60
Control	6018	RPL13 protein-like	gi|58760388,gi|62751646,gi|74267768,gi|75060396	33,783.70	99.90%	2	2	2	0.02%	7.82%	LATQLTGPVMPIR	3.19	1,412.79
Control	6018	RPL13 protein-like	gi|58760388,gi|62751646,gi|74267768,gi|75060396	33,783.70	99.90%	2	2	2	0.02%	7.82%	VITEEEKNFK	3.07	1,236.65
Control	6018	syndecan binding protein (syntenin)	gi|115497576,gi|146231800,gi|74267862	32,372.10	99.80%	2	2	2	0.02%	17.80%	DSQIADILSTAGNIVTITIMPAFIFEHIIK	4.16	3,287.76
Control	6018	syndecan binding protein (syntenin)	gi|115497576,gi|146231800,gi|74267862	32,372.10	99.80%	2	2	2	0.02%	17.80%	SIDNGIFVQLVQANSPSSLVGLR	3.61	2,414.30
Control	6018	Nicastrin	gi|74267600,gi|77735901	79,055.00	99.80%	2	2	3	0.03%	2.65%	ALAGVATVLAR	3.22	1,041.64
Control	6018	Nicastrin	gi|74267600,gi|77735901	79,055.00	99.80%	2	2	3	0.03%	2.65%	LLYGFLVR	2.54	980.5928
Control	6018	ribosomal protein S13-like	gi|58760415,gi|70778778,gi|74267772,gi|75060393	17,205.30	99.90%	2	2	2	0.02%	16.60%	KGLTPSQIGVILR	3.94	1,381.85
Control	6018	ribosomal protein S13-like	gi|58760415,gi|70778778,gi|74267772,gi|75060393	17,205.30	99.90%	2	2	2	0.02%	16.60%	LTSDDVKEQIYK	3.91	1,438.74

Control	6018	RecName: Full=ATP synthase subunit O, mitochondrial; AltName: Full=Oligomycin sensitivity conferral protein; Short=OSCP; Flags: Precursor	gi|143811365,gi|157881386,gi|159164706,gi|163451,gi|27806307,gi|28189911,gi|74268299	23,332.20	100.00%	3	4	6	0.06%	19.70%	FSPLTSNLINLLAENGR	3.69	1,859.00
Control	6018	RecName: Full=ATP synthase subunit O, mitochondrial; AltName: Full=Oligomycin sensitivity conferral protein; Short=OSCP; Flags: Precursor	gi|143811365,gi|157881386,gi|159164706,gi|163451,gi|27806307,gi|28189911,gi|74268299	23,332.20	100.00%	3	4	6	0.06%	19.70%	LVRPPVQIYGIEGR	3.85	1,596.92
Control	6018	RecName: Full=ATP synthase subunit O, mitochondrial; AltName: Full=Oligomycin sensitivity conferral protein; Short=OSCP; Flags: Precursor	gi|143811365,gi|157881386,gi|159164706,gi|163451,gi|27806307,gi|28189911,gi|74268299	23,332.20	100.00%	3	4	6	0.06%	19.70%	YATALYSAASK	2.77	1,145.58
Control	6018	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	4	8	0.08%	18.80%	DFSLEQLR	2.52	1,007.52
Control	6018	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	4	8	0.08%	18.80%	FYGPAGPYGIFAGR	4.3	1,472.73

Control	6018	PGRMC 2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	4	8	0.08%	18.80%	GLGAGAGAGEESPAASLPR	4.99	1,667.83
Control	6018	PGRMC 2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	4	8	0.08%	18.80%	RGLGAGAGAGEESPAASLPR	4.12	1,823.94
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	AEDIPQMDDAFSQTVK	3.16	1,810.82
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	ALSQIHEAAVR	4.29	1,194.66
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	FGKPDPIVSVIFKDEK	3.96	1,819.00
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	FKGFPPPVLSEDGSSIR	2.64	1,832.95
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	GNNPFFDELFFYNVHLTPSELMDEIISIR	4.51	3,473.67
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	IDVGFVYDEPGHAVMR	3.71	1,820.86
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	ILHQHLGPPEER	3.99	1,425.76
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	ILVELSTLLEK	3.55	1,257.77
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	IPAHQVLYSTSGGDASGK	5.16	1,787.89
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	ISVYDYDTFTR	2.71	1,379.65

Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	IYRAEDIPQMDDAFSQTVK	3.34	2,243.07
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	LDAVNTLLVMAER	3.05	1,460.78
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	MAPSETHGAAAIFK	4.44	1,446.70
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	NDVVGTTYLHLSK	3.47	1,446.76
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	SDENEDPSVVGEFK	3.74	1,551.68
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	SLLTEADAGHTEFTDEVYQNESR	5.94	2,612.17
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	TLHSSFQPNISQGR	3.66	1,571.79
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	TQGLVPEHVETR	3.8	1,365.71
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	VEMTLEVLNEKEADERPAGK	3.54	2,274.13
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	VFLPKEELYMPPLVIK	3.12	1,932.09
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	VGETIIDLENR	3.18	1,258.66

Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	VIEDRDNYIPNTLNPVFGR	3.76	2,232.14
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	VIIELFDNDQVGKDEFLGR	5.73	2,207.13
Control	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	24	29	36	0.35%	17.40%	VIVESASNIPK	3.02	1,156.66
Control	6018	TXNDC13 protein	gi|148878448,gi|149642897	38,865.40	100.00%	3	3	3	0.03%	12.10%	FFVTTLPAFFHAK	3.04	1,525.82
Control	6018	TXNDC13 protein	gi|148878448,gi|149642897	38,865.40	100.00%	3	3	3	0.03%	12.10%	VDVIQEPGLSGR	3.21	1,269.68
Control	6018	TXNDC13 protein	gi|148878448,gi|149642897	38,865.40	100.00%	3	3	3	0.03%	12.10%	YRGPGVYEDLQNYILEK	3.4	2,057.03
Control	6018	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	4	4	5	0.05%	24.30%	ADFREPNAEVPRPIPHIGADYIPTEEER	3.44	3,218.59
Control	6018	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	4	4	5	0.05%	24.30%	FKNLENSPLGEALR	2.84	1,587.85
Control	6018	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	4	4	5	0.05%	24.30%	NLENSPLGEALR	3.37	1,312.69
Control	6018	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	4	4	5	0.05%	24.30%	SVPLAATSMLITQGLISK	3.89	1,846.04
Control	6018	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	5	5	6	0.06%	16.60%	IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK	5.59	3,829.95
Control	6018	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	5	5	6	0.06%	16.60%	IILDLISESPIK	3.2	1,340.80

Control	6018	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	5	5	6	0.06%	16.60%	IITITGTQDQIQNAQYLLQNSVK	5.08	2,589.39
Control	6018	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	5	5	6	0.06%	16.60%	RPAEDMEEEQAFKR	3.84	1,751.80
Control	6018	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	5	5	6	0.06%	16.60%	TDYNASVSVPDSSGPER	3.32	1,780.80
Control	6018	RecName: Full=DnaJ homolog subfamily C member 11	gi|110808198,gi|114050887,gi|84708894	63,220.40	100.00%	3	3	3	0.03%	12.20%	GTISVGIDATDLFDRYEEEYEDVSGSGFPQIEINK	4.38	3,893.82
Control	6018	RecName: Full=DnaJ homolog subfamily C member 11	gi|110808198,gi|114050887,gi|84708894	63,220.40	100.00%	3	3	3	0.03%	12.20%	GVLHQVMALDSEALR	3.7	1,654.86
Control	6018	RecName: Full=DnaJ homolog subfamily C member 11	gi|110808198,gi|114050887,gi|84708894	63,220.40	100.00%	3	3	3	0.03%	12.20%	LFNLVHQAYEVLSDPQTR	3.41	2,130.10
Control	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	12	15	17	0.17%	15.60%	FKMLAELYGSDPQEELVY	3.01	2,148.02

Control	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	12	15	17	0.17%	15.60%	KPLIGSVLAK	2.55	1,025.67
Control	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	12	15	17	0.17%	15.60%	KPLIGSVLAKDPDAAQR	3.82	1,779.01
Control	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	12	15	17	0.17%	15.60%	MLAELYGSDPQEELVY	1.77	1,872.86
Control	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	12	15	17	0.17%	15.60%	NLESPSSFTIK	2.38	1,222.63
Control	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	12	15	17	0.17%	15.60%	PSLYAQVQKPPR	2.43	1,383.77
Control	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	12	15	17	0.17%	15.60%	TSDKGQFFGITK	2.45	1,328.68
Control	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	12	15	17	0.17%	15.60%	VDKNTGDVYALER	4.26	1,479.74
Control	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	12	15	17	0.17%	15.60%	VGSPLGSLFVEDPDEPQNR	2.23	2,056.00
Control	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	12	15	17	0.17%	15.60%	VGSPLGSLFVEDPDEPQNRK	2.69	2,184.09
Control	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	12	15	17	0.17%	15.60%	YSFVQGEYR	2.71	1,148.54
Control	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	12	15	17	0.17%	15.60%	YTFSVPEDIR	3.14	1,226.61

Control	6018	RecName: Full=Alpha-enolase; AltName: Full=2-phospho-D-glycerate hydro-lyase; AltName: Full=Non-neural enolase; Short=NNE; AltName: Full=Enolase 1; AltName: Full=Phosphopyruvate hydratase	gi|109940077,gi|74354056,gi|87196501	47,309.10	99.80%	2	2	2	0.02%	7.60%	DATNVGDEGGFAPNILENK	5.4	1,960.92
Control	6018	RecName: Full=Alpha-enolase; AltName: Full=2-phospho-D-glycerate hydro-lyase; AltName: Full=Non-neural enolase; Short=NNE; AltName: Full=Enolase 1; AltName: Full=Phosphopyruvate hydratase	gi|109940077,gi|74354056,gi|87196501	47,309.10	99.80%	2	2	2	0.02%	7.60%	VVIGMDVAASEFYR	3.66	1,572.77
Control	6018	LOC515309 protein	gi|148878460,gi|149773584	31,548.40	100.00%	3	4	4	0.04%	15.20%	FAEVYFAQSQQK	3.43	1,445.71
Control	6018	LOC515309 protein	gi|148878460,gi|149773584	31,548.40	100.00%	3	4	4	0.04%	15.20%	KEEEEEEEEYDEGSNLKR	5.99	2,241.96
Control	6018	LOC515309 protein	gi|148878460,gi|149773584	31,548.40	100.00%	3	4	4	0.04%	15.20%	SNPEDQILYQTER	3.75	1,592.76
Control	6018	PREDICTED: lamin B2	gi|194668843	70,532.10	99.80%	2	2	2	0.02%	6.69%	ETENGEEGEDEAAEFGEEDLFHQQGDPR	2.97	3,164.28
Control	6018	PREDICTED: lamin B2	gi|194668843	70,532.10	99.80%	2	2	2	0.02%	6.69%	TTLVNADGEEVAMR	4.18	1,521.72

Control	6018	SCO cytochrome oxidase deficient homolog 1 (yeast)	gi|119223914,gi|122692513,gi|134035032	33,641.50	99.80%	2	3	3	0.03%	12.10%	LIGLTGTKEEIDQVAR	4.64	1,742.97
Control	6018	SCO cytochrome oxidase deficient homolog 1 (yeast)	gi|119223914,gi|122692513,gi|134035032	33,641.50	99.80%	2	3	3	0.03%	12.10%	SIGKPLLGGPFSLTTHTGEPK	3.24	2,137.17
Control	6018	LMAN1 protein	gi|148744096,gi|149773586	58,038.50	100.00%	4	4	5	0.05%	10.40%	GAGAPGQQGQTFQQELDTVVNTQHEILR	2.55	3,022.50
Control	6018	LMAN1 protein	gi|148744096,gi|149773586	58,038.50	100.00%	4	4	5	0.05%	10.40%	RGAGAPGQQGQTFQQELDTVVNTQHEILR	3.46	3,178.60
Control	6018	LMAN1 protein	gi|148744096,gi|149773586	58,038.50	100.00%	4	4	5	0.05%	10.40%	YQEEFEHFQQELDK	3.88	1,869.83
Control	6018	LMAN1 protein	gi|148744096,gi|149773586	58,038.50	100.00%	4	4	5	0.05%	10.40%	YVSSLTEEISK	3.52	1,255.64
Control	6018	acyl-CoA synthetase long-chain family member 5	gi|115497154,gi|152941112,gi|94534758	76,013.10	100.00%	3	3	3	0.03%	5.86%	ALVLISNVEK	2.78	1,085.66
Control	6018	acyl-CoA synthetase long-chain family member 5	gi|115497154,gi|152941112,gi|94534758	76,013.10	100.00%	3	3	3	0.03%	5.86%	GAMLTHANIVSNASGFLK	2.95	1,846.95
Control	6018	acyl-CoA synthetase long-chain family member 5	gi|115497154,gi|152941112,gi|94534758	76,013.10	100.00%	3	3	3	0.03%	5.86%	TLKPTLFPTVPR	2.17	1,369.82
Control	6018	PREDICTED: similar to ER lipid raft associated 1 isoform 2	gi|194678978	39,049.70	99.80%	2	2	2	0.02%	11.80%	DLNVMAPGLTIQAVR	3.6	1,613.87
Control	6018	PREDICTED: similar to ER lipid raft associated 1 isoform 2	gi|194678978	39,049.70	99.80%	2	2	2	0.02%	11.80%	EALEPSGESPIQNK	4.18	1,498.74

Control	6018	PREDICTED: similar to ER lipid raft associated 1 isoform 2	gi|194678978	39,049.70	99.80%	2	2	2	0.02%	11.80%	SVQTTLQTDEVK	2.82	1,348.70
Control	6018	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	100.00%	3	4	6	0.06%	10.20%	LQTVQSADQVLVLR	4.74	1,569.90
Control	6018	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	100.00%	3	4	6	0.06%	10.20%	QVVLVGQEPVLFSGSVR	5.25	1,814.02
Control	6018	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	100.00%	3	4	6	0.06%	10.20%	VNFQNVSFAYPSRPDQPALQGLTFTLSPGQMTALVGPNGSGK	3.58	4,408.20
Control	6018	PREDICTED: similar to rearranged L-myc fusion	gi|119920765	217,470.40	99.80%	2	2	2	0.02%	1.83%	EKCSNVAVCFDGTK	2.96	1,500.68
Control	6018	PREDICTED: similar to rearranged L-myc fusion	gi|119920765	217,470.40	99.80%	2	2	2	0.02%	1.83%	NSITHGSFSGSLQGYPSSGAK	1.75	2,081.99
Control	6018	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	gi|165973956,gi|2493087,gi|81294315	10,254.50	99.80%	2	3	5	0.05%	27.30%	DFTPSGIAGAFQR	3.71	1,366.68
Control	6018	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	gi|165973956,gi|2493087,gi|81294315	10,254.50	99.80%	2	3	5	0.05%	27.30%	LGELPSWILMR	2.8	1,330.72
Control	6018	Solute carrier family 39 (zinc transporter), member 7	gi|112362085,gi|115749633,gi|146231764,gi|63169171	42,835.10	99.80%	2	2	2	0.02%	8.77%	DGPVRPQNAEEEKAGSDLR	2.6	2,068.01

Control	6018	Solute carrier family 39 (zinc transporter), member 7	gi|112362085,gi|115749633,gi|146231764,gi|63169171	42,835.10	99.80%	2	2	2	0.02%	8.77%	EKQSSEEEEKEAGALR	2.58	1,819.87
Control	6018	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	9	12	0.12%	31.10%	AGAGSATLSMAYAGAR	3.97	1,470.70
Control	6018	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	9	12	0.12%	31.10%	ANAFVAELKDLDPAR	3.67	1,629.86
Control	6018	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	9	12	0.12%	31.10%	IFGVTTLDIVR	3.43	1,233.72
Control	6018	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	9	12	0.12%	31.10%	LTLYDIAHTPGVAADLSHIETR	5.82	2,393.25
Control	6018	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	9	12	0.12%	31.10%	MIAEAIPELK	2.46	1,130.61

Control	6018	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	9	12	0.12%	31.10%	VAVLGASGGIGQPLSLLLK	6.85	1,793.09
Control	6018	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	9	12	0.12%	31.10%	VNVPVIGGHAGK	3.4	1,147.66
Control	6018	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	6	21	0.21%	27.60%	FGLIPEEFFQFLYPK	3.38	1,874.97
Control	6018	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	6	21	0.21%	27.60%	HYLFDVQR	2.81	1,077.55
Control	6018	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	6	21	0.21%	27.60%	LNEQKIAQLEEVK	3.37	1,541.85
Control	6018	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	6	21	0.21%	27.60%	NNIAMALEVTYR	4.1	1,410.70

Control	6018	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	6	21	0.21%	27.60%	PVPPLPEHGGK	1.74	1,127.62
Control	6018	Ribosomal protein S8	gi|119224110,gi|58760384,gi|59858489,gi|70778956,gi|74268417,gi|75070020	24,188.40	100.00%	2	2	3	0.03%	13.50%	IIDVVYNASNNELVR	4.41	1,718.91
Control	6018	Ribosomal protein S8	gi|119224110,gi|58760384,gi|59858489,gi|70778956,gi|74268417,gi|75070020	24,188.40	100.00%	2	2	3	0.03%	13.50%	ISSLLEEQFQQGK	4.55	1,506.78
Control	6018	RPS17 protein	gi|148745739,gi|149642675,gi|151554859,gi|166219437	15,564.50	99.80%	2	2	2	0.02%	36.30%	LLDFGSLSNLQVTQPTVGMNFK	5.31	2,425.24
Control	6018	RPS17 protein	gi|148745739,gi|149642675,gi|151554859,gi|166219437	15,564.50	99.80%	2	2	2	0.02%	36.30%	RDNYVPEVSALDQEIIEVDPDTKEMLK	3.01	3,162.55
Control	6018	PREDICTED: similar to oxysterol 7alpha-hydroxylase	gi|194672764	90,479.20	99.80%	2	2	2	0.02%	4.22%	AMAVLRDEIDHLLQSTGQK	3.42	2,141.10
Control	6018	PREDICTED: similar to oxysterol 7alpha-hydroxylase	gi|194672764	90,479.20	99.80%	2	2	2	0.02%	4.22%	FLFGIPYPDSDVLFR	2.6	1,785.92
Control	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	9	11	16	0.16%	28.80%	AVFVDLEPTVIDEVR	4.98	1,701.91
Control	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	9	11	16	0.16%	28.80%	DVNAAIATIK	3.39	1,015.58
Control	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	9	11	16	0.16%	28.80%	EIIDLVLDR	2.45	1,085.62
Control	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	9	11	16	0.16%	28.80%	IHFPLATYAPVISAEK	3.1	1,756.96
Control	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	9	11	16	0.16%	28.80%	LDHKFDLMYAK	3.05	1,396.69
Control	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	9	11	16	0.16%	28.80%	LISQIVSSITASLR	3.6	1,487.88

Control	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	9	11	16	0.16%	28.80%	NLDIERPTYTNLNR	3.29	1,718.88
Control	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	9	11	16	0.16%	28.80%	QLFHPEQLITGKEDAANNYAR	3.53	2,415.21
Control	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	9	11	16	0.16%	28.80%	TIGGGDDSFNTFFSETGAGK	4	2,007.89
Control	6018	tricarboxylate carrier protein	gi|1765906,gi|2497986,gi|27807191	33,859.10	99.80%	2	2	2	0.02%	7.72%	GLSSLLYGSIPK	2.96	1,234.70
Control	6018	tricarboxylate carrier protein	gi|1765906,gi|2497986,gi|27807191	33,859.10	99.80%	2	2	2	0.02%	7.72%	GTYQGLTATVLK	2.81	1,251.69
Control	6018	PREDICTED: similar to transmembrane protein 165	gi|76619924	34,667.10	99.80%	2	2	3	0.03%	13.30%	MSPDEGQEELEEVQAELK	3.67	2,076.93
Control	6018	PREDICTED: similar to transmembrane protein 165	gi|76619924	34,667.10	99.80%	2	2	3	0.03%	13.30%	NKEPPAPAQQLQPQPAAVQGPEPAR	5.32	2,619.36
Control	6018	RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8; AltName: Full=NADH-ubiquinone oxidoreductase 19 kDa subunit; AltName: Full=Complex I-19kD;	gi|1171870,gi|28461275,gi|599681,gi|86827664	20,073.10	99.80%	2	3	3	0.03%	18.60%	ARPEPNPEVEGDLKPAR	7.18	1,874.97

Control	6018	RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8; AltName: Full=NADH-ubiquinone oxidoreductase 19 kDa subunit; AltName: Full=Complex I-19kD;	gi|1171870,gi|28461275,gi|599681,gi|86827664	20,073.10	99.80%	2	3	3	0.03%	18.60%	VKTDRPLPENPYHSR	3.85	1,808.94
Control	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	11	14	17	0.17%	12.40%	AAFQASCETFCVGEEAK	2.58	1,790.77

Control	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	11	14	17	0.17%	12.40%	ATILYASETGR	3.59	1,181.62
Control	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	11	14	17	0.17%	12.40%	AVDTRLEELGGER	3.04	1,444.74

Control	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	11	14	17	0.17%	12.40%	DFINQYYSSIK	3.15	1,377.67
Control	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	11	14	17	0.17%	12.40%	DFINQYYSSIKR	2.98	1,533.77

Control	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	11	14	17	0.17%	12.40%	ESSNTDSAGALGTLR	4.57	1,478.71
Control	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	11	14	17	0.17%	12.40%	LLSTLAEEPSEQQELETLSQDPR	3.48	2,613.29

Control	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	11	14	17	0.17%	12.40%	LSTQAEGLQLLPGLIHVHR	4.65	2,082.18
Control	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	11	14	17	0.17%	12.40%	TYVQDILR	2.86	1,007.55

Control	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	11	14	17	0.17%	12.40%	VEDPPPPTESVAVEQLEK	4.73	1,963.99
Control	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	11	14	17	0.17%	12.40%	VLTAFSREPDSPK	3.53	1,446.76
Control	6018	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	3	4	7	0.07%	10.20%	IGGIGTVPVGR	2.83	1,025.61

Control	6018	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	3	4	7	0.07%	10.20%	VETGVLKPGMVVTFAPVNVTTEVK	4.06	2,531.38
Control	6018	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	3	4	7	0.07%	10.20%	YYVTIIDAPGHR	2.92	1,404.73
Control	6018	cell division cycle 42 (GTP binding protein, 25kDa)	gi|114052486,gi|122063301,gi|86821687	21,240.70	99.80%	2	3	6	0.06%	19.90%	NVFDEAILAALEPPEPK	4.68	1,852.97
Control	6018	cell division cycle 42 (GTP binding protein, 25kDa)	gi|114052486,gi|122063301,gi|86821687	21,240.70	99.80%	2	3	6	0.06%	19.90%	TPFLLVGTQIDLRDDPSTIEK	3.59	2,358.26
Control	6018	RecName: Full=Golgi SNAP receptor complex member 1	gi|108935998,gi|83638559,gi|84370083	28,524.90	100.00%	5	5	5	0.05%	20.00%	ENMTSQRGMLKSIQSK	2.87	1,837.93
Control	6018	RecName: Full=Golgi SNAP receptor complex member 1	gi|108935998,gi|83638559,gi|84370083	28,524.90	100.00%	5	5	5	0.05%	20.00%	FPAVNSLIQR	3.41	1,144.65
Control	6018	RecName: Full=Golgi SNAP receptor complex member 1	gi|108935998,gi|83638559,gi|84370083	28,524.90	100.00%	5	5	5	0.05%	20.00%	LIEETISIAMATK	2.99	1,435.77
Control	6018	RecName: Full=Golgi SNAP receptor complex member 1	gi|108935998,gi|83638559,gi|84370083	28,524.90	100.00%	5	5	5	0.05%	20.00%	MNTLANRFPAVNSLIQR	4.02	1,961.04

Control	6018	RecName: Full=Golgi SNAP receptor complex member 1	gi|108935998,gi|83638559,gi|84370083	28,524.90	100.00%	5	5	5	0.05%	20.00%	NSDRLIEETISIAMATK	3.32	1,907.97
Control	6018	minor histocompatibility antigen 13	gi|164448616	41,537.10	100.00%	3	3	5	0.05%	15.60%	GEVTEMFSYEESNPKDPAAVTETR	3.07	2,703.21
Control	6018	minor histocompatibility antigen 13	gi|164448616	41,537.10	100.00%	3	3	5	0.05%	15.60%	LVFPQDLLEK	2.64	1,201.68
Control	6018	minor histocompatibility antigen 13	gi|164448616	41,537.10	100.00%	3	3	5	0.05%	15.60%	QYQLLFTQGSGENKEEIINYEFDTK	4.99	2,994.44
Control	6018	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	5	6	8	0.08%	35.80%	EDGNEEDKENQGDETQGQQPPQR	3.93	2,628.10
Control	6018	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	5	6	8	0.08%	35.80%	GAEAANVTGPGGVPVQGSK	4.91	1,695.87
Control	6018	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	5	6	8	0.08%	35.80%	NDTKEDVFVHQTAIK	4.13	1,744.89
Control	6018	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	5	6	8	0.08%	35.80%	NYQQNYQNSESGEKNEGSESAPEGQAQQR	6.06	3,257.40
Control	6018	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	5	6	8	0.08%	35.80%	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	4.69	3,239.53
Control	6018	PREDICTED: similar to Feline leukemia virus subgroup C receptor-related protein 1 (Feline leukemia virus subgroup C receptor) (hFLVCR)	gi|194674242	59,731.10	99.80%	2	2	2	0.02%	3.60%	DPGEETPGGEGTLVPR	3.07	1,610.77

Control	6018	PREDICTED: similar to Feline leukemia virus subgroup C receptor-related protein 1 (Feline leukemia virus subgroup C receptor) (hFLVCR)	gi|194674242	59,731.10	99.80%	2	2	2	0.02%	3.60%	LLPKDPGEETPGGEGTLVPR	3.71	2,062.08
Control	6018	H3 histone, family 3A	gi|59858289,gi|62177168,gi|95769331	15,310.70	100.00%	3	6	11	0.11%	38.20%	EIAQDFKTDLR	3.49	1,335.69
Control	6018	H3 histone, family 3A	gi|59858289,gi|62177168,gi|95769331	15,310.70	100.00%	3	6	11	0.11%	38.20%	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	5.48	3,380.68
Control	6018	H3 histone, family 3A	gi|59858289,gi|62177168,gi|95769331	15,310.70	100.00%	3	6	11	0.11%	38.20%	YRPGTVALR	2.51	1,032.59
Control	6018	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	100.00%	4	4	4	0.04%	13.70%	FTSLGLLPR	2.76	1,003.59
Control	6018	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	100.00%	4	4	4	0.04%	13.70%	LTEDGLPLGINLGK	4.56	1,439.81
Control	6018	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	100.00%	4	4	4	0.04%	13.70%	VFRLPEDQAIINR	4.19	1,570.87
Control	6018	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	100.00%	4	4	4	0.04%	13.70%	VPIVGVGGVSSGQDALEK	5.46	1,711.92

Control	6018	PREDICTED: eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) isoform 1	gi|119906216,gi|146231746,gi|172047287	32,883.70	99.80%	2	2	2	0.02%	8.03%	GVVQDLQQAVSK	2.75	1,271.70
Control	6018	PREDICTED: eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) isoform 1	gi|119906216,gi|146231746,gi|172047287	32,883.70	99.80%	2	2	2	0.02%	8.03%	IASLEVENQSLR	3.86	1,358.73
Control	6018	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	3	3	4	0.04%	6.54%	AENLGEVLR	2.53	1,000.54
Control	6018	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	3	3	4	0.04%	6.54%	ISEDYYVHLIADNLPVATR	3.88	2,189.12
Control	6018	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	3	3	4	0.04%	6.54%	IVNTPFQVLMNSEK	3.81	1,635.84
Control	6018	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	100.00%	4	4	7	0.07%	21.00%	AITIFQERDPANIK	3.51	1,615.88
Control	6018	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	100.00%	4	4	7	0.07%	21.00%	GAAQNIIPASTGAAK	4.38	1,369.74

Control	6018	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	100.00%	4	4	7	0.07%	21.00%	IVSNASCTTNCLAPLAK	3.05	1,705.86
Control	6018	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	100.00%	4	4	7	0.07%	21.00%	VIHDHFGIVEGLMTTVHAITATQK	4.9	2,634.37
Control	6018	14-3-3 protein eta chain	gi|162592,gi|55976654,gi|73586681,gi|73853758	28,193.60	99.80%	2	2	2	0.02%	12.20%	AVTELNEPLSNEDR	4.02	1,586.77
Control	6018	14-3-3 protein eta chain	gi|162592,gi|55976654,gi|73586681,gi|73853758	28,193.60	99.80%	2	2	2	0.02%	12.20%	LAEQAERYDDMASAMK	4.05	1,844.82
Control	6018	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	100.00%	3	4	5	0.05%	8.25%	FFLSAGLIDKVDNFK	4.74	1,713.92
Control	6018	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	100.00%	3	4	5	0.05%	8.25%	LEDPHVDIIR	2.55	1,206.65
Control	6018	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	100.00%	3	4	5	0.05%	8.25%	YPEVGDLR	2.57	948.4786
Control	6018	intergral membrane protein 1	gi|114051696,gi|122136222,gi|152941168,gi|86823970	80,641.10	100.00%	3	3	4	0.04%	4.68%	FESVIHEFDPYFNYR	4.93	1,962.90
Control	6018	intergral membrane protein 1	gi|114051696,gi|122136222,gi|152941168,gi|86823970	80,641.10	100.00%	3	3	4	0.04%	4.68%	FYSLLDPSYAK	2.68	1,303.66
Control	6018	intergral membrane protein 1	gi|114051696,gi|122136222,gi|152941168,gi|86823970	80,641.10	100.00%	3	3	4	0.04%	4.68%	IIFDDFR	2.38	925.4779
Control	6018	Myeloid-associated differentiation marker	gi|111308557,gi|115497460	35,291.10	100.00%	3	4	7	0.07%	14.60%	ARPGEITGYMATVPGLLK	3.21	1,890.02

Control	6018	Myeloid-associated differentiation marker	gi|111308557,gi|115497460	35,291.10	100.00%	3	4	7	0.07%	14.60%	LVFVRV	2.2	732.4766
Control	6018	Myeloid-associated differentiation marker	gi|111308557,gi|115497460	35,291.10	100.00%	3	4	7	0.07%	14.60%	TTVTTTMSSSSGLGSPTIVGSPR	4.52	2,240.11
Control	6018	Myosin regulatory light chain MRCL3	gi|109659359,gi|134024635,gi|139948749,gi|148744185,gi|194678093,gi|205829192,gi|59858321,gi|62751407	19,848.30	99.80%	2	3	3	0.03%	16.90%	ATSNVFAMFDQSQIQEFK	4.82	2,106.98
Control	6018	Myosin regulatory light chain MRCL3	gi|109659359,gi|134024635,gi|139948749,gi|148744185,gi|194678093,gi|205829192,gi|59858321,gi|62751407	19,848.30	99.80%	2	3	3	0.03%	16.90%	FTDEEVDELYR	3.24	1,415.63
Control	6018	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	14	0.14%	14.10%	DAEAWFNEK	2.95	1,109.49
Control	6018	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	14	0.14%	14.10%	IRLENEIQTYR	4.32	1,434.77

Control	6018	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	14	0.14%	14.10%	LASYLDKVR	2.97	1,064.61
Control	6018	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	14	0.14%	14.10%	QSLEASLAETEGR	4.34	1,390.68
Control	6018	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	14	0.14%	14.10%	QSVEADINGLR	3.36	1,201.62
Control	6018	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	14	0.14%	14.10%	RVLDELTLTK	3.02	1,187.70
Control	6018	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	14	0.14%	14.10%	SQYEQLAEKNR	4.01	1,365.68

Control	6018	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	14	0.14%	14.10%	VLDELTLTK	3.07	1,031.60
Control	6018	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	5	6	7	0.07%	11.40%	DLDELSRYPEDKITPENLPQILLQLK	5.92	3,080.65
Control	6018	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	5	6	7	0.07%	11.40%	DSFDDRGPSLNPVLDYDHGSR	4.06	2,362.07
Control	6018	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	5	6	7	0.07%	11.40%	VIHLSNLPHSGYSDSAVLK	2.86	2,037.08
Control	6018	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	5	6	7	0.07%	11.40%	VVHIMDFQR	3.02	1,160.59
Control	6018	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	5	6	7	0.07%	11.40%	YQLLQLVEPFGVISNHLILNK	3.71	2,438.38
Control	6018	PREDICTED: similar to dynein, cytoplasmic, heavy polypeptide 1 isoform 3	gi|194677009	531,935.00	99.80%	2	2	2	0.02%	0.88%	VAAPDVVVPTLDTVR	3.68	1,551.87
Control	6018	PREDICTED: similar to dynein, cytoplasmic, heavy polypeptide 1 isoform 3	gi|194677009	531,935.00	99.80%	2	2	2	0.02%	0.88%	VLTLSEDSPYETLHSFISNAVAPFFK	3.18	2,912.47
Control	6018	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	5	8	13	0.13%	29.00%	EAGNHSSGAGLVQINK	2.73	1,581.80
Control	6018	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	5	8	13	0.13%	29.00%	GKESEKELALLK	3.18	1,344.77

Control	6018	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	5	8	13	0.13%	29.00%	GVGDDQLGEESEERDDHLLPM	3.22	2,357.02
Control	6018	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	5	8	13	0.13%	29.00%	HTLADNFNPVSEER	5.46	1,628.77
Control	6018	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	5	8	13	0.13%	29.00%	SFESTVGQSPDMYSYVFR	4.87	2,115.93
Control	6018	ADP-ribosylation-like factor 6 interacting protein 5	gi|59858163,gi|62460474,gi|74354855,gi|75057806	21,648.60	99.80%	2	3	8	0.08%	13.80%	FARPDFR	1.79	908.4737
Control	6018	ADP-ribosylation-like factor 6 interacting protein 5	gi|59858163,gi|62460474,gi|74354855,gi|75057806	21,648.60	99.80%	2	3	8	0.08%	13.80%	TPMGIVLDALEQQEETITK	5.85	2,132.08
Control	6018	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	5	5	6	0.06%	12.10%	EKPYFPIPEDYTFIQNVPLEDR	5.28	2,710.34
Control	6018	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	5	5	6	0.06%	12.10%	GYFEYIEENKYSR	3.07	1,697.78
Control	6018	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	5	5	6	0.06%	12.10%	LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR	5.08	3,142.43

Control	6018	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	5	5	6	0.06%	12.10%	NFILDQTNVSAAAQR	3.74	1,647.84
Control	6018	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	5	5	6	0.06%	12.10%	SSGPTSLFAVTVAPPGAR	2.59	1,714.91
Control	6018	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	gi|124829038,gi|125630707,gi|171769867	51,147.90	100.00%	3	4	4	0.04%	9.27%	ADYLQNYEFPHLQNFIK	3.37	2,140.05
Control	6018	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	gi|124829038,gi|125630707,gi|171769867	51,147.90	100.00%	3	4	4	0.04%	9.27%	LLLVSFDGFR	3.48	1,166.66
Control	6018	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	gi|124829038,gi|125630707,gi|171769867	51,147.90	100.00%	3	4	4	0.04%	9.27%	VLEEIDEHIGELVHR	3.49	1,787.93
Control	6018	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	4	4	4	0.04%	9.65%	EESREPAPASPAPAGVEIR	3.42	1,962.99
Control	6018	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	4	4	4	0.04%	9.65%	MDENQFVAVTSTNAAK	3.65	1,741.81
Control	6018	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	4	4	4	0.04%	9.65%	NLHQSGFSLSGTQVDEGVR	3.29	2,030.99
Control	6018	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	4	4	4	0.04%	9.65%	TLDFDALSVGQR	2.94	1,321.67
Control	6018	TOMM22 protein	gi|151556851,gi|154152189	15,275.00	100.00%	5	7	14	0.14%	52.10%	GDAEKPEEELEEEDDEELDETLSER	4.02	2,935.23
Control	6018	TOMM22 protein	gi|151556851,gi|154152189	15,275.00	100.00%	5	7	14	0.14%	52.10%	LQMEQQQQLQQR	4.31	1,557.78

Control	6018	TOMM22 protein	gi|151556851,gi|154152189	15,275.00	100.00%	5	7	14	0.14%	52.10%	LWGLTEMFPER	2.79	1,394.68
Control	6018	TOMM22 protein	gi|151556851,gi|154152189	15,275.00	100.00%	5	7	14	0.14%	52.10%	QILLGPNTGLSGGMPGALPSLPGK	4.75	2,291.24
Control	6018	TOMM22 protein	gi|151556851,gi|154152189	15,275.00	100.00%	5	7	14	0.14%	52.10%	QILLGPNTGLSGGMPGALPSLPGKI	3.86	2,388.33
Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	AIAELGIYPAVDPLDSTSR	4.68	1,988.03
Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	DQEGQDVLLFIDNIFR	5.22	1,921.97
Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	FTQAGSEVSALLGR	5.04	1,435.75
Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	3.05	3,350.64

Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	3.35	3,714.89
Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	IMDPNIVGSEHYDVAR	3.76	1,831.86
Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	IMNVIGEPIDER	3.63	1,401.70
Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	IMNVIGEPIDERGPIK	3.52	1,796.96
Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	IPSAVGYQPTLATDMGTMQER	5.21	2,282.08

Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	IPVGPETLGR	2.77	1,038.59
Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	IVAVIGAVVDVQFDEGLPPILNALEVQGR	3.14	3,031.68
Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	LVLEVAQHLGESTVR	3.07	1,650.92
Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	QFAAIHAEAPEFVEMSVEQEILVTGIK	3.98	3,002.52
Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	SLQDIIAILGMDELSEEDKLTVSR	4.01	2,691.38

Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	TIAMDGTEGLVR	3.14	1,278.64
Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	TVLIMELINNVAK	3.53	1,457.84
Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	VALTGLTVAEYFR	4.49	1,439.79
Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	VALTGLTVAEYFRDQEGQDVLLFIDNIFR	3.34	3,342.74
Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	VALVYGQMNEPPGAR	3.87	1,617.81

Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	VLDSGAPIRIPVGPETLGR	3.42	1,947.10
Control	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	21	23	42	0.41%	71.60%	VVDLLAPYAK	2.63	1,088.64
Control	6018	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	5	8	10	0.10%	18.80%	AEQINQAAGEASAVLAK	4.85	1,670.87
Control	6018	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	5	8	10	0.10%	18.80%	ASYGVEDPEYAVTQLAQTTMR	3.49	2,346.09
Control	6018	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	5	8	10	0.10%	18.80%	ILEPGLNILIPVLDR	4.18	1,675.02
Control	6018	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	5	8	10	0.10%	18.80%	STDASLDEELDR	3.22	1,350.60
Control	6018	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	5	8	10	0.10%	18.80%	STDASLDEELDRVK	2.47	1,577.77

Control	6018	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	5	6	6	0.06%	6.27%	IPVQLVFK	2.42	943.5976
Control	6018	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	5	6	6	0.06%	6.27%	LGEVPITVTAVSPAASDAVTQR	3.4	2,182.17
Control	6018	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	5	6	6	0.06%	6.27%	SPVTLTAYIVTSLLGYK	4.15	1,826.03
Control	6018	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	5	6	6	0.06%	6.27%	SYSQSILLDLTDSTLQTTLK	4.13	2,227.17
Control	6018	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	5	6	6	0.06%	6.27%	VGSPFELVVIGNK	4.87	1,358.77
Control	6018	S100 calcium binding protein A16	gi|111307529,gi|115497862,gi|122142422	11,758.80	100.00%	3	3	5	0.05%	43.70%	AVVVLVENFYK	3.17	1,280.72
Control	6018	S100 calcium binding protein A16	gi|111307529,gi|115497862,gi|122142422	11,758.80	100.00%	3	3	5	0.05%	43.70%	ISFDEYWTLIGGITSPIANLIR	3.57	2,479.32
Control	6018	S100 calcium binding protein A16	gi|111307529,gi|115497862,gi|122142422	11,758.80	100.00%	3	3	5	0.05%	43.70%	LIQNLDANHDGR	2.39	1,365.69
Control	6018	CHMP4B protein	gi|116874509,gi|190360743	24,919.20	99.80%	2	2	3	0.03%	13.40%	EALENANTNTEVLK	4.14	1,545.78
Control	6018	CHMP4B protein	gi|116874509,gi|190360743	24,919.20	99.80%	2	2	3	0.03%	13.40%	QLAQIDGTLSTIEFQR	3.24	1,819.96
Control	6018	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	100.00%	4	5	20	0.20%	21.70%	FLVGFTNK	2.42	925.5142
Control	6018	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	100.00%	4	5	20	0.20%	21.70%	GEDFPANNIVK	3.54	1,203.60
Control	6018	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	100.00%	4	5	20	0.20%	21.70%	GTEDFIVESLDASFR	4.52	1,685.80
Control	6018	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	100.00%	4	5	20	0.20%	21.70%	QATFEYSFIPAEPMGGRPFGLVINLNYK	2.48	3,175.59
Control	6018	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	12	12	0.12%	25.40%	FGTFHSPALEDADFDGKPMVLVAGQYSTGK	3.7	3,201.52

Control	6018	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	12	12	0.12%	25.40%	GYDFPAVLR	2.37	1,037.54
Control	6018	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	12	12	0.12%	25.40%	LEGHGLPTNLPR	3.11	1,303.71
Control	6018	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	12	12	0.12%	25.40%	LFELEEQDLFR	4.45	1,438.72
Control	6018	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	12	12	0.12%	25.40%	LFELEEQDLFRDIQGLPR	4.07	2,218.15
Control	6018	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	12	12	0.12%	25.40%	LSDVDRDGMLDDEEFALASHLIEAK	3.58	2,805.33
Control	6018	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	12	12	0.12%	25.40%	MQELLMAHDFTK	2.22	1,463.70
Control	6018	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	12	12	0.12%	25.40%	SKYDEIFYNLAPADGK	4.15	1,830.89
Control	6018	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	9	12	12	0.12%	25.40%	TSFIQYLLEQEVPGSR	3.36	1,866.96
Control	6018	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	99.80%	2	2	2	0.02%	5.21%	ALGVEQDLALPAIAVIGDQSSGK	3.55	2,252.21
Control	6018	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	99.80%	2	2	2	0.02%	5.21%	SSVLEALSGVALPR	4.9	1,398.80
Control	6018	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	8	8	13	0.13%	29.50%	KQDAFYKEQLAR	3.74	1,496.79
Control	6018	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	8	8	13	0.13%	29.50%	LSENVIDR	2.65	945.5
Control	6018	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	8	8	13	0.13%	29.50%	QNTQQTLSCSALASQYMR	4.84	2,045.94
Control	6018	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	8	8	13	0.13%	29.50%	RVAEELALEQAK	3.21	1,356.75

Control	6018	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	8	8	13	0.13%	29.50%	RVAEELALEQAKK	4.68	1,484.84
Control	6018	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	8	8	13	0.13%	29.50%	RVTFEADENENITVVK	3.29	1,863.94
Control	6018	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	8	8	13	0.13%	29.50%	VAEELALEQAK	4.03	1,200.65
Control	6018	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	8	8	13	0.13%	29.50%	VAEELALEQAKK	4.13	1,328.74
Control	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	11	14	29	0.28%	18.50%	IGFGSFVEK	2.25	983.5197
Control	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	11	14	29	0.28%	18.50%	LLVFSTDAGFHFAGDGK	2.57	1,781.89
Control	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	11	14	29	0.28%	18.50%	LPEGVTINYK	3.45	1,133.62
Control	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	11	14	29	0.28%	18.50%	LQPEDITQIQPQQLVLQLR	5.99	2,260.27
Control	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	11	14	29	0.28%	18.50%	LSENNIQTIFAVTEEFQPVYK	4.84	2,470.25
Control	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	11	14	29	0.28%	18.50%	NVLSLTDKGEVFNELVGK	4.87	1,962.05
Control	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	11	14	29	0.28%	18.50%	SAVTTVVNPKYEGK	4	1,492.80
Control	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	11	14	29	0.28%	18.50%	SGEPQTFTLK	2.51	1,107.57
Control	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	11	14	29	0.28%	18.50%	SKGTAEKLQPEDITQIQPQQLVLQLR	3.12	2,961.64
Control	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	11	14	29	0.28%	18.50%	SLGTDLMNEMR	2.17	1,282.58
Control	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	11	14	29	0.28%	18.50%	TVMPYISTTPAK	2.63	1,324.68
Control	6018	TPM3 protein	gi|79153472	29,015.30	100.00%	4	4	4	0.04%	11.30%	IQLVEEELDR	3.33	1,243.65

Control	6018	TPM3 protein	gi|79153472	29,015.30	100.00%	4	4	4	0.04%	11.30%	IQLVEEELDRAQER	4	1,727.89
Control	6018	TPM3 protein	gi|79153472	29,015.30	100.00%	4	4	4	0.04%	11.30%	RIQLVEEELDRAQER	3.04	1,883.99
Control	6018	TPM3 protein	gi|79153472	29,015.30	100.00%	4	4	4	0.04%	11.30%	YSQKEDKYEEEIK	3.48	1,688.80
Control	6018	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	3	4	5	0.05%	12.30%	LSQNNFALGYK	3.6	1,254.65
Control	6018	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	3	4	5	0.05%	12.30%	LTLDTIFVPNTGK	3.78	1,418.79

Control	6018	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	3	4	5	0.05%	12.30%	LTLDTIFVPNTGKK	3.36	1,546.88
Control	6018	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	3	4	5	0.05%	12.30%	LTLSALIDGK	3.22	1,030.61
Control	6018	SLC25A3 protein	gi|151556064	39,986.50	100.00%	4	6	13	0.13%	11.90%	IQTQPGYANTLR	3.59	1,361.72
Control	6018	SLC25A3 protein	gi|151556064	39,986.50	100.00%	4	6	13	0.13%	11.90%	LPRPPPPEMPESLK	4.78	1,603.85
Control	6018	SLC25A3 protein	gi|151556064	39,986.50	100.00%	4	6	13	0.13%	11.90%	LPRPPPPEMPESLKK	3.87	1,731.95
Control	6018	SLC25A3 protein	gi|151556064	39,986.50	100.00%	4	6	13	0.13%	11.90%	VLYSNMLGEENAYLWR	2.65	1,973.94
Control	6018	Mitogen-activated protein kinase kinase 1 interacting protein 1	gi|109658269,gi|115496109,gi|122133616	13,632.00	99.80%	2	2	2	0.02%	30.60%	ELAPLFEELR	2.42	1,216.66
Control	6018	Mitogen-activated protein kinase kinase 1 interacting protein 1	gi|109658269,gi|115496109,gi|122133616	13,632.00	99.80%	2	2	2	0.02%	30.60%	VANDNAPEHALRPGFLSTFALATDQGSK	2.69	2,927.46

Control	6018	ALCAM/CD166	gi|13111304,gi|41386784,gi|47605539	64,749.10	100.00%	3	3	3	0.03%	6.35%	SVQYDDVPEYKDR	2.2	1,613.74
Control	6018	ALCAM/CD166	gi|13111304,gi|41386784,gi|47605539	64,749.10	100.00%	3	3	3	0.03%	6.35%	VDVPQNLMFGK	2.73	1,263.64
Control	6018	ALCAM/CD166	gi|13111304,gi|41386784,gi|47605539	64,749.10	100.00%	3	3	3	0.03%	6.35%	VFKQPSKPEIVSK	2.33	1,486.86
Control	6018	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor 1; AltName: Full=p40; AltName: Full=Protein C10	gi|122066007,gi|28189773,gi|73587277	18,591.70	99.80%	2	2	2	0.02%	17.50%	AIVAIENPADVSVISSR	3.64	1,740.95
Control	6018	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor 1; AltName: Full=p40; AltName: Full=Protein C10	gi|122066007,gi|28189773,gi|73587277	18,591.70	99.80%	2	2	2	0.02%	17.50%	FAAATGATPIAGR	4.85	1,203.65
Control	6018	alpha isoform of regulatory subunit A, protein phosphatase 2	gi|146231714,gi|79153525,gi|82697383	65,273.60	99.80%	2	2	2	0.02%	5.60%	IGPILDNSTLQSEVKPVLEK	2.2	2,180.22
Control	6018	alpha isoform of regulatory subunit A, protein phosphatase 2	gi|146231714,gi|79153525,gi|82697383	65,273.60	99.80%	2	2	2	0.02%	5.60%	VLAMSGDPNYLHR	2.62	1,488.73

Control	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	5	6	8	0.08%	31.80%	GIVDQSQQAYQEAFEISK	4.25	2,040.99
Control	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	5	6	8	0.08%	31.80%	GIVDQSQQAYQEAFEISKK	2.73	2,169.08
Control	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	5	6	8	0.08%	31.80%	LAEQAERYDDMAACMK	3.11	1,860.79
Control	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	5	6	8	0.08%	31.80%	SVTEQGAELSNEER	4.93	1,548.71
Control	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	5	6	8	0.08%	31.80%	TAFDEAIAELDTLSEESYKDSTLIMQLLR	5.05	3,318.63

Control	6018	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	5	5	6	0.06%	20.20%	IALTDNALIAR	3.49	1,170.68
Control	6018	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	5	5	6	0.06%	20.20%	KVPAVPETLK	2.32	1,081.66
Control	6018	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	5	5	6	0.06%	20.20%	KVPAVPETLKK	2.64	1,209.76
Control	6018	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	5	5	6	0.06%	20.20%	SVNELIYKR	2.79	1,121.63
Control	6018	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	5	5	6	0.06%	20.20%	TTHFVEGGDAGNREDQINR	3.04	2,115.98
Control	6018	TAPBPL protein	gi|151553600,gi|156120889	47,099.80	99.80%	2	2	2	0.02%	7.47%	LPLSPQGTVR	2.72	1,067.62
Control	6018	TAPBPL protein	gi|151553600,gi|156120889	47,099.80	99.80%	2	2	2	0.02%	7.47%	QVPVPDDGSLEGLTDFQVDTLTK	3.54	2,474.23
Control	6018	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	3	3	4	0.04%	12.70%	ADLINNLGTIAK	4.23	1,242.71
Control	6018	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	3	3	4	0.04%	12.70%	EDQTEYLEER	2.7	1,311.57
Control	6018	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	3	3	4	0.04%	12.70%	GVVDSEDLPLNISR	4.57	1,513.79
Control	6018	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	3	3	4	0.04%	12.70%	HLEINPDHSIIETLR	3.49	1,786.94
Control	6018	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	3	3	4	0.04%	12.70%	NPDDITNEEYGEFYK	3.6	1,833.78
Control	6018	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	3	3	4	0.04%	12.70%	TLTIVDTGIGMTK	4.31	1,365.73

Control	6018	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	3	3	4	0.04%	12.70%	YESLTDPSKLDSGK	3.95	1,539.75
Control	6018	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	4	4	13	0.13%	30.20%	AMGIMNSFVNDIFER	2.85	1,759.81
Control	6018	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	4	4	13	0.13%	30.20%	ESYSVYVYK	2.3	1,137.55
Control	6018	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	4	4	13	0.13%	30.20%	KESYSVYVYK	3.27	1,265.64
Control	6018	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	4	4	13	0.13%	30.20%	STITSREIQTAVR	2.96	1,461.80
Control	6018	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	3	3	3	0.03%	9.20%	EATESFASDPILYRPVAVALDTKGPEIR	4.04	3,045.59
Control	6018	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	3	3	3	0.03%	9.20%	GDLGIEIPAEK	3.22	1,141.61
Control	6018	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	3	3	3	0.03%	9.20%	IYVDDGLISLLVK	4	1,447.84
Control	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	10	19	0.19%	25.60%	AMGNLQIDFADPSR	4.36	1,534.73
Control	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	10	19	0.19%	25.60%	AMGNLQIDFADPSRADDAR	2.83	2,078.96

Control	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	10	19	0.19%	25.60%	AVVYSNTIQSIMAIVK	3.56	1,752.96
Control	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	10	19	0.19%	25.60%	EYQLNDSAAYYLNDLER	5.22	2,076.95
Control	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	10	19	0.19%	25.60%	IAQSDYIPTQQDVLR	3.7	1,746.90
Control	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	10	19	0.19%	25.60%	LLLLGAGESGK	3.36	1,057.63
Control	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	10	19	0.19%	25.60%	SREYQLNDSAAYYLNDLER	4.91	2,320.08
Control	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	10	19	0.19%	25.60%	YDEAASYIQSK	2.91	1,274.59

Control	6018	Paraoxonase 2	gi|109939919,gi|61553203,gi|61888862,gi|71648804	39,404.60	100.00%	3	4	6	0.06%	12.70%	LLIGTLYHR	2.57	1,085.65
Control	6018	Paraoxonase 2	gi|109939919,gi|61553203,gi|61888862,gi|71648804	39,404.60	100.00%	3	4	6	0.06%	12.70%	VVAEGFDSANGINISPDKK	4.43	1,961.00
Control	6018	Paraoxonase 2	gi|109939919,gi|61553203,gi|61888862,gi|71648804	39,404.60	100.00%	3	4	6	0.06%	12.70%	YIYVADILAHEIHVLEK	2.23	2,026.10
Control	6018	RecName: Full=Complement component 1 Q subcomponent-binding protein, mitochondrial; Flags: Precursor	gi|115311784,gi|74354078,gi|77736001	30,588.80	100.00%	4	5	8	0.08%	24.50%	AEEQEPELTSTPNFVVEVTK	4.46	2,247.10
Control	6018	RecName: Full=Complement component 1 Q subcomponent-binding protein, mitochondrial; Flags: Precursor	gi|115311784,gi|74354078,gi|77736001	30,588.80	100.00%	4	5	8	0.08%	24.50%	AFVDFLSDEIKEEK	1.97	1,669.83
Control	6018	RecName: Full=Complement component 1 Q subcomponent-binding protein, mitochondrial; Flags: Precursor	gi|115311784,gi|74354078,gi|77736001	30,588.80	100.00%	4	5	8	0.08%	24.50%	GVDNTFADELVELSTALEHQEYISFLEDLK	4.74	3,425.66

Control	6018	RecName: Full=Complement component 1 Q subcomponent-binding protein, mitochondrial; Flags: Precursor	gi|115311784,gi|74354078,gi|77736001	30,588.80	100.00%	4	5	8	0.08%	24.50%	GVDNTFADELVELSTALEHQEYISFLEDLKGFVK	4.04	3,856.92
Control	6018	ARF1 protein	gi|146327384,gi|28603778,gi|59858233,gi|62751462	20,583.70	99.80%	2	2	2	0.02%	16.00%	ILMVGLDAAGK	2.85	1,103.61
Control	6018	ARF1 protein	gi|146327384,gi|28603778,gi|59858233,gi|62751462	20,583.70	99.80%	2	2	2	0.02%	16.00%	MLAEDELRDAVLLVFANK	3.6	2,063.08
Control	6018	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	99.80%	2	2	2	0.02%	5.57%	SEIDLLDIR	2.83	1,073.58
Control	6018	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	99.80%	2	2	2	0.02%	5.57%	TLISILTER	2.55	1,045.63
Control	6018	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	5	6	9	0.09%	11.00%	GLNTIPLFVQLLYSPIENIQR	3.79	2,428.36
Control	6018	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	5	6	9	0.09%	11.00%	LHYGLPVVVK	3.01	1,124.68

Control	6018	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	5	6	9	0.09%	11.00%	LLNDEDQVVVNK	3.08	1,385.73
Control	6018	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	5	6	9	0.09%	11.00%	MLGSPVDSVLFYAITTLHNLLLHQEGAK	3.31	3,083.62
Control	6018	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	5	6	9	0.09%	11.00%	TSMGGTQQQFVEGVR	4.45	1,640.77
Control	6018	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	gi|117306519,gi|118151180,gi|158512477	51,340.60	100.00%	4	4	4	0.04%	15.30%	EPEAPPEDKESESEAKADGETASDSESR	2.05	2,977.27
Control	6018	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	gi|117306519,gi|118151180,gi|158512477	51,340.60	100.00%	4	4	4	0.04%	15.30%	LVQQFLTLRPDQQLHIFNTLK	1.71	2,552.44
Control	6018	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	gi|117306519,gi|118151180,gi|158512477	51,340.60	100.00%	4	4	4	0.04%	15.30%	SHLTDKGMLTAATEDK	3.37	1,733.84
Control	6018	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	gi|117306519,gi|118151180,gi|158512477	51,340.60	100.00%	4	4	4	0.04%	15.30%	VAREPEAPPEDKESESEAK	2.42	2,097.99
Control	6018	SET translocation (myeloid leukemia-associated)	gi|152941192,gi|83638675,gi|84370163	32,099.40	99.80%	2	2	2	0.02%	8.66%	IDFYFDENPYFENK	3.27	1,840.81

Control	6018	SET translocation (myeloid leukemia-associated)	gi|152941192,gi|83638675,gi|84370163	32,099.40	99.80%	2	2	2	0.02%	8.66%	VEVTEFEDIK	3.67	1,208.60
Control	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	10	10	11	0.11%	5.05%	FNQMLNQIPNDYHSSR	3.99	1,979.90
Control	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	10	10	11	0.11%	5.05%	GLTSSEPVSIMEK	3.13	1,393.69
Control	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	10	10	11	0.11%	5.05%	GPGDLEAPSNLVLSER	4.06	1,653.84
Control	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	10	10	11	0.11%	5.05%	IIYSPTVGDPIDEYTTVPGR	3.65	2,193.11
Control	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	10	10	11	0.11%	5.05%	ITYQPSTGEGNEQTTTIGGR	4.58	2,110.01
Control	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	10	10	11	0.11%	5.05%	IVEVFEIGPK	2.74	1,130.65
Control	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	10	10	11	0.11%	5.05%	LKPDTPYTITVSSLYPDGEGGR	3.53	2,366.19
Control	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	10	10	11	0.11%	5.05%	NIGVEVFSLGIK	3.32	1,275.73
Control	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	10	10	11	0.11%	5.05%	NNVILQPLQPDTPYK	3.68	1,739.93
Control	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	10	10	11	0.11%	5.05%	SLPADVIHTVIENLQPETK	2.88	2,104.13

Control	6018	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	3	4	5	0.05%	13.10%	ANVDKVFFDLMR	4.93	1,470.74
Control	6018	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	3	4	5	0.05%	13.10%	VFFDLMR	2.07	943.4707
Control	6018	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	3	4	5	0.05%	13.10%	VKEDENVPFLLVGNK	5.18	1,700.92
Control	6018	NADH dehydrogenase (ubiquinone) 39 kDa subunit	gi|230,gi|28603782,gi|464254,gi|74267974	37,737.50	99.80%	2	2	2	0.02%	10.60%	LLQYADALEHLLSTGQGVVLER	3.66	2,425.31
Control	6018	NADH dehydrogenase (ubiquinone) 39 kDa subunit	gi|230,gi|28603782,gi|464254,gi|74267974	37,737.50	99.80%	2	2	2	0.02%	10.60%	LQYGPLAYILGEK	3.49	1,464.81
Control	6018	PREDICTED: similar to small GTP binding protein RAB23	gi|194677545	37,951.40	99.80%	2	2	3	0.03%	9.91%	LKQQIAENPESMHSSSNK	4.18	2,043.98
Control	6018	PREDICTED: similar to small GTP binding protein RAB23	gi|194677545	37,951.40	99.80%	2	2	3	0.03%	9.91%	VVAEVGDIPTALVQNK	3.88	1,652.92
Control	6018	RecName: Full=Transmembrane emp24 domain-containing protein 1; Flags: Precursor	gi|114152289,gi|83638714,gi|84370158	25,119.90	99.80%	2	4	6	0.06%	11.50%	KADGVHTVEPTEAGDYK	3.94	1,816.87

Control	6018	RecName: Full=Transmembrane emp24 domain-containing protein 1; Flags: Precursor	gi|114152289,gi|83638714,gi|84370158	25,119.90	99.80%	2	4	6	0.06%	11.50%	SIQVLTLLR	3.08	1,042.66
Control	6018	growth and transformation-dependent protein	gi|114051522,gi|126258169,gi|84201630	17,719.20	100.00%	3	3	3	0.03%	20.50%	FKKEDEIPETVSFEMLDAAK	3.34	2,343.14
Control	6018	growth and transformation-dependent protein	gi|114051522,gi|126258169,gi|84201630	17,719.20	100.00%	3	3	3	0.03%	20.50%	NETLTSLNLEK	2.64	1,261.66
Control	6018	growth and transformation-dependent protein	gi|114051522,gi|126258169,gi|84201630	17,719.20	100.00%	3	3	3	0.03%	20.50%	RNETLTSLNLEK	3.74	1,417.76
Control	6018	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	5	6	7	0.07%	9.72%	DAFLGSFLYEYSR	4.52	1,567.74
Control	6018	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	5	6	7	0.07%	9.72%	FKDLGEEHFK	3.56	1,249.62
Control	6018	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	5	6	7	0.07%	9.72%	HLVDEPQNLIK	3.22	1,305.72
Control	6018	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	5	6	7	0.07%	9.72%	KVPQVSTPTLVEVSR	4.17	1,639.94

Control	6018	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	5	6	7	0.07%	9.72%	LVNELTEFAK	3.36	1,163.63
Control	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	12	15	32	0.31%	26.90%	IIGAVDQIQLTQAQLEER	4.82	2,025.10
Control	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	12	15	32	0.31%	26.90%	IREGQVEVLK	3.92	1,170.68
Control	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	12	15	32	0.31%	26.90%	KLEVNEAELLR	4.4	1,313.74
Control	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	12	15	32	0.31%	26.90%	KSFTPDHVVYAR	2.85	1,419.74
Control	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	12	15	32	0.31%	26.90%	LEVNEAELLR	3.36	1,185.65
Control	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	12	15	32	0.31%	26.90%	QAEMEGAVQSIQGELSK	4.26	1,820.87
Control	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	12	15	32	0.31%	26.90%	SDQVNGVLVLSLLDK	4.06	1,599.90
Control	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	12	15	32	0.31%	26.90%	SDQVNGVLVLSLLDKIIGAVDQIQLTQAQLEER	5.54	3,605.98
Control	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	12	15	32	0.31%	26.90%	SFTPDHVVYAR	3.07	1,291.64
Control	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	12	15	32	0.31%	26.90%	VMIYQDEVK	3.21	1,140.56

Control	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	12	15	32	0.31%	26.90%	VMIYQDEVKLPAK	3.57	1,549.83
Control	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	12	15	32	0.31%	26.90%	VPPFTFHVK	1.97	1,071.60
Control	6018	RNA binding motif (RNP1, RRM) protein 3	gi|73587236,gi|77735675	9,735.50	100.00%	3	3	3	0.03%	55.60%	ALEDHFSSFGPISEVVVVK	4.93	2,060.07
Control	6018	RNA binding motif (RNP1, RRM) protein 3	gi|73587236,gi|77735675	9,735.50	100.00%	3	3	3	0.03%	55.60%	GFGFITFTNPEHASNAMR	3.57	2,012.93
Control	6018	RNA binding motif (RNP1, RRM) protein 3	gi|73587236,gi|77735675	9,735.50	100.00%	3	3	3	0.03%	55.60%	LFVGGLNFNTDER	3.48	1,481.74
Control	6018	ITGA3 protein	gi|151556279,gi|156120449	45,035.90	99.80%	2	2	2	0.02%	6.34%	EAGNPGSLFGYSVALHR	4.05	1,774.89
Control	6018	ITGA3 protein	gi|151556279,gi|156120449	45,035.90	99.80%	2	2	2	0.02%	6.34%	YLLLAGAPR	2.73	973.583
Control	6018	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	100.00%	3	6	13	0.13%	16.70%	KYMEENDLLKK	4.37	1,426.72
Control	6018	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	100.00%	3	6	13	0.13%	16.70%	LQAAVDGPSDKKEE	3.31	1,486.74
Control	6018	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	100.00%	3	6	13	0.13%	16.70%	VNLQNNPGAVEHFHMK	3.99	1,850.90
Control	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	18	65	0.63%	56.90%	AKDFSLILDDVAITELSFSR	4.77	2,240.18
Control	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	18	65	0.63%	56.90%	AQVSLLIR	2.6	899.5673
Control	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	18	65	0.63%	56.90%	DLQMVNISLR	3.47	1,204.64
Control	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	18	65	0.63%	56.90%	ESVFTVEGGHR	2.67	1,217.59

Control	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	18	65	0.63%	56.90%	FNASQLITQR	3.87	1,177.63
Control	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	18	65	0.63%	56.90%	IGGVQQDTILAEGLHFR	4.49	1,853.99
Control	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	18	65	0.63%	56.90%	IPWFQYPIIYDIR	3.69	1,723.92
Control	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	18	65	0.63%	56.90%	IVQAEGEAEAAR	4.01	1,243.63
Control	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	18	65	0.63%	56.90%	IYLTADNLVLNLQDESFTR	4.96	2,225.15
Control	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	18	65	0.63%	56.90%	LGLDYEER	3.07	994.4841
Control	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	18	65	0.63%	56.90%	LLLGAGAVAYGIR	5.37	1,273.76
Control	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	18	65	0.63%	56.90%	QKIVQAEGEAEAAR	4.05	1,499.78
Control	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	18	65	0.63%	56.90%	VLPSIVNEVLK	2.56	1,210.74
Control	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	18	65	0.63%	56.90%	VLSRPNAMELPSMYQR	3.52	1,907.95
Control	6018	TAP1 protein	gi|151557007	81,933.30	100.00%	4	6	10	0.10%	8.13%	GVVGAALGFR	3.3	946.5469
Control	6018	TAP1 protein	gi|151557007	81,933.30	100.00%	4	6	10	0.10%	8.13%	SSQVAIEVLSAMPTVR	3.77	1,703.90
Control	6018	TAP1 protein	gi|151557007	81,933.30	100.00%	4	6	10	0.10%	8.13%	STVAALLQNLYQPTEGQVLLDGEPLPK	4.64	2,894.55
Control	6018	TAP1 protein	gi|151557007	81,933.30	100.00%	4	6	10	0.10%	8.13%	SVLFITQR	2.6	963.5622
Control	6018	MOSPD2 protein	gi|151556011,gi|155369632,gi|156120441	56,360.50	99.80%	2	2	2	0.02%	6.50%	ALIVLTNVTK	2.69	1,071.68
Control	6018	MOSPD2 protein	gi|151556011,gi|155369632,gi|156120441	56,360.50	99.80%	2	2	2	0.02%	6.50%	GPLLHISPAEELYFGSTDSGEK	3.12	2,347.15

Control	6018	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	11	13	0.13%	35.40%	AEDGSVIDYELIDQDAR	3.91	1,908.88
Control	6018	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	11	13	0.13%	35.40%	AYTNFDAERDALNIETAIK	4.61	2,155.07

Control	6018	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	11	13	0.13%	35.40%	GVDEVTIVNILTNR	4.32	1,542.85
Control	6018	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	11	13	0.13%	35.40%	LSLEGDHSTPPSAYGSVK	4.56	1,844.90

Control	6018	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	11	13	0.13%	35.40%	RAEDGSVIDYELIDQDAR	5.54	2,064.98
Control	6018	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	11	13	0.13%	35.40%	SALSGHLETVILGLLK	4.25	1,650.98

Control	6018	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	11	13	0.13%	35.40%	SLYYYIQQDTKGDYQK	3.33	2,012.96
Control	6018	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	11	13	0.13%	35.40%	TDLEKDIVSDTSGDFRK	5.28	1,925.95

Control	6018	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	9	11	13	0.13%	35.40%	TKGVDEVTIVNILTNR	3.65	1,771.99
Control	6018	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	4	6	7	0.07%	13.90%	ELIEVLQPLIAEHQAR	3.13	1,859.04
Control	6018	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	4	6	7	0.07%	13.90%	ISFPAIQAAPSFSNSFPQIFR	3.8	2,325.20

Control	6018	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	4	6	7	0.07%	13.90%	MSASDPNSSIFLTDTAK	3.69	1,800.83
Control	6018	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	4	6	7	0.07%	13.90%	NAAKDEIDSAVK	3.24	1,260.64
Control	6018	PREDICTED: similar to Transmembrane protein 16F	gi|119892265	106,290.10	99.80%	2	2	2	0.02%	4.72%	LLQVDESIIKPEQEFFTAPFEK	3.13	2,608.35
Control	6018	PREDICTED: similar to Transmembrane protein 16F	gi|119892265	106,290.10	99.80%	2	2	2	0.02%	4.72%	TPEFEEFNGKPDSLYFNDGQR	4.43	2,490.12
Control	6018	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	5	6	8	0.08%	16.90%	ALSSSLDDTEVK	3.15	1,264.63
Control	6018	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	5	6	8	0.08%	16.90%	ALSSSLDDTEVKK	4.33	1,392.72
Control	6018	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	5	6	8	0.08%	16.90%	FRGPFTDVVTTNLK	4.88	1,594.86
Control	6018	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	5	6	8	0.08%	16.90%	GPFTDVVTTNLK	4.12	1,291.69
Control	6018	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	5	6	8	0.08%	16.90%	VEQVLSLEPQHELK	4.73	1,648.89

Control	6018	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	3	3	4	0.04%	10.10%	APDFVFYAPR	3.65	1,182.59
Control	6018	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	3	3	4	0.04%	10.10%	FYPEDVSEELIQDITQR	2.56	2,082.00
Control	6018	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	3	3	4	0.04%	10.10%	TAMSTPHVAEPAENEQDEQDENGAEASAELR	5.73	3,342.43
Control	6018	PDZ and LIM domain 1	gi|148877479	35,802.30	99.80%	2	2	3	0.03%	13.40%	SAVPFTASPASSSAPR	4.29	1,532.77
Control	6018	PDZ and LIM domain 1	gi|148877479	35,802.30	99.80%	2	2	3	0.03%	13.40%	VITNQYNNPAGLYSSENISSFNNALESK	3.1	3,074.47
Control	6018	PREDICTED: similar to Keratin, type I cytoskeletal 24 (Cytokeratin-24) (Keratin-24) (Type I keratin-24)	gi|194676109	55,111.70	99.80%	2	3	4	0.04%	5.33%	KVLDDLTMTR	3.23	1,207.64
Control	6018	PREDICTED: similar to Keratin, type I cytoskeletal 24 (Cytokeratin-24) (Keratin-24) (Type I keratin-24)	gi|194676109	55,111.70	99.80%	2	3	4	0.04%	5.33%	SDLEMQIESLTEELAYLK	3.86	2,112.04
Control	6018	H2A histone family, member Y	gi|114052404,gi|87578157	39,516.80	99.80%	2	4	6	0.06%	13.70%	AASADSTTEGTPADGFTVLSTK	4.73	2,127.01
Control	6018	H2A histone family, member Y	gi|114052404,gi|87578157	39,516.80	99.80%	2	4	6	0.06%	13.70%	IGVGAPVYMAAVLEYLTAEILELAGNAAR	5.75	2,991.59
Control	6018	PREDICTED: transmembrane protein 33 isoform 2	gi|119893815,gi|119922774	27,968.00	99.80%	2	2	2	0.02%	8.10%	ALLANALTSALR	4.11	1,213.73

Control	6018	PREDICTED: transmembrane protein 33 isoform 2	gi|119893815,gi|119922774	27,968.00	99.80%	2	2	2	0.02%	8.10%	LPHFQLSR	2.39	997.5578
Control	6018	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	5	10	0.10%	45.00%	DSLLQDGEFTMDLR	3.62	1,655.76
Control	6018	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	5	10	0.10%	45.00%	SSFFVNGLTLGGQK	4.62	1,454.76
Control	6018	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	5	10	0.10%	45.00%	STGGAPTFNITVTMTAK	4.05	1,712.85
Control	6018	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	5	10	0.10%	45.00%	TFVNITPAEVGILVGK	5.08	1,657.95

Control	6018	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	5	10	0.10%	45.00%	TFVNITPAEVGILVGKDR	3.02	1,929.08
Control	6018	PREDICTED: ATPase type 13A1 isoform 1	gi|76620985	132,577.20	99.80%	2	3	3	0.03%	2.92%	FLPVAFPVGNAFSFYQSNR	4.59	2,161.09
Control	6018	PREDICTED: ATPase type 13A1 isoform 1	gi|76620985	132,577.20	99.80%	2	3	3	0.03%	2.92%	SIDGSISEPLAQGSPK	3.79	1,585.81
Control	6018	Cell adhesion molecule 1	gi|83638798,gi|84370145	45,751.20	99.90%	2	2	3	0.03%	7.19%	GADDAADADTAIINAEGGQNNSEEKK	3.62	2,604.17
Control	6018	Cell adhesion molecule 1	gi|83638798,gi|84370145	45,751.20	99.90%	2	2	3	0.03%	7.19%	GADDAADADTAIINAEGGQNNSEEKKEYFI	5.23	3,156.42
Control	6018	Brain abundant, membrane attached signal protein 1	gi|115304757,gi|1930063,gi|27807507,gi|6686271	22,992.60	100.00%	2	2	3	0.03%	12.80%	AQAPAAPADEVKPAETPAANSDQTVAVK	3.37	2,747.38
Control	6018	Brain abundant, membrane attached signal protein 1	gi|115304757,gi|1930063,gi|27807507,gi|6686271	22,992.60	100.00%	2	2	3	0.03%	12.80%	AQAPAAPADEVKPAETPAANSDQTVAVKE	2.96	2,876.43
Control	6018	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	4	6	8	0.08%	25.30%	ALNLPSSGEGLAFFTFPNIASATK	5.42	2,453.27
Control	6018	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	4	6	8	0.08%	25.30%	LVMASLYHIYVALEEEIER	3.98	2,294.17
Control	6018	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	4	6	8	0.08%	25.30%	NKENPVYTPLYFPEELHR	6.72	2,246.12

Control	6018	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	4	6	8	0.08%	25.30%	YLGDLSGGQVLK	2.87	1,249.68
Control	6018	HADHA protein	gi|74268185	83,232.60	100.00%	3	3	3	0.03%	6.68%	DAMFSNLIGQLDYR	3.19	1,658.78
Control	6018	HADHA protein	gi|74268185	83,232.60	100.00%	3	3	3	0.03%	6.68%	MPSQPDVSSDEDIQYR	3.07	1,882.81
Control	6018	HADHA protein	gi|74268185	83,232.60	100.00%	3	3	3	0.03%	6.68%	TVLGSPEVLLGILPGAGATQR	3.81	2,049.17
Control	6018	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	4	4	4	0.04%	4.70%	FVFGTTPEDILR	3.16	1,394.73
Control	6018	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	4	4	4	0.04%	4.70%	GGVNDNFQGVLQNVR	4.08	1,616.81
Control	6018	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	4	4	4	0.04%	4.70%	IEDANLIPPVPDKK	2.91	1,548.86
Control	6018	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	4	4	4	0.04%	4.70%	KVTEENKELANELR	3.01	1,672.89
Control	6018	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	100.00%	4	6	6	0.06%	23.90%	EDTESLEIFQNEVAR	3.39	1,779.84
Control	6018	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	100.00%	4	6	6	0.06%	23.90%	FSQMLHPIFEEASNVIKEEYPNANQVVFAR	5.24	3,523.73

Control	6018	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	100.00%	4	6	6	0.06%	23.90%	LHREFHHGPDPTDTAPGEEVQDVASSPPESSFQK	2.28	3,728.72
Control	6018	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	100.00%	4	6	6	0.06%	23.90%	SDPIQELHDLAEITPDR	4.58	2,050.01
Control	6018	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32, gi|59857977	33,881.70	100.00%	4	5	6	0.06%	22.50%	AVIGMTAGATGAFVGTPAEVALIR	3.64	2,289.23
Control	6018	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32, gi|59857977	33,881.70	100.00%	4	5	6	0.06%	22.50%	AVVVNAAQLASYSQSK	3.18	1,635.87

Control	6018	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32, gi|59857977	33,881.70	100.00%	4	5	6	0.06%	22.50%	FLFGGLAGMGATVFVQPLDLVK	4.16	2,296.24
Control	6018	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32, gi|59857977	33,881.70	100.00%	4	5	6	0.06%	22.50%	NVFNALFR	2.34	980.5311
Control	6018	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	3	3	4	0.04%	14.20%	GGALLTSTSGPGFHLMLPFITSYK	2.83	2,511.30
Control	6018	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	3	3	4	0.04%	14.20%	SVQTTLQTDEVK	2.82	1,348.70
Control	6018	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	3	3	4	0.04%	14.20%	VAQVAEITFGQK	2.93	1,290.71
Control	6018	GLI pathogenesis-related 2	gi|111307081,gi|115497826	17,191.20	100.00%	2	2	2	0.02%	16.90%	ASASDGSSFVVAR	2.59	1,253.61
Control	6018	GLI pathogenesis-related 2	gi|111307081,gi|115497826	17,191.20	100.00%	2	2	2	0.02%	16.90%	EAQQYSEALASTR	3.42	1,453.69
Control	6018	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	10	13	0.13%	17.70%	ATLNAFLHR	2.84	1,042.58
Control	6018	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	10	13	0.13%	17.70%	GLLLFVDEADAFLR	3.26	1,578.85
Control	6018	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	10	13	0.13%	17.70%	ITVLEALR	2.67	914.567

Control	6018	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	10	13	0.13%	17.70%	LKEYEAAVEQLKGDQIR	4.21	1,990.06
Control	6018	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	10	13	0.13%	17.70%	NVLMYGPPGTGK	3.35	1,249.62
Control	6018	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	10	13	0.13%	17.70%	QQQLLNEENLR	2.64	1,384.72
Control	6018	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	10	13	0.13%	17.70%	RLLSKPQDALEGVVLSPSLEAR	3.55	2,378.34
Control	6018	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	10	13	0.13%	17.70%	TAGTLFGEGFR	3.68	1,155.58
Control	6018	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	9	10	13	0.13%	12.90%	DISTNYYASQK	3.06	1,289.60
Control	6018	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	9	10	13	0.13%	12.90%	EEASDYLELDTIK	3.69	1,525.73
Control	6018	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	9	10	13	0.13%	12.90%	ELISNASDALDK	3.35	1,275.64
Control	6018	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	9	10	13	0.13%	12.90%	ELISNASDALDKIR	3.7	1,544.83
Control	6018	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	9	10	13	0.13%	12.90%	FQSSHHPSDMTSLDQYVER	5.34	2,280.00
Control	6018	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	9	10	13	0.13%	12.90%	GVVDSDDLPLNVSR	4.71	1,485.75
Control	6018	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	9	10	13	0.13%	12.90%	LIINSLYK	2.32	963.5874
Control	6018	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	9	10	13	0.13%	12.90%	NLLHVTDTGVGMTR	4.41	1,529.77

Control	6018	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	9	10	13	0.13%	12.90%	SILFVPTSAPR	3.08	1,187.68
Control	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	9	9	10	0.10%	11.20%	ALSAIADLLTNEHER	2.76	1,652.86
Control	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	9	9	10	0.10%	11.20%	APSRQDVYGPQPQVR	4.16	1,697.87
Control	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	9	9	10	0.10%	11.20%	FHPEPYGLEDDQR	2.93	1,602.72
Control	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	9	9	10	0.10%	11.20%	FVGDADLER	2.56	1,021.50
Control	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	9	9	10	0.10%	11.20%	KPTEDPTNDTVDFPKR	4.5	1,859.91
Control	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	9	9	10	0.10%	11.20%	NFHYPPDGYSR	2.8	1,352.60
Control	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	9	9	10	0.10%	11.20%	QDVYGPQPQVR	2.62	1,286.65
Control	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	9	9	10	0.10%	11.20%	SLDNNYSTLNER	3.07	1,425.66
Control	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	9	9	10	0.10%	11.20%	VSPQDASPLLANGTLTR	2.96	1,739.93
Control	6018	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	5	6	14	0.14%	15.30%	DPLVIELGQK	3.35	1,111.64
Control	6018	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	5	6	14	0.14%	15.30%	IFDTSLTRDPLVIELGQK	5.17	2,045.13
Control	6018	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	5	6	14	0.14%	15.30%	RVIIPSHLAYGK	4.84	1,353.80

Control	6018	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	5	6	14	0.14%	15.30%	VIIPSHLAYGK	2.78	1,197.70
Control	6018	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	5	6	14	0.14%	15.30%	VIIPSHLAYGKR	1.95	1,353.80
Control	6018	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	2	2	3	0.03%	6.58%	EEQKDFVSLYQDFENFYTR	4.05	2,458.12
Control	6018	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	2	2	3	0.03%	6.58%	NIGVVVVGFPATPIIESR	6.04	1,868.06
Control	6018	endoglin	gi|115497110,gi|92097469	69,885.10	99.80%	2	3	6	0.06%	3.25%	FSFLLR	1.75	782.4559
Control	6018	endoglin	gi|115497110,gi|92097469	69,885.10	99.80%	2	3	6	0.06%	3.25%	LQAPGIPLQLAYDSK	4.56	1,613.89
Control	6018	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	3	3	4	0.04%	5.31%	DKLNPQSTYSEA	3.58	1,352.63
Control	6018	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	3	3	4	0.04%	5.31%	SFEGNNNYDTPELR	4.21	1,655.73
Control	6018	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	3	3	4	0.04%	5.31%	TGPIQDHTGDGNFIYSQADENQK	5.54	2,535.14
Control	6018	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	3	3	3	0.03%	7.96%	GGTGADPVQTVTGGLR	3.72	1,485.77
Control	6018	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	3	3	3	0.03%	7.96%	LIEAVDNMLTNK	3.38	1,376.71
Control	6018	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	3	3	3	0.03%	7.96%	SISIIDSPGILSGEK	4.02	1,515.83
Control	6018	RPS7 protein	gi|148877374,gi|149642623,gi|205806695	22,109.50	100.00%	3	3	4	0.04%	17.50%	DVNFEFPEFQL	2.98	1,384.64
Control	6018	RPS7 protein	gi|148877374,gi|149642623,gi|205806695	22,109.50	100.00%	3	3	4	0.04%	17.50%	TLTAVHDAILEDLVFPSEIVGK	4.33	2,367.28
Control	6018	RPS7 protein	gi|148877374,gi|149642623,gi|205806695	22,109.50	100.00%	3	3	4	0.04%	17.50%	TLTAVHDAILEDLVFPSEIVGKR	4.73	2,523.38

Control	6018	ERGIC and golgi 2	gi|113912114,gi|115497448	42,596.10	99.80%	2	2	2	0.02%	9.28%	IDHLSFGELVPGIINPLDGTEK	3.55	2,364.25
Control	6018	ERGIC and golgi 2	gi|113912114,gi|115497448	42,596.10	99.80%	2	2	2	0.02%	9.28%	ISADTHQFAVTER	2.44	1,474.73
Control	6018	heme oxygenase (decycling) 2	gi|164448721	37,538.70	100.00%	3	4	4	0.04%	14.10%	AFEFNMQVFNELDQAGSLLAK	3.92	2,388.15
Control	6018	heme oxygenase (decycling) 2	gi|164448721	37,538.70	100.00%	3	4	4	0.04%	14.10%	LPTQDGLPVHDGK	2.55	1,376.72
Control	6018	heme oxygenase (decycling) 2	gi|164448721	37,538.70	100.00%	3	4	4	0.04%	14.10%	YMGDLSGGQVLKK	3.02	1,411.73
Control	6018	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	gi|59858119,gi|60650208,gi|60650268,gi|61889066,gi|75070049,gi|88954151	42,933.90	99.80%	2	2	2	0.02%	10.70%	FTRPIIAGMEFSR	4.77	1,540.79
Control	6018	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	gi|59858119,gi|60650208,gi|60650268,gi|61889066,gi|75070049,gi|88954151	42,933.90	99.80%	2	2	2	0.02%	10.70%	SDNSSHPQKDDGDNPETIMSSGNVNSSS	4.05	2,922.19
Control	6018	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	3	4	4	0.04%	8.01%	SISHYHETLGEALQGVELEFSGLDIK	4.09	2,872.44
Control	6018	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	3	4	4	0.04%	8.01%	VNAVPRPIPEK	2.13	1,219.72
Control	6018	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	3	4	4	0.04%	8.01%	YLDPSFFQHR	2.35	1,309.63

Control	6018	PREDICTED: similar to Transmembrane emp24 domain-containing protein 2 precursor (Membrane protein p24A)	gi|194674620	22,715.40	99.80%	2	2	9	0.09%	12.40%	IVMFTIDIGEAPK	3.97	1,449.77
Control	6018	PREDICTED: similar to Transmembrane emp24 domain-containing protein 2 precursor (Membrane protein p24A)	gi|194674620	22,715.40	99.80%	2	2	9	0.09%	12.40%	YTFAAHMDGTYK	4	1,420.62
Control	6018	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	5	7	7	0.07%	6.12%	EATSTFTNITYR	3.46	1,403.68
Control	6018	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	5	7	7	0.07%	6.12%	GTGDSSQITQVSPQR	3.97	1,560.76
Control	6018	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	5	7	7	0.07%	6.12%	HVLTLTDQVTR	3.04	1,282.71

Control	6018	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	5	7	7	0.07%	6.12%	ILEARPLSDKGTGDSSQITQVSPQR	6.1	2,683.40
Control	6018	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	5	7	7	0.07%	6.12%	PLSDKGTGDSSQITQVSPQR	5.58	2,101.05
Control	6018	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	7	7	11	0.11%	14.80%	ADLVNNLGTIAK	3.67	1,228.69
Control	6018	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	7	7	11	0.11%	14.80%	EDQTEYLEER	2.7	1,311.57
Control	6018	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	7	7	11	0.11%	14.80%	ELISNASDALDK	3.35	1,275.64
Control	6018	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	7	7	11	0.11%	14.80%	ELISNASDALDKIR	3.7	1,544.83
Control	6018	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	7	7	11	0.11%	14.80%	GVVDSEDLPLNISR	4.57	1,513.79
Control	6018	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	7	7	11	0.11%	14.80%	HSQFIGYPITLYLEK	2.97	1,808.96
Control	6018	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	7	7	11	0.11%	14.80%	NPDDITQEEYGEFYK	2.83	1,847.80
Control	6018	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	7	7	11	0.11%	14.80%	TLTLVDTGIGMTK	4.31	1,365.73
Control	6018	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	7	7	11	0.11%	14.80%	YESLTDPSKLDSGK	3.95	1,539.75

Control	6018	RecName: Full=Adiponectin; AltName: Full=Adipocyte, C1q and collagen domain-containing protein; AltName: Full=30 kDa adipocyte complement-related protein; AltName: Full=Adipocyte complement-related 30	gi|114158576,gi|146186777,gi|73697558	26,115.60	100.00%	3	4	5	0.05%	16.20%	IFYNQQNHYDGTTGK	3.9	1,785.82
Control	6018	RecName: Full=Adiponectin; AltName: Full=Adipocyte, C1q and collagen domain-containing protein; AltName: Full=30 kDa adipocyte complement-related protein; AltName: Full=Adipocyte complement-related 30	gi|114158576,gi|146186777,gi|73697558	26,115.60	100.00%	3	4	5	0.05%	16.20%	NVDQASGSVLLYLEK	3.63	1,635.86

Control	6018	RecName: Full=Adiponectin; AltName: Full=Adipocyte, C1q and collagen domain-containing protein; AltName: Full=30 kDa adipocyte complement-related protein; AltName: Full=Adipocyte complement-related 30	gi|114158576,gi|146186777,gi|73697558	26,115.60	100.00%	3	4	5	0.05%	16.20%	SAFSVGLER	2.24	965.505
Control	6018	Solute carrier family 1 (neutral amino acid transporter), member 5	gi|115305216,gi|15145909,gi|21541958,gi|27807087	56,431.20	99.80%	2	2	3	0.03%	4.45%	EVLDSFLDLVR	2.76	1,305.71
Control	6018	Solute carrier family 1 (neutral amino acid transporter), member 5	gi|115305216,gi|15145909,gi|21541958,gi|27807087	56,431.20	99.80%	2	2	3	0.03%	4.45%	NIFPSNLVSAAFR	2.31	1,435.77
Control	6018	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	5	0.05%	14.20%	ALDLFSDNAPPPELLEIINEDVAKK	2.51	2,751.45
Control	6018	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	5	0.05%	14.20%	GSFSEQGINEFLR	3.79	1,483.72

Control	6018	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	5	0.05%	14.20%	GSTAPVGGGAFPTISTR	3.49	1,575.81
Control	6018	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	5	0.05%	14.20%	LAAVDATVNQVLASR	3.58	1,527.85
Control	6018	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	5	0.05%	14.20%	TGEAIVDAALSALR	2.68	1,386.76
Control	6018	hypothetical protein LOC506149	gi|114052080,gi|122136337,gi|85057041	11,432.50	99.80%	2	2	3	0.03%	22.40%	MSFGLLR	2.03	839.4445
Control	6018	hypothetical protein LOC506149	gi|114052080,gi|122136337,gi|85057041	11,432.50	99.80%	2	2	3	0.03%	22.40%	VFSIVIPFLYVGTLISK	2.8	1,896.12
Control	6018	cytochrome c oxidase subunit 2	gi|33321665,gi|70988004,gi|70988018,gi|70988032,gi|70988046,gi|70988060,gi|70988074,gi|70988088,gi|70988102,gi|70988116,gi|70988130	26,004.80	99.80%	2	3	3	0.03%	24.20%	ILYMMDEINNPSLTVK	3.65	1,896.94
Control	6018	cytochrome c oxidase subunit 2	gi|33321665,gi|70988004,gi|70988018,gi|70988032,gi|70988046,gi|70988060,gi|70988074,gi|70988088,gi|70988102,gi|70988116,gi|70988130	26,004.80	99.80%	2	3	3	0.03%	24.20%	LNQTTLMSSRPGLYYGQCSEICGSNHSFMPIVLELVPLK	2.99	4,342.14

Control	6018	Deoxyribonuclease I-like 1	gi|151553571	35,175.30	99.80%	2	2	2	0.02%	8.86%	IVLHGEHLQSLLR	2.24	1,514.88
Control	6018	Deoxyribonuclease I-like 1	gi|151553571	35,175.30	99.80%	2	2	2	0.02%	8.86%	VLPSLVLVPLHTTPK	3.89	1,614.00
ATP	6006	Chain B, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591027,gi|110591030,gi|114686,gi|27807305,gi|599873,gi|74356487	18,544.10	99.80%	2	2	2	0.02%	19.40%	IQEYEKELEK	3.29	1,308.67
ATP	6006	Chain B, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591027,gi|110591030,gi|114686,gi|27807305,gi|599873,gi|74356487	18,544.10	99.80%	2	2	2	0.02%	19.40%	NIIPFDQMTIEDLNEVFPETK	2.52	2,509.22
ATP	6006	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	10	11	17	0.18%	15.20%	AQILLDCGEDNICVPDLQLEVFGEQNHVYLGDK	4.26	3,687.77
ATP	6006	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	10	11	17	0.18%	15.20%	DLDGNGYPDLIVGSFGVDK	3.65	1,980.96
ATP	6006	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	10	11	17	0.18%	15.20%	DVPGRSPASSGPQILK	3.96	1,608.87
ATP	6006	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	10	11	17	0.18%	15.20%	FGSSLTPLGDLDQDGYNDVAIGAAFGGENR	3.68	3,056.42

ATP	6006	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	10	11	17	0.18%	15.20%	GGRDLDGNGYPDLIVGSFGVDK	3.09	2,251.10
ATP	6006	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	10	11	17	0.18%	15.20%	LAGMEPTPTLTLTGQDEFGR	4.59	2,150.04
ATP	6006	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	10	11	17	0.18%	15.20%	QATLTQTLLIQNGAR	4.05	1,627.91
ATP	6006	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	10	11	17	0.18%	15.20%	TIQFDFQILSK	3.15	1,339.73
ATP	6006	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	10	11	17	0.18%	15.20%	VTAPPEAEYSGLVR	3.35	1,488.77
ATP	6006	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	10	11	17	0.18%	15.20%	VYIYLQR	2.7	954.5407

ATP	6006	PREDICTED: similar to EGF-like repeats and discoidin I-like domains 3	gi|119895885	52,071.20	100.00%	2	2	2	0.02%	9.03%	DKVFQGNFDNDTHRK	3.2	1,820.87
ATP	6006	PREDICTED: similar to EGF-like repeats and discoidin I-like domains 3	gi|119895885	52,071.20	100.00%	2	2	2	0.02%	9.03%	GTNEDMVFHGNVDNNTPYANSFTPPIK	3.23	2,995.35
ATP	6006	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	2	4	9	0.09%	14.00%	YVDSEGHLYTVPIR	2.64	1,648.83
ATP	6006	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	2	4	9	0.09%	14.00%	YVDSEGHLYTVPIREQGNIYKPNNK	5.57	2,934.47
ATP	6006	RTN3 protein	gi|115305093,gi|122132179,gi|146231798,gi|151554368,gi|32880223,gi|38327594	25,478.60	99.80%	2	3	4	0.04%	5.49%	TQIDHYVGIAR	3.41	1,272.67
ATP	6006	RTN3 protein	gi|115305093,gi|122132179,gi|146231798,gi|151554368,gi|32880223,gi|38327594	25,478.60	99.80%	2	3	4	0.04%	5.49%	YKTQIDHYVGIAR	3.54	1,563.83
ATP	6006	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	6	7	8	0.08%	23.40%	DNFHGLAIFLDTYPNDETTER	3.45	2,468.14
ATP	6006	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	6	7	8	0.08%	23.40%	DNVDDPTGNFR	3.22	1,249.54
ATP	6006	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	6	7	8	0.08%	23.40%	DRLVPGPVFGSK	2.69	1,271.71
ATP	6006	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	6	7	8	0.08%	23.40%	LPTGYYFGASAGTGDLSDNHDIISMK	4.91	2,746.27
ATP	6006	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	6	7	8	0.08%	23.40%	NRDHDTFLAVR	3.24	1,343.68
ATP	6006	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	6	7	8	0.08%	23.40%	SPKDNVDDPTGNFR	3.99	1,561.72

ATP	6006	RPS9 protein	gi|151554648,gi|151554779,gi|155372029,gi|189044386,gi|190576593,gi|197215709,gi|217418300	22,574.50	99.70%	2	2	2	0.02%	9.79%	LIGEYGLR	2.25	920.5201
ATP	6006	RPS9 protein	gi|151554648,gi|151554779,gi|155372029,gi|189044386,gi|190576593,gi|197215709,gi|217418300	22,574.50	99.70%	2	2	2	0.02%	9.79%	QVVNIPSFIVR	2.59	1,271.75
ATP	6006	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	3	3	4	0.04%	6.83%	EIILVDDYSNDPEDGALLGK	3.39	2,176.07
ATP	6006	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	3	3	4	0.04%	6.83%	EIILVDDYSNDPEDGALLGKIEK	3.62	2,546.29
ATP	6006	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	3	3	4	0.04%	6.83%	QHPYTFPGGSGTVFAR	3.14	1,721.84
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	ADIGVAMGIAGSDVSK	4.92	1,506.75
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	AVAGDASESALLK	4.07	1,231.65
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	AVFQANQDNLPILK	3.52	1,570.86

ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	AVFQANQDNLPILKR	2.36	1,726.96
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	EQPLDEELKDAFQNAYLELGGLGER	3.9	2,834.38
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	EVSMDDHKLSLDELHR	3.79	1,939.92
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	EVSMDDHKLSLDELHRK	2.75	2,068.01
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	GIVVYTGDR	2.74	979.5208
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	GIVVYTGDRTVMGR	1.69	1,539.80
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	GVGIISEGNETVEDIAAR	4.84	1,829.92
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	IVEIPFNSTNK	2.87	1,261.68
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	IVEIPFNSTNKYQLSIHK	2.15	2,131.15
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	KADIGVAMGIAGSDVSK	4.26	1,634.84

ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	LNIPVSQVNPR	4.68	1,236.71
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	LSLDELHR	2.55	982.5317
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	MSINAEEVVVGDLVEVK	3.78	1,846.95
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	NMVPQQALVIR	3.5	1,284.71
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	QAADMILLDDNFASIVTGVEEGR	3.54	2,480.20
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	QAADMILLDDNFASIVTGVEEGRLIFDNLKK	5.3	3,451.78
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	QGAIVAVTGDGVNDSPALK	4.79	1,811.95
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	QGAIVAVTGDGVNDSPALKK	3.83	1,940.05
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	RAVAGDASESALLK	3.01	1,387.75
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	SPDFTNENPLETR	4.22	1,519.70

ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	VDNSSLTGESEPQTR	3.62	1,619.75
ATP	6006	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	25	44	68	0.72%	26.20%	VIMVTGDHPITAK	4.6	1,397.75
ATP	6006	PREDICTED: similar to C4b-binding protein alpha chain precursor (C4bp) (Proline-rich protein) (PRP)	gi|76677514	21,762.00	100.00%	3	4	4	0.04%	15.40%	DQYVSPETVTVR	3.09	1,393.70
ATP	6006	PREDICTED: similar to C4b-binding protein alpha chain precursor (C4bp) (Proline-rich protein) (PRP)	gi|76677514	21,762.00	100.00%	3	4	4	0.04%	15.40%	LSLEIEKLEQEKR	1.78	1,614.91
ATP	6006	PREDICTED: similar to C4b-binding protein alpha chain precursor (C4bp) (Proline-rich protein) (PRP)	gi|76677514	21,762.00	100.00%	3	4	4	0.04%	15.40%	LSVEKDQYVSPETVTVR	3.69	1,950.02
ATP	6006	COL18A1 protein	gi|133778103,gi|134085613,gi|157742960	135,049.70	100.00%	2	2	2	0.02%	2.33%	LFVAQAGGADPEKFQGLISELR	4.49	2,346.25
ATP	6006	COL18A1 protein	gi|133778103,gi|134085613,gi|157742960	135,049.70	100.00%	2	2	2	0.02%	2.33%	LQDLYSIVR	3.18	1,106.62
ATP	6006	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	3	3	3	0.03%	25.60%	AFDLLVDRPVTLVR	2.38	1,613.94

ATP	6006	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	3	3	3	0.03%	25.60%	AYQDRYHDLGAHYSAR	3.01	1,922.89
ATP	6006	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	3	3	3	0.03%	25.60%	DYKVDQEIVNIIQER	3.02	1,861.97
ATP	6006	ribosomal protein L18	gi|59858459,gi|62752012,gi|75060915,gi|75775560,gi|89573893	21,518.10	99.80%	2	3	3	0.03%	11.20%	TNRPPLSLSR	3.27	1,140.65
ATP	6006	ribosomal protein L18	gi|59858459,gi|62752012,gi|75060915,gi|75775560,gi|89573893	21,518.10	99.80%	2	3	3	0.03%	11.20%	TNSTFNQVVLK	2.84	1,250.67
ATP	6006	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	7	10	13	0.14%	13.30%	AFEESLSTLK	2.44	1,124.58
ATP	6006	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	7	10	13	0.14%	13.30%	HTLGENIADNGGLK	4.14	1,438.73
ATP	6006	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	7	10	13	0.14%	13.30%	NEIVFPAGILQAPFYTR	3.88	1,936.03
ATP	6006	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	7	10	13	0.14%	13.30%	RRDEELIYHK	2.28	1,358.72
ATP	6006	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	7	10	13	0.14%	13.30%	TPESSHEGLITDPHSPSR	4.07	1,946.92

ATP	6006	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	7	10	13	0.14%	13.30%	VFNDYTAVPDLYFENAMR	3.47	2,181.00
ATP	6006	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	7	10	13	0.14%	13.30%	VLTGYLNYMVQLGK	2.85	1,614.86
ATP	6006	secretory carrier membrane protein 3 isoform 1	gi|61553277,gi|71649517,gi|73586519,gi|78369651	38,260.60	99.80%	2	3	3	0.03%	9.80%	AQQEFAAGVFSNPAVR	3.92	1,691.85
ATP	6006	secretory carrier membrane protein 3 isoform 1	gi|61553277,gi|71649517,gi|73586519,gi|78369651	38,260.60	99.80%	2	3	3	0.03%	9.80%	TAAANAAAGAAENAFRAP	2.71	1,644.81
ATP	6006	anchor attachment protein 1	gi|61555046,gi|66792846,gi|74267686	67,439.00	99.80%	2	2	2	0.02%	3.89%	KLPFPDETHER	2.97	1,368.69
ATP	6006	anchor attachment protein 1	gi|61555046,gi|66792846,gi|74267686	67,439.00	99.80%	2	2	2	0.02%	3.89%	SVGLEVYTQSFSR	3.84	1,472.74
ATP	6006	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	4	5	5	0.05%	14.20%	GHAAPTPTPVKPPR	2.73	1,425.80
ATP	6006	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	4	5	5	0.05%	14.20%	KGHAAPTPTPVKPPR	1.93	1,553.89
ATP	6006	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	4	5	5	0.05%	14.20%	LEANHGLLVAR	3.37	1,192.68
ATP	6006	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	4	5	5	0.05%	14.20%	RIQSNLGALSR	3.08	1,214.70
ATP	6006	PREDICTED: similar to Thrombospondin type-1 domain-containing protein 7A	gi|194665998	183,582.80	99.80%	2	2	2	0.02%	2.91%	GNQTALCGGGVQTREAYCVQANENLLSLNTHKDK	2.94	3,632.75

ATP	6006	PREDICTED: similar to Thrombospondin type-1 domain-containing protein 7A	gi|194665998	183,582.80	99.80%	2	2	2	0.02%	2.91%	LKPLTLAYDGDADM	4.64	1,538.74
ATP	6006	SCAMP2 protein	gi|151554759,gi|156120987	36,685.40	99.80%	2	2	2	0.02%	9.76%	ELQNTVANLHVR	2.24	1,393.75
ATP	6006	SCAMP2 protein	gi|151554759,gi|156120987	36,685.40	99.80%	2	2	2	0.02%	9.76%	TGASFQQAQEEFSQGIFSSR	2.54	2,205.02
ATP	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	14	26	95	1.00%	62.10%	DNIQGITKPAIR	4.08	1,325.75
ATP	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	14	26	95	1.00%	62.10%	DNIQGITKPAIRR	2.45	1,481.85
ATP	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	14	26	95	1.00%	62.10%	ISGLIYEETR	4.19	1,180.62
ATP	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	14	26	95	1.00%	62.10%	ISGLIYEETRGVLK	4.57	1,577.89
ATP	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	14	26	95	1.00%	62.10%	KTVTAMDVVYALK	4.56	1,454.79

ATP	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	14	26	95	1.00%	62.10%	KTVTAMDVVYALKR	3.98	1,610.89
ATP	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	14	26	95	1.00%	62.10%	RISGLIYEETRGVLK	3.31	1,733.99
ATP	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	14	26	95	1.00%	62.10%	RKTVTAMDVVYALK	3.96	1,610.89
ATP	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	14	26	95	1.00%	62.10%	TVTAMDVVYALK	4.08	1,326.70
ATP	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	14	26	95	1.00%	62.10%	TVTAMDVVYALKR	3.25	1,482.80
ATP	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	14	26	95	1.00%	62.10%	VFLENVIR	3.72	989.5778
ATP	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	14	26	95	1.00%	62.10%	VFLENVIRDAVTYTEHAK	5.34	2,105.10

ATP	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	14	26	95	1.00%	62.10%	VFLENVIRDAVTYTEHAKR	4.96	2,261.20
ATP	6006	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	14	26	95	1.00%	62.10%	VLRDNIQGITKPAIR	4.31	1,694.01
ATP	6006	RecName: Full=Cleft lip and palate transmembrane protein 1 homolog	gi|110278913,gi|114051439,gi|84708720	75,864.60	99.80%	2	3	3	0.03%	4.48%	ALNTFIDDLFAFVIK	4.01	1,726.94
ATP	6006	RecName: Full=Cleft lip and palate transmembrane protein 1 homolog	gi|110278913,gi|114051439,gi|84708720	75,864.60	99.80%	2	3	3	0.03%	4.48%	NLLTGETEADPEMIK	3.25	1,676.81
ATP	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	8	10	12	0.13%	16.60%	ALEHHRSEIQAEQDR	2.86	1,818.88
ATP	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	8	10	12	0.13%	16.60%	AVDEAADALLK	2.55	1,115.59
ATP	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	8	10	12	0.13%	16.60%	LAQQEKQEQVKIESLAK	3.95	1,970.09
ATP	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	8	10	12	0.13%	16.60%	QHIALALEK	4.2	1,022.60
ATP	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	8	10	12	0.13%	16.60%	SVIENAKKEEVAGAK	4.64	1,572.86
ATP	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	8	10	12	0.13%	16.60%	TASADLPTVPLGSAVEAIR	3.25	1,868.01

ATP	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	8	10	12	0.13%	16.60%	TDHPETGEGKPKPATSEEASSTSVR	3.61	2,598.23
ATP	6006	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	8	10	12	0.13%	16.60%	VVSQYHELVVQAR	4.6	1,527.83
ATP	6006	Endoplasmic reticulum protein 29	gi|109658363,gi|115495555,gi|143811387	28,789.90	99.80%	2	2	2	0.02%	17.80%	GHGIYLGMPGCLPAYDTLAGEFIRASGVEARQSLLK	3.01	3,806.94
ATP	6006	Endoplasmic reticulum protein 29	gi|109658363,gi|115495555,gi|143811387	28,789.90	99.80%	2	2	2	0.02%	17.80%	SLNILTAFQK	3.33	1,134.65
ATP	6006	ATAD1 protein	gi|154426126,gi|76671592	41,750.40	99.80%	2	3	3	0.03%	11.40%	EYVNSTSEESHDEDEIRPVQQQDLHR	2.5	3,140.42
ATP	6006	ATAD1 protein	gi|154426126,gi|76671592	41,750.40	99.80%	2	3	3	0.03%	11.40%	LQPSIIFIDEIDSFLR	4.1	1,906.03
ATP	6006	PREDICTED: similar to CUB domain containing protein 1	gi|194677155	93,109.80	100.00%	3	3	3	0.03%	4.31%	AFMIIQEQR	3.07	1,151.59
ATP	6006	PREDICTED: similar to CUB domain containing protein 1	gi|194677155	93,109.80	100.00%	3	3	3	0.03%	4.31%	LSLALVPAQK	2.69	1,039.65
ATP	6006	PREDICTED: similar to CUB domain containing protein 1	gi|194677155	93,109.80	100.00%	3	3	3	0.03%	4.31%	STDTPLLDAHEPTEPGE	2.59	1,808.82
ATP	6006	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	3	5	5	0.05%	13.50%	GLFTGLTPR	2.61	961.5467
ATP	6006	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	3	5	5	0.05%	13.50%	SAATLITHPFHVITLR	3.24	1,777.01

ATP	6006	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	3	5	5	0.05%	13.50%	VLIQVGYEPLAPTVGR	3.72	1,711.97
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	AAALRPEEDGAFRPSEAFETLQK	3.62	2,533.27
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	AEESAAHLPEEIR	3.31	1,451.71
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	AEESAAHLPEEIRR	3.14	1,607.81
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	AEESAAHLPEEIRRLEEELGQLK	3.31	2,647.37
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	ALKEVVKEIQTSVK	4.09	1,571.94
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	ASVGQVESDLK	3.56	1,132.58
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	ASVGQVESDLKMLR	2.61	1,548.81
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	DLSDGIHVVK	2.71	1,082.58

ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	EELGQGLQGVEQK	3.7	1,414.72
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	ELVSLKQEQQR	3.48	1,357.74
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	ERDFTSLENTVEER	4.56	1,724.81
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	ERDFTSLENTVEERLTELTK	4.26	2,410.21
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	FKEAADSEHHTLQALTEK	4.7	2,055.01
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	GLGEAQLSLAGDVDELK	3.8	1,714.89
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	GLGEAQLSLAGDVDELKR	4.54	1,870.99
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	GLGEAQLSLAGDVDELKRR	1.99	2,027.09

ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	GLLEDLRNDLDR	1.98	1,428.74
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	GLLEDLRNDLDRLFVK	3.08	1,916.06
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	ILRAEESAAHLPEEIR	3.69	1,833.98
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	ILRAEESAAHLPEEIRR	2.95	1,990.08
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	KPPPAPQQHPPPPAPHPQQQHPPQHPQNQAHGK	3.29	3,630.83
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	LEEELGQLK	3	1,058.57
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	LQNEILKDLSDGIHVVK	3.66	1,921.08
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	LQNEILKDLSDGIHVVKDAR	3.59	2,263.24

ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	LQSVEDGVQAAR	3.86	1,272.65
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	QREELGQGLQGVEQK	5.15	1,698.88
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	QREELGQGLQGVEQKVQSLQATFGTFESLVR	4.04	3,462.80
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	RLEEELGQLK	3.32	1,214.67
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	SINDNIAIFTDVQK	3.04	1,577.82
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	SINDNIAIFTDVQKR	4.24	1,733.92
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	STIQTMESDVYTEVK	3.3	1,746.81
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	STIQTMESDVYTEVKELVSLKQEQQR	3.74	3,085.54

ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	TAVDSLVAYSVK	2.73	1,252.68
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	TAVDSLVAYSVKIETNENNLESAK	4.2	2,595.31
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	VQEQVHTLLGR	3.45	1,279.71
ATP	6006	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	36	53	83	0.87%	54.70%	VQSLQATFGTFESLVR	5.12	1,782.94
ATP	6006	similar to peptidylprolyl isomerase A (cyclophilin A)	gi|28189771,gi|58760424,gi|75948300	17,851.80	99.80%	2	3	3	0.03%	16.50%	SIYGEKFDDENFILK	2.51	1,817.90
ATP	6006	similar to peptidylprolyl isomerase A (cyclophilin A)	gi|28189771,gi|58760424,gi|75948300	17,851.80	99.80%	2	3	3	0.03%	16.50%	VSFELFADKVPK	3.36	1,379.76
ATP	6006	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	3	3	3	0.03%	18.20%	LEDPDGNVLYK	2.35	1,262.63
ATP	6006	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	3	3	3	0.03%	18.20%	SVIDYQTHFR	2.62	1,265.63
ATP	6006	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	3	3	3	0.03%	18.20%	TVYFDFQVGEDPPLFPSENR	2.99	2,357.11
ATP	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	13	17	0.18%	46.30%	AATFGLILDDVSLTHLTFGKEFTEAVEAK	3.64	3,123.63
ATP	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	13	17	0.18%	46.30%	DLQNVNITLR	4.04	1,185.66
ATP	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	13	17	0.18%	46.30%	FDAGELITQR	3.92	1,149.59

ATP	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	13	17	0.18%	46.30%	IFTSIGEDYDER	3.57	1,444.66
ATP	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	13	17	0.18%	46.30%	IFTSIGEDYDERVLPSITTEILK	2.65	2,639.38
ATP	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	13	17	0.18%	46.30%	ILFRPVASQLPR	3.17	1,396.84
ATP	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	13	17	0.18%	46.30%	KLEAAEDIAYQLSR	3.82	1,606.84
ATP	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	13	17	0.18%	46.30%	NITYLPAGQSVLLQLPQ	4.19	1,855.03
ATP	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	13	17	0.18%	46.30%	NVPVITGSKDLQNVNITLR	5.19	2,081.17
ATP	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	13	17	0.18%	46.30%	SRNITYLPAGQSVLLQLPQ	4.09	2,098.17
ATP	6006	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	13	17	0.18%	46.30%	VLPSITTEILK	2.53	1,213.74
ATP	6006	ras-related C3 botulinum toxin substrate 1	gi|27806443,gi|51702785,gi|6007014,gi|73587375	21,432.60	100.00%	3	4	5	0.05%	14.10%	KLTPITYPQGLAMAK	2.94	1,647.91
ATP	6006	ras-related C3 botulinum toxin substrate 1	gi|27806443,gi|51702785,gi|6007014,gi|73587375	21,432.60	100.00%	3	4	5	0.05%	14.10%	LDLRDDKDTIEK	2.1	1,460.76
ATP	6006	ras-related C3 botulinum toxin substrate 1	gi|27806443,gi|51702785,gi|6007014,gi|73587375	21,432.60	100.00%	3	4	5	0.05%	14.10%	LTPITYPQGLAMAK	3.27	1,519.82
ATP	6006	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	3	4	4	0.04%	27.90%	ALAAAGYDVEKNNSR	4.65	1,578.79

ATP	6006	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	3	4	4	0.04%	27.90%	KALAAAGYDVEKNNSR	4.5	1,706.88
ATP	6006	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	3	4	4	0.04%	27.90%	KASGPPVSELITK	3.24	1,326.76
ATP	6006	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	5	5	5	0.05%	19.80%	ILHVNGFNGEGGEDPQAAR	5.4	2,110.00
ATP	6006	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	5	5	5	0.05%	19.80%	LLLLGAGESGK	3.7	1,057.63
ATP	6006	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	5	5	5	0.05%	19.80%	SKIEDYFPEFAR	2.41	1,501.73
ATP	6006	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	5	5	5	0.05%	19.80%	VLTSGIFETK	2.54	1,094.61
ATP	6006	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	5	5	5	0.05%	19.80%	YFIRDEFLR	1.5	1,258.66
ATP	6006	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	5	5	5	0.05%	19.80%	YTTPEDATPEPGEDPR	1.92	1,774.78
ATP	6006	PREDICTED: similar to Transmembrane 9 superfamily member 2 precursor (p76), partial	gi|194671915	72,962.00	100.00%	2	4	4	0.04%	4.40%	IYYHVVETGSMGAR	4.36	1,598.76
ATP	6006	PREDICTED: similar to Transmembrane 9 superfamily member 2 precursor (p76), partial	gi|194671915	72,962.00	100.00%	2	4	4	0.04%	4.40%	RPSENLGQVLFGER	4.74	1,601.84
ATP	6006	interferon stimulated gene 17 [Ovis aries]	gi|12082402,gi|57619183	17,482.10	100.00%	3	3	3	0.03%	19.70%	EVLQEGVPLVHQGLK	4	1,645.93

ATP	6006	interferon stimulated gene 17 [Ovis aries]	gi|12082402,gi|57619183	17,482.10	100.00%	3	3	3	0.03%	19.70%	INVPAFQQR	2.54	1,072.59
ATP	6006	interferon stimulated gene 17 [Ovis aries]	gi|12082402,gi|57619183	17,482.10	100.00%	3	3	3	0.03%	19.70%	LAHLDSREVLQEGVPLVHQGLK	2.78	2,438.35
ATP	6006	RPL12 protein	gi|148744191,gi|42564206,gi|45430019,gi|47117092,gi|74354972	17,801.10	99.80%	2	2	2	0.02%	18.80%	HSGNITFDEIVNIAR	3.23	1,685.86
ATP	6006	RPL12 protein	gi|148744191,gi|42564206,gi|45430019,gi|47117092,gi|74354972	17,801.10	99.80%	2	2	2	0.02%	18.80%	QAQIEVVPSASALIIK	3.41	1,666.97
ATP	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	16	20	27	0.28%	28.60%	AEVQNLGGELVVSGVDSAMSLIQAAK	3.68	2,602.34
ATP	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	16	20	27	0.28%	28.60%	AHVLAASVEQATENFLEKGDK	3.56	2,257.15
ATP	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	16	20	27	0.28%	28.60%	ALKPEVDKLNIMAAK	2.38	1,656.94
ATP	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	16	20	27	0.28%	28.60%	ESQFLKEELVAAVEDVRK	2.2	2,090.11
ATP	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	16	20	27	0.28%	28.60%	GKGPLKNTSDVISAAK	3.24	1,585.89
ATP	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	16	20	27	0.28%	28.60%	HVNPVQALSEFKAMDSI	2.91	1,901.94
ATP	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	16	20	27	0.28%	28.60%	IAEQVASFQEEK	3.71	1,378.68
ATP	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	16	20	27	0.28%	28.60%	LLILADMADVYK	3.27	1,380.74
ATP	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	16	20	27	0.28%	28.60%	NAGTEQDLGIQYK	2.72	1,436.70

ATP	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	16	20	27	0.28%	28.60%	NLMNAVVQTVK	2.92	1,232.67
ATP	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	16	20	27	0.28%	28.60%	QALQDLLSEYMGNAGRK	2.92	1,909.94
ATP	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	16	20	27	0.28%	28.60%	QIIVDPLSFSEER	3.28	1,532.80
ATP	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	16	20	27	0.28%	28.60%	TSVQTEDDQLIAGQSAR	3.78	1,818.88
ATP	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	16	20	27	0.28%	28.60%	VIHVVTSEMDNYEPGVYTEK	4.57	2,326.09
ATP	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	16	20	27	0.28%	28.60%	VKAEVQNLGGELVVSGVDSAMSLIQAAK	4.54	2,829.50
ATP	6006	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	16	20	27	0.28%	28.60%	VLTDAVDDITSIDDFLAVSENHILEDVNK	4.03	3,200.58
ATP	6006	RecName: Full=Transmembrane and coiled-coil domain-containing protein 1	gi|109895213,gi|74354058,gi|77736477	21,158.30	99.80%	2	2	2	0.02%	15.40%	LPFTPLSYIQGLSHR	3.77	1,728.94
ATP	6006	RecName: Full=Transmembrane and coiled-coil domain-containing protein 1	gi|109895213,gi|74354058,gi|77736477	21,158.30	99.80%	2	2	2	0.02%	15.40%	QAGGFLGPPPPSGK	2.88	1,309.69
ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	AKFEELNMDLFR	4.89	1,528.75

ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	DAGTIAGLNVMR	3.25	1,233.63
ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	ELEEIVQPIISK	3.42	1,397.79
ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	FEELNMDLFR	3.11	1,329.61
ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	IDTRNELESYAYSLK	4.24	1,801.90
ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	IINEPTAAAIAYGLDK	4.01	1,659.90
ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	IINEPTAAAIAYGLDKR	3.83	1,816.00
ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	ITITNDQNRLTPEEIER	3.51	2,042.05
ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	ITPSYVAFTPEGER	3.18	1,566.78

ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	KKELEEIVQPIISK	3.81	1,653.98
ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	KSQIFSTASDNQPTVTIK	3.48	1,965.03
ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	KVTHAVVTVPAYFNDAQR	3.39	2,016.07
ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	MVNDAEKFAEEDKK	3	1,669.77
ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	NQLTSNPENTVFDAK	3.36	1,677.81
ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	NQLTSNPENTVFDAKR	3.73	1,833.91
ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	SQIFSTASDNQPTVTIK	3.34	1,836.93
ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	TFAPEEISAMVLTK	4.15	1,552.79

ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	TKPYIQVDVGGGQTK	4.17	1,590.85
ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	VLEDSDLKKSDIDEIVLVGGSTR	5.91	2,488.31
ATP	6006	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	20	31	37	0.39%	33.40%	VTHAVVTVPAYFNDAQR	3.49	1,887.97
ATP	6006	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	6	7	7	0.07%	12.10%	LNTIPLFVQLLYSSVENIQR	4.35	2,347.30
ATP	6006	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	6	7	7	0.07%	12.10%	LNYGIPAIVK	2.32	1,087.65
ATP	6006	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	6	7	7	0.07%	12.10%	LVQLLVK	2.37	812.5605
ATP	6006	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	6	7	7	0.07%	12.10%	NLSDVATKQEGLESVLK	2.49	1,830.98

ATP	6006	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	6	7	7	0.07%	12.10%	SAIVHLINYQDDAELATR	3.03	2,029.04
ATP	6006	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	6	7	7	0.07%	12.10%	TLVTQNSGVEALIHAILR	3.14	1,935.10
ATP	6006	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	27.80%	AALVDLEPGTMDSVR	3.14	1,589.78
ATP	6006	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	27.80%	GHYTEGAELVDSVLDVVRK	3.22	2,087.08
ATP	6006	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	27.80%	LAVNMVPFPR	3.84	1,159.63
ATP	6006	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	27.80%	LHFFMPGFAPLTAR	3.24	1,620.84
ATP	6006	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	27.80%	MSATFIGNSTAIQELFKR	2.81	2,030.04
ATP	6006	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	27.80%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	3.15	4,479.06
ATP	6006	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	27.80%	YLTVAAVFR	2.35	1,039.59
ATP	6006	phospholipid scramblase 3	gi|114051405,gi|120419474,gi|92098369	32,206.90	99.80%	2	3	3	0.03%	10.90%	EALTDTDDFGLQFPLDLDVR	2.74	2,280.10
ATP	6006	phospholipid scramblase 3	gi|114051405,gi|120419474,gi|92098369	32,206.90	99.80%	2	3	3	0.03%	10.90%	FSIQDADRQTLLR	2.48	1,562.83
ATP	6006	PREDICTED: similar to histone, H2A	gi|76651181,gi|76689692	14,148.10	99.80%	2	2	3	0.03%	35.40%	AGLQFPVGR	3.16	944.5313
ATP	6006	PREDICTED: similar to histone, H2A	gi|76651181,gi|76689692	14,148.10	99.80%	2	2	3	0.03%	35.40%	HLQLAIR	2.43	850.5258

ATP	6006	PREDICTED: similar to histone, H2A	gi|76651181,gi|76689692	14,148.10	99.80%	2	2	3	0.03%	35.40%	HLQLAIRNDEELNKLLGR	3.81	2,132.19
ATP	6006	PREDICTED: similar to histone, H2A	gi|76651181,gi|76689692	14,148.10	99.80%	2	2	3	0.03%	35.40%	NDEELNKLLGR	3.02	1,300.69
ATP	6006	PREDICTED: similar to histone, H2A	gi|76651181,gi|76689692	14,148.10	99.80%	2	2	3	0.03%	35.40%	VTIAQGGVLPNIQAVLLPK	5.02	1,931.17
ATP	6006	syntaxin 7	gi|118150840,gi|122140829,gi|73586654	29,638.60	100.00%	3	3	3	0.03%	13.00%	EFGSLPTTPSDQR	2.95	1,434.69
ATP	6006	syntaxin 7	gi|118150840,gi|122140829,gi|73586654	29,638.60	100.00%	3	3	3	0.03%	13.00%	TLNQLGTPQDSPELR	3.61	1,668.86
ATP	6006	syntaxin 7	gi|118150840,gi|122140829,gi|73586654	29,638.60	100.00%	3	3	3	0.03%	13.00%	TLNQLGTPQDSPELRQQLQQK	2.3	2,422.27
ATP	6006	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	5	6	6	0.06%	29.10%	FLTKGDNNAVDDRGLYK	2.44	1,925.97
ATP	6006	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	5	6	6	0.06%	29.10%	GDLLFLTNRVEDPIR	2.98	1,757.95
ATP	6006	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	5	6	6	0.06%	29.10%	GDLLFLTNRVEDPIRVGEIVVFR	3.52	2,657.48
ATP	6006	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	5	6	6	0.06%	29.10%	MLSLDFLDDVRR	1.95	1,495.76
ATP	6006	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	5	6	6	0.06%	29.10%	VGEIVVFR	2.5	918.5407
ATP	6006	PREDICTED: brain protein 44	gi|119889010,gi|194665199	14,264.40	99.80%	2	4	4	0.04%	18.90%	LRPLYNHPAGPR	3.67	1,390.77
ATP	6006	PREDICTED: brain protein 44	gi|119889010,gi|194665199	14,264.40	99.80%	2	4	4	0.04%	18.90%	VLDKVELLLPEK	3.48	1,395.85
ATP	6006	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	11	13	0.14%	17.70%	EDFESLLHSAK	1.68	1,275.62

ATP	6006	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	11	13	0.14%	17.70%	FLVVLNFGDVGQLAR	4.96	1,647.92
ATP	6006	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	11	13	0.14%	17.70%	FTGLSKEELLK	3.53	1,264.71
ATP	6006	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	11	13	0.14%	17.70%	LLIAGTDSSDLQQILR	4.58	1,742.97
ATP	6006	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	11	13	0.14%	17.70%	NQEDDLTETNLEQIDPIFGSK	4.44	2,406.13
ATP	6006	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	11	13	0.14%	17.70%	NQEDDLTETNLEQIDPIFGSKEDFESLLHSAK	4.77	3,662.73
ATP	6006	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	11	13	0.14%	17.70%	SVSEDRLLIAGTDSSDLQQILR	4.77	2,416.27
ATP	6006	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	11	13	0.14%	17.70%	VDLLLSTQPGR	2.44	1,198.68
ATP	6006	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	9	11	13	0.14%	17.70%	VILDLTPNYK	3.53	1,175.67
ATP	6006	MHC class I antigen	gi|84095083	40,657.50	100.00%	5	7	13	0.14%	19.30%	EGEDQTQDMELVETRPSGDGTFQK	2.32	2,713.19
ATP	6006	MHC class I antigen	gi|84095083	40,657.50	100.00%	5	7	13	0.14%	19.30%	FIAVGYVDDTQFVR	4.62	1,629.83
ATP	6006	MHC class I antigen	gi|84095083	40,657.50	100.00%	5	7	13	0.14%	19.30%	GYRQDAYDGRDYIALNEDLR	4.02	2,403.13
ATP	6006	MHC class I antigen	gi|84095083	40,657.50	100.00%	5	7	13	0.14%	19.30%	QDAYDGRDYIALNEDLR	3.03	2,026.95
ATP	6006	MHC class I antigen	gi|84095083	40,657.50	100.00%	5	7	13	0.14%	19.30%	YLENGKDTLLR	2.07	1,321.71
ATP	6006	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	3	3	3	0.03%	4.31%	ALLELQLEPEELYQTFQR	3.4	2,220.15

ATP	6006	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	3	3	3	0.03%	4.31%	FSVSPVVR	2.04	890.5093
ATP	6006	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	3	3	3	0.03%	4.31%	VFSGLVSTGLK	2.98	1,107.64
ATP	6006	RecName: Full=Serine palmitoyltransferase 1; AltName: Full=Serine-palmitoyl-CoA transferase 1; Short=SPT 1; Short=SPT1; AltName: Full=Long chain base biosynthesis protein 1; Short=L	gi|122139929,gi|75948211,gi|77736443	52,771.80	99.80%	2	4	4	0.04%	5.92%	LLKEQEIEDQKNPR	3.79	1,739.93
ATP	6006	RecName: Full=Serine palmitoyltransferase 1; AltName: Full=Serine-palmitoyl-CoA transferase 1; Short=SPT 1; Short=SPT1; AltName: Full=Long chain base biosynthesis protein 1; Short=L	gi|122139929,gi|75948211,gi|77736443	52,771.80	99.80%	2	4	4	0.04%	5.92%	VVVTVEQTEEDLEK	2.98	1,617.82

ATP	6006	RecName: Full=Synaptic glycoprotein SC2; AltName: Full=Trans-2,3-enoyl-CoA reductase; Short=TER	gi|122140918,gi|73586600,gi|77736441	36,056.10	99.80%	2	2	2	0.02%	7.79%	LPVGTTATLYFR	4.05	1,338.74
ATP	6006	RecName: Full=Synaptic glycoprotein SC2; AltName: Full=Trans-2,3-enoyl-CoA reductase; Short=TER	gi|122140918,gi|73586600,gi|77736441	36,056.10	99.80%	2	2	2	0.02%	7.79%	MKHYEVEILDAK	3.46	1,491.75
ATP	6006	RecName: Full=Calcium/calmodulin-dependent protein kinase type II beta chain; Short=CaM-kinase II beta chain; Short=CaM kinase II subunit beta; Short=CaMK-II subunit beta	gi|118572489,gi|75773666,gi|78369262	60,464.50	99.80%	2	2	2	0.02%	9.23%	DLKPENLLLASK	2.71	1,340.78

ATP	6006	RecName: Full=Calcium/calmodulin-dependent protein kinase type II beta chain; Short=CaM-kinase II beta chain; Short=CaM kinase II subunit beta; Short=CaMK-II subunit beta	gi|118572489,gi|75773666,gi|78369262	60,464.50	99.80%	2	2	2	0.02%	9.23%	LYQQIKAGAYDFPSPEWDTVTPEAKNLINQMLTINPAK	3.42	4,321.19
ATP	6006	PREDICTED: similar to Calpain-5 (nCL-3) (htra-3) isoform 1	gi|76636134	72,988.00	99.90%	2	2	2	0.02%	4.69%	ANADDLQALHTLHLR	3.53	1,687.89
ATP	6006	PREDICTED: similar to Calpain-5 (nCL-3) (htra-3) isoform 1	gi|76636134	72,988.00	99.90%	2	2	2	0.02%	4.69%	NSRQPSDLPGTVAVR	3.09	1,596.85
ATP	6006	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	7	10	13	0.14%	41.20%	AVEFQEAQAYAEDNSLLFMETSAK	4.27	2,708.24
ATP	6006	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	7	10	13	0.14%	41.20%	GVDLQENNPASR	2.03	1,299.63
ATP	6006	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	7	10	13	0.14%	41.20%	KLPKNEPQNAAGAPGR	3.27	1,647.89
ATP	6006	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	7	10	13	0.14%	41.20%	LVLLGESAVGK	2.87	1,085.66
ATP	6006	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	7	10	13	0.14%	41.20%	NRGVDLQENNPASR	4.8	1,569.77

ATP	6006	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	7	10	13	0.14%	41.20%	QASPNIVIALAGNK	3.65	1,395.80
ATP	6006	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	7	10	13	0.14%	41.20%	YHSLAPMYYR	2.55	1,316.61
ATP	6006	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	3	4	7	0.07%	21.60%	ELNVMFIETSAK	3.3	1,397.70
ATP	6006	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	3	4	7	0.07%	21.60%	GSDVIIMLVGNKTDLADKR	3.5	2,061.10
ATP	6006	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	3	4	7	0.07%	21.60%	VAAALPGMESTQDR	2.17	1,461.70
ATP	6006	Chain F, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Oxidized State	gi|149241541,gi|149241554,gi|149241571,gi|149241584,gi|149241601,gi|149241614	10,651.90	99.80%	2	2	2	0.02%	12.20%	GQDPYNILAPK	2.8	1,215.64
ATP	6006	Chain F, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Oxidized State	gi|149241541,gi|149241554,gi|149241571,gi|149241584,gi|149241601,gi|149241614	10,651.90	99.80%	2	2	2	0.02%	12.20%	KGQDPYNILAPK	2.97	1,343.73

ATP	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	5	8	0.08%	28.50%	DLTDYLMK	2.38	1,014.48
ATP	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	5	8	0.08%	28.50%	GYSFTTTAER	3.24	1,132.53
ATP	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	5	8	0.08%	28.50%	GYSFTTTAEREIVR	1.81	1,629.82
ATP	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	5	8	0.08%	28.50%	HQGVMVGMGQKDCYVGDEAQSK	3.01	2,383.05
ATP	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	5	8	0.08%	28.50%	HQGVMVGMGQKDCYVGDEAQSKR	4.14	2,539.15
ATP	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	5	8	0.08%	28.50%	IKIIAPPER	2.89	1,036.65
ATP	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	5	8	0.08%	28.50%	IKIIAPPERK	2.84	1,164.75
ATP	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	5	8	0.08%	28.50%	LDLAGRDLTDYLMK	3.45	1,639.84

ATP	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	5	8	0.08%	28.50%	SYELPDGQVITIGNER	4	1,790.89
ATP	6006	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	5	8	0.08%	28.50%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	5.71	3,199.61
ATP	6006	Transducin (beta)-like 2	gi|112362303,gi|115495815	49,894.00	99.80%	2	2	2	0.02%	5.83%	APIVNIGIADTGK	3.51	1,268.72
ATP	6006	Transducin (beta)-like 2	gi|112362303,gi|115495815	49,894.00	99.80%	2	2	2	0.02%	5.83%	LQQQLTQAQEALK	2.89	1,498.82
ATP	6006	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	8	12	12	0.13%	11.00%	FKASGVEGTDVVK	4.28	1,336.71
ATP	6006	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	8	12	12	0.13%	11.00%	GKFNTSDVSAIEK	3.22	1,395.71
ATP	6006	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	8	12	12	0.13%	11.00%	KIDKYLYAMR	2.57	1,316.70
ATP	6006	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	8	12	12	0.13%	11.00%	LSDETLLDIMNR	3.51	1,435.71
ATP	6006	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	8	12	12	0.13%	11.00%	NKEGLHNAKEILTR	3.4	1,622.90
ATP	6006	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	8	12	12	0.13%	11.00%	QIEETLAHFSLTK	3.5	1,516.80
ATP	6006	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	8	12	12	0.13%	11.00%	SANLVAATLGAILSR	4.31	1,456.85
ATP	6006	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	8	12	12	0.13%	11.00%	TTVGVDGSLYK	2.57	1,139.59
ATP	6006	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	3	5	5	0.05%	6.87%	INENTGSVSVTR	3.23	1,276.65
ATP	6006	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	3	5	5	0.05%	6.87%	SIVVSPILIPENQR	3.95	1,564.91

ATP	6006	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	3	5	5	0.05%	6.87%	TLEGPVPLEVIVIDQNDNRPIFR	3.23	2,634.43
ATP	6006	EGF, latrophilin and seven transmembrane domain containing 1	gi|115305144,gi|116004035	77,458.50	99.80%	2	2	2	0.02%	3.34%	IRHIEEPVALLR	4.06	1,445.86
ATP	6006	EGF, latrophilin and seven transmembrane domain containing 1	gi|115305144,gi|116004035	77,458.50	99.80%	2	2	2	0.02%	3.34%	LIHTAEQATLR	3.18	1,252.70
ATP	6006	PREDICTED: similar to ER lumen protein retaining receptor 3 (KDEL receptor 3) (KDEL endoplasmic reticulum protein retention receptor 3)	gi|119893224	24,969.50	99.80%	2	2	2	0.02%	11.20%	ILGDLSHLLAMILLLGK	4.6	1,836.10
ATP	6006	PREDICTED: similar to ER lumen protein retaining receptor 3 (KDEL receptor 3) (KDEL endoplasmic reticulum protein retention receptor 3)	gi|119893224	24,969.50	99.80%	2	2	2	0.02%	11.20%	LSLPMPI	1.83	786.4432

ATP	6006	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	11	14	14	0.15%	22.10%	FAIQTDPNSNDGLVTVVKPIDFETNR	3.51	2,890.46
ATP	6006	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	11	14	14	0.15%	22.10%	FLEAGIYEVPIIITDSGNPPK	3.16	2,273.21
ATP	6006	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	11	14	14	0.15%	22.10%	GPFPQELVR	2.5	1,042.57

ATP	6006	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	11	14	14	0.15%	22.10%	LDERPIHAEPQYPVR	2.38	1,819.95
ATP	6006	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	11	14	14	0.15%	22.10%	MYVLTVAAENQVPLAK	3.12	1,762.94
ATP	6006	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	11	14	14	0.15%	22.10%	QLLIDPEDDVR	2.61	1,312.67

ATP	6006	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	11	14	14	0.15%	22.10%	QLLIDPEDDVRDNILK	2.01	1,896.01
ATP	6006	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	11	14	14	0.15%	22.10%	SAAPHPGDIGDFINEGLK	4.4	1,837.91
ATP	6006	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	11	14	14	0.15%	22.10%	YDEEGGGEEDQDYDLSQLQQPDTVEPDAIKPVGIR	4.67	3,905.78

ATP	6006	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	11	14	14	0.15%	22.10%	YSVTGPGADQPPTGIFIINPISGQLSVTKPLDR	3.22	3,438.83
ATP	6006	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	11	14	14	0.15%	22.10%	YSVTGPGADQPPTGIFIINPISGQLSVTKPLDRELIAR	3.65	4,021.18
ATP	6006	RecName: Full=Cytochrome c1, heme protein, mitochondrial; AltName: Full=Ubiquinol-cytochrome-c reductase complex cytochrome c1 subunit; Short=Cytochrome c-1; AltName: Full=Cytochrome b-c1 complex	gi|109940069,gi|114793904,gi|71042588,gi|75765182,gi|75765193,gi|82407279,gi|82407290,gi|83638779,gi|84000289	35,279.50	99.90%	2	3	4	0.04%	11.10%	LSDYFPKPYPNPEAAR	3.68	1,864.92

ATP	6006	RecName: Full=Cytochrome c1, heme protein, mitochondrial; AltName: Full=Ubiquinol-cytochrome-c reductase complex cytochrome c1 subunit; Short=Cytochrome c-1; AltName: Full=Cytochrome b-c1 complex	gi|109940069,gi|114793904,gi|71042588,gi|75765182,gi|75765193,gi|82407279,gi|82407290,gi|83638779,gi|84000289	35,279.50	99.90%	2	3	4	0.04%	11.10%	MGLKMLLMMGLLLPLVYAMK	2.7	2,266.26
ATP	6006	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	100.00%	3	4	7	0.07%	40.80%	ELAEAQEDTILK	3.86	1,359.70
ATP	6006	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	100.00%	3	4	7	0.07%	40.80%	RIERELAEAQEDTILK	2.66	1,914.03
ATP	6006	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	100.00%	3	4	7	0.07%	40.80%	YSALFLGMAYGAK	4.07	1,407.70
ATP	6006	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	8	10	10	0.11%	27.10%	FDEGRNNFEGEVTKEK	2.66	1,898.89
ATP	6006	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	8	10	10	0.11%	27.10%	FLESGGQDGAGDDDDLEDLEEAEEPDLEEDDDQKAVKDEL	5.48	4,394.84
ATP	6006	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	8	10	10	0.11%	27.10%	GNFDEALAAHK	1.64	1,172.57
ATP	6006	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	8	10	10	0.11%	27.10%	HNQLPLVIEFTEQTAPK	3.9	1,965.04
ATP	6006	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	8	10	10	0.11%	27.10%	ILFIFIDSDHTDNQR	2.12	1,833.91
ATP	6006	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	8	10	10	0.11%	27.10%	LITLEEEMTK	2.74	1,222.62
ATP	6006	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	8	10	10	0.11%	27.10%	VDATEESDLAQQYGVR	3.35	1,780.83
ATP	6006	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	8	10	10	0.11%	27.10%	YQLDKDGVVLFKK	3.4	1,552.87

ATP	6006	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	3	4	5	0.05%	16.10%	FTRNEFNLESK	3.65	1,384.69
ATP	6006	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	3	4	5	0.05%	16.10%	GAVGALLVYDIAK	3.49	1,289.75
ATP	6006	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	3	4	5	0.05%	16.10%	VVLIGDSGVGK	2.54	1,043.61
ATP	6006	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	99.80%	2	2	2	0.02%	9.72%	IPDEFDNDPILVQQLR	3.14	1,911.98
ATP	6006	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	99.80%	2	2	2	0.02%	9.72%	TVLEHYALEEDPLEAFKQR	2.63	2,288.16
ATP	6006	PREDICTED: ATP-binding cassette, sub-family B (MDR/TAP), member 1	gi|194685301	144,522.00	100.00%	3	3	3	0.03%	3.57%	ILLLDEATSALDTESEAVVQAALDK	3.35	2,615.37
ATP	6006	PREDICTED: ATP-binding cassette, sub-family B (MDR/TAP), member 1	gi|194685301	144,522.00	100.00%	3	3	3	0.03%	3.57%	STVVQLLER	2.53	1,044.60
ATP	6006	PREDICTED: ATP-binding cassette, sub-family B (MDR/TAP), member 1	gi|194685301	144,522.00	100.00%	3	3	3	0.03%	3.57%	YGREDVTMDEIQK	3.33	1,599.73

ATP	6006	PREDICTED: similar to DIP2 disco-interacting protein 2 homolog B	gi|119892137	171,462.20	99.80%	2	2	2	0.02%	3.24%	DLGQIEENDLVR	3.16	1,400.70
ATP	6006	PREDICTED: similar to DIP2 disco-interacting protein 2 homolog B	gi|119892137	171,462.20	99.80%	2	2	2	0.02%	3.24%	GEPLGVICNWPPALESALQRWGTTQAKCPCLTALDVTGK	3.6	4,124.08
ATP	6006	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	33,055.70	100.00%	3	3	3	0.03%	19.10%	NASEMIDKLTLTFNR	3.66	1,768.89
ATP	6006	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	33,055.70	100.00%	3	3	3	0.03%	19.10%	TEEKPIFSLDTISSAESMSIYDDIDADVLR	4.33	3,376.60
ATP	6006	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	33,055.70	100.00%	3	3	3	0.03%	19.10%	VYGVGSLALYEK	4.07	1,298.70
ATP	6006	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	2	2	3	0.03%	17.10%	TLMNLGGLAVAR	3.16	1,231.68
ATP	6006	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	2	2	3	0.03%	17.10%	YFSDNQLQEGKNVIGLQMGTNR	4.82	2,528.22

ATP	6006	PREDICTED: similar to Heparan sulfate 2-O-sulfotransferase 1 (2-O-sulfotransferase) (2OST), partial	gi|119889909	37,063.70	99.80%	2	2	2	0.02%	8.28%	EKDGDLYILAQNFFYEK	3.34	2,093.02
ATP	6006	PREDICTED: similar to Heparan sulfate 2-O-sulfotransferase 1 (2-O-sulfotransferase) (2OST), partial	gi|119889909	37,063.70	99.80%	2	2	2	0.02%	8.28%	LVSYYYFLR	2.37	1,223.65
ATP	6006	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	8	9	0.09%	9.75%	FVKEMNLFR	2.53	1,199.62
ATP	6006	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	8	9	0.09%	9.75%	IMKVEYHLLSPYVSPR	4.53	1,948.04
ATP	6006	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	8	9	0.09%	9.75%	LAADEEENVDSNMR	3.01	1,608.68
ATP	6006	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	8	9	0.09%	9.75%	MLNENSYVPR	2.11	1,238.58
ATP	6006	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	8	9	0.09%	9.75%	SSVGTSLLLTLAR	2.51	1,317.77
ATP	6006	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	8	9	0.09%	9.75%	VEYHLLSPYVSPR	3.71	1,559.82
ATP	6006	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	8	9	0.09%	9.75%	VSASPLLYSLIEK	4.52	1,419.81

ATP	6006	Leucine rich repeat containing 8 family, member A	gi|115304767,gi|116003833	93,997.70	100.00%	3	3	3	0.03%	3.58%	FIVIDGLR	2.4	932.5565
ATP	6006	Leucine rich repeat containing 8 family, member A	gi|115304767,gi|116003833	93,997.70	100.00%	3	3	3	0.03%	3.58%	IEAPALAFLR	2.7	1,100.65
ATP	6006	Leucine rich repeat containing 8 family, member A	gi|115304767,gi|116003833	93,997.70	100.00%	3	3	3	0.03%	3.58%	MANLTELELIR	2.89	1,318.70
ATP	6006	Caveolin 2	gi|157279219,gi|38322700,gi|51512145,gi|56119130,gi|66774044	18,142.30	100.00%	3	3	6	0.06%	27.20%	ADVQLFMDDDSYSR	2.91	1,677.71
ATP	6006	Caveolin 2	gi|157279219,gi|38322700,gi|51512145,gi|56119130,gi|66774044	18,142.30	100.00%	3	3	6	0.06%	27.20%	SFSSVSLQLSHD	3.98	1,306.63
ATP	6006	Caveolin 2	gi|157279219,gi|38322700,gi|51512145,gi|56119130,gi|66774044	18,142.30	100.00%	3	3	6	0.06%	27.20%	VGFEDVIAEPVSTHSFDK	2.63	1,976.96
ATP	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	gi|146231724,gi|77736299	40,519.40	99.80%	2	2	2	0.02%	10.20%	ISQTNYIPTQQDVLR	2.83	1,775.93
ATP	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	gi|146231724,gi|77736299	40,519.40	99.80%	2	2	2	0.02%	10.20%	LKIDFGEAAR	3.83	1,119.62

ATP	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	gi|146231724,gi|77736299	40,519.40	99.80%	2	2	2	0.02%	10.20%	LLLLGAGESGK	3.7	1,057.63
ATP	6006	Chromosome 9 open reading frame 46 ortholog	gi|74354529,gi|77735799	17,091.30	99.80%	2	2	2	0.02%	17.00%	GMITFESLEK	3.28	1,170.57
ATP	6006	Chromosome 9 open reading frame 46 ortholog	gi|74354529,gi|77735799	17,091.30	99.80%	2	2	2	0.02%	17.00%	MKGEAENILETEKSK	3.66	1,722.86
ATP	6006	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	5	5	6	0.06%	24.90%	DLLEDKILHSHLVDYFPEFDGPQR	2.07	2,883.43

ATP	6006	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	5	5	6	0.06%	24.90%	IATSGYLPTQQDVLR	3.62	1,661.89
ATP	6006	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	5	5	6	0.06%	24.90%	IIHGAGYSEEDKRGFTK	2.48	1,907.96

ATP	6006	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	5	5	6	0.06%	24.90%	LLLLGTGESGK	3.43	1,087.64
ATP	6006	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	5	5	6	0.06%	24.90%	VRVPTTGIIEYPFDLENIIFR	5.2	2,492.36
ATP	6006	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	3	4	4	0.04%	28.50%	IALMPLLQAEKDRR	2.28	1,669.94
ATP	6006	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	3	4	4	0.04%	28.50%	LQIEDFEAR	2.58	1,120.56

ATP	6006	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	3	4	4	0.04%	28.50%	VKQDMPPVGGYGPIDYKR	4.29	2,036.03
ATP	6006	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	4	4	4	0.04%	21.80%	FFVVSSESR	2.95	1,057.53
ATP	6006	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	4	4	4	0.04%	21.80%	RKPDEVLDDEDIGSAPLK	5.11	1,997.02
ATP	6006	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	4	4	4	0.04%	21.80%	TELHIPNVDLK	3.06	1,278.71
ATP	6006	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	4	4	4	0.04%	21.80%	VLKEDALPDLKTEYEVDSEDR	2.63	2,464.21
ATP	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	9	10	11	0.12%	33.30%	AVLVDLEPGTMDSVR	3.53	1,617.82
ATP	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	9	10	11	0.12%	33.30%	GHYTEGAELVDSVLDVVRK	3.22	2,087.08
ATP	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	9	10	11	0.12%	33.30%	IMNTFSVVPSPK	3	1,335.70
ATP	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	9	10	11	0.12%	33.30%	INVYYNEATGGK	3.35	1,328.65
ATP	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	9	10	11	0.12%	33.30%	LAVNMVPFPR	3.84	1,159.63
ATP	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	9	10	11	0.12%	33.30%	LHFFMPGFAPLTSR	3.49	1,636.83
ATP	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	9	10	11	0.12%	33.30%	MSATFIGNSTAIQELFKR	2.81	2,030.04
ATP	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	9	10	11	0.12%	33.30%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	3.15	4,479.06
ATP	6006	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	9	10	11	0.12%	33.30%	YLTVAAVFR	2.35	1,039.59

ATP	6006	RecName: Full=LAG1 longevity assurance homolog 2	gi|109892506,gi|73587265,gi|77736279	44,887.70	100.00%	3	3	4	0.04%	12.10%	LRAPPNPTLEHFYMTSGKQPK	3.42	2,428.24
ATP	6006	RecName: Full=LAG1 longevity assurance homolog 2	gi|109892506,gi|73587265,gi|77736279	44,887.70	100.00%	3	3	4	0.04%	12.10%	NRPLANGHPILNNNHR	3.71	1,836.97
ATP	6006	RecName: Full=LAG1 longevity assurance homolog 2	gi|109892506,gi|73587265,gi|77736279	44,887.70	100.00%	3	3	4	0.04%	12.10%	QADVELLSR	2.09	1,030.55
ATP	6006	RecName: Full=Peptidyl-prolyl cis-trans isomerase B; Short=PPIase; Short=Rotamase; AltName: Full=Cyclophilin B; AltName: Full=S-cyclophilin; Short=SCYLP; Flags: Precursor	gi|215274238,gi|27806469,gi|529242,gi|59858297,gi|74268324	23,726.00	99.80%	2	2	2	0.02%	12.50%	TVDNFVALATGEK	3.54	1,364.71

ATP	6006	RecName: Full=Peptidyl-prolyl cis-trans isomerase B; Short=PPIase; Short=Rotamase; AltName: Full=Cyclophilin B; AltName: Full=S-cyclophilin; Short=SCYLP; Flags: Precursor	gi|215274238,gi|27806469,gi|529242,gi|59858297,gi|74268324	23,726.00	99.80%	2	2	2	0.02%	12.50%	VIKDFMIQGGDFTR	3.77	1,642.83
ATP	6006	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	4	4	4	0.04%	14.00%	LLAELPASVHALTGVDLSK	2.22	1,934.10
ATP	6006	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	4	4	4	0.04%	14.00%	MALVLDALPR	3.67	1,114.63
ATP	6006	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	4	4	4	0.04%	14.00%	QVLLAQAEAEK	2.92	1,199.66
ATP	6006	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	4	4	4	0.04%	14.00%	SILGTLTVEQIYQDRDQFAK	3.07	2,325.21
ATP	6006	PREDICTED: similar to 1-acylglycerophosphocholine O-acyltransferase 1 (Lung-type acyl-CoA:lysophosphatidylcholine acyltransferase 1) (Lysophosphatidylcholine acyltransferase 1) (Acyltransferase-like 2)	gi|194676422	54,069.40	99.80%	2	2	2	0.02%	5.98%	MFGSQDGSVEEHALSSILK	2.42	2,050.98

ATP	6006	PREDICTED: similar to 1-acylglycerophosphocholine O-acyltransferase 1 (Lung-type acyl-CoA:lysophosphatidylcholine acyltransferase 1) (Lysophosphatidylcholine acyltransferase 1) (Acyltransferase-like 2)	gi|194676422	54,069.40	99.80%	2	2	2	0.02%	5.98%	TLDTIQLAFK	2.7	1,149.65
ATP	6006	Chain C, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591028,gi|110591031,gi|114687,gi|163036,gi|27807291,gi|55670489,gi|73586602	12,514.70	99.90%	2	2	3	0.03%	22.20%	QTSGGPVDAGPEYQQDLDRELFK	3.42	2,550.21
ATP	6006	Chain C, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591028,gi|110591031,gi|114687,gi|163036,gi|27807291,gi|55670489,gi|73586602	12,514.70	99.90%	2	2	3	0.03%	22.20%	RQTSGGPVDAGPEYQQDLDRELFK	3.44	2,706.31
ATP	6006	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	5	6	6	0.06%	5.34%	AFMTADLPNELIELLEK	3.72	1,963.01

ATP	6006	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	5	6	6	0.06%	5.34%	ISGETIFVTAPHEATAGIIGVNR	3.9	2,353.25
ATP	6006	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	5	6	6	0.06%	5.34%	KFDVNTSAVQVLIEHIGNLDR	4.51	2,368.26
ATP	6006	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	5	6	6	0.06%	5.34%	LLYNNVSNFGR	3.64	1,296.67
ATP	6006	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	5	6	6	0.06%	5.34%	RPISADSAIMNPASK	3.03	1,573.80
ATP	6006	coiled-coil domain containing 47	gi|146231852,gi|73586661,gi|78369308,gi|97045772	55,725.10	99.80%	2	2	2	0.02%	6.83%	ELLESNFTLVGDDGTNKEATSTGK	3.15	2,526.22
ATP	6006	coiled-coil domain containing 47	gi|146231852,gi|73586661,gi|78369308,gi|97045772	55,725.10	99.80%	2	2	2	0.02%	6.83%	QDLLNVLAR	2.18	1,041.61

ATP	6006	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	5	7	7	0.07%	17.70%	ALTEELSALKR	3.2	1,230.71
ATP	6006	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	5	7	7	0.07%	17.70%	FDAVIGYK	2.26	912.4826
ATP	6006	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	5	7	7	0.07%	17.70%	KSVTGEIVLITGAGHGIGR	4.87	1,865.06
ATP	6006	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	5	7	7	0.07%	17.70%	NPSTSLGPTLEPEEVVNK	4.38	1,910.97
ATP	6006	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	5	7	7	0.07%	17.70%	SVTGEIVLITGAGHGIGR	3.51	1,736.97
ATP	6006	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	4	4	4	0.04%	24.70%	AELNEFLTR	2.86	1,092.57
ATP	6006	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	4	4	4	0.04%	24.70%	ELAEDGYSGVEVR	3.29	1,423.67
ATP	6006	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	4	4	4	0.04%	24.70%	FVDGLMIHSGDPVNYYVDTAVR	4.66	2,484.19
ATP	6006	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	4	4	4	0.04%	24.70%	GGKPEPPAMPQPVPTA	2.93	1,589.80
ATP	6006	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	2	2	2	0.02%	4.10%	FLQDTIEEMALK	3.59	1,453.72
ATP	6006	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	2	2	2	0.02%	4.10%	KLEEGGPVYSPPAQAAVR	2.8	1,868.99
ATP	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	13	23	0.24%	38.90%	GLKLTFDSSFSPNTGKK	3.67	1,826.96
ATP	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	13	23	0.24%	38.90%	LTFDSSFSPNTGK	3.78	1,400.67

ATP	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	13	23	0.24%	38.90%	LTFDSSFSPNTGKK	2.26	1,528.76
ATP	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	13	23	0.24%	38.90%	LTLSALLDGK	3.09	1,030.61
ATP	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	13	23	0.24%	38.90%	LTLSALLDGKNVNAGGHK	3.39	1,808.00
ATP	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	13	23	0.24%	38.90%	TDEFQLHTNVNDGTEFGGSIYQK	3.42	2,600.19
ATP	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	13	23	0.24%	38.90%	TKSENGLEFTSSGSANTETTK	4.02	2,189.02
ATP	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	13	23	0.24%	38.90%	VNNSSLIGLGYTQTLKPGIK	4.67	2,103.18
ATP	6006	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	9	13	23	0.24%	38.90%	VTQSNFAVGYK	3.57	1,213.62
ATP	6006	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	8	10	19	0.20%	31.30%	DIFNKGFGFGLVK	3.55	1,441.78
ATP	6006	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	8	10	19	0.20%	31.30%	GFGFGLVK	2.04	824.4666
ATP	6006	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	8	10	19	0.20%	31.30%	LTFDTTFSPNTGK	3.72	1,428.70
ATP	6006	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	8	10	19	0.20%	31.30%	LTFDTTFSPNTGKK	2.54	1,556.80
ATP	6006	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	8	10	19	0.20%	31.30%	LTLSALVDGK	3.3	1,016.60
ATP	6006	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	8	10	19	0.20%	31.30%	TGDFQLHTNVNDGTEFGGSIYQK	4.21	2,528.17

ATP	6006	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	8	10	19	0.20%	31.30%	VNNSSLIGVGYTQTLRPGVK	5.45	2,103.16
ATP	6006	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	8	10	19	0.20%	31.30%	YQLDPTASISAK	3.51	1,293.67
ATP	6006	endothelial cell-specific molecule 2	gi|114053335,gi|86438024	20,621.00	99.80%	2	3	5	0.05%	13.20%	ESEDPQKPGSSGLSESGSTANGEK	4.05	2,378.06
ATP	6006	endothelial cell-specific molecule 2	gi|114053335,gi|86438024	20,621.00	99.80%	2	3	5	0.05%	13.20%	NKESEDPQKPGSSGLSESGSTANGEK	2.19	2,620.20
ATP	6006	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	4	5	5	0.05%	5.44%	GFPLVTVQR	2.08	1,016.59
ATP	6006	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	4	5	5	0.05%	5.44%	GLGEHELDEDEEDYESSAK	4.5	2,151.88
ATP	6006	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	4	5	5	0.05%	5.44%	IFGELSSYEDFLDAR	3.44	1,761.83
ATP	6006	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	4	5	5	0.05%	5.44%	KYFAATQFEPLAAR	3.31	1,612.85
ATP	6006	CYB5B protein	gi|158455068,gi|76640228	26,782.70	99.80%	2	2	2	0.02%	22.40%	FLDEHPGGEEVLMEQAGGDATESFEDVGHSSDAR	4.09	3,634.55
ATP	6006	CYB5B protein	gi|158455068,gi|76640228	26,782.70	99.80%	2	2	2	0.02%	22.40%	QYYIGDVHPNDLKPGGGSK	2.48	2,045.01

<table>
<tr><td>ATP</td><td>6006</td><td>Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor</td><td>gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288</td><td>46,506.00</td><td>100.00%</td><td>3</td><td>3</td><td>3</td><td>0.03%</td><td>9.11%</td><td>MALIGLGVSHPVLK</td><td>2.18</td><td>1,450.85</td></tr>
<tr><td>ATP</td><td>6006</td><td>Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor</td><td>gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288</td><td>46,506.00</td><td>100.00%</td><td>3</td><td>3</td><td>3</td><td>0.03%</td><td>9.11%</td><td>QVAEQFLNIR</td><td>2.86</td><td>1,217.66</td></tr>
<tr><td>ATP</td><td>6006</td><td>Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor</td><td>gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288</td><td>46,506.00</td><td>100.00%</td><td>3</td><td>3</td><td>3</td><td>0.03%</td><td>9.11%</td><td>TIAQGNLSNPDVQAAK</td><td>3.98</td><td>1,626.84</td></tr>
<tr><td>ATP</td><td>6006</td><td>Flotillin 1</td><td>gi|115305033,gi|116004001,gi|118572320,gi|75775078</td><td>47,334.80</td><td>100.00%</td><td>6</td><td>6</td><td>7</td><td>0.07%</td><td>21.50%</td><td>AQQVAVQEQEIAR</td><td>3.68</td><td>1,469.77</td></tr>
<tr><td>ATP</td><td>6006</td><td>Flotillin 1</td><td>gi|115305033,gi|116004001,gi|118572320,gi|75775078</td><td>47,334.80</td><td>100.00%</td><td>6</td><td>6</td><td>7</td><td>0.07%</td><td>21.50%</td><td>ITLVSSGSGAMGAAK</td><td>4.81</td><td>1,365.70</td></tr>
<tr><td>ATP</td><td>6006</td><td>Flotillin 1</td><td>gi|115305033,gi|116004001,gi|118572320,gi|75775078</td><td>47,334.80</td><td>100.00%</td><td>6</td><td>6</td><td>7</td><td>0.07%</td><td>21.50%</td><td>MRGEAEAFAIGAR</td><td>3.39</td><td>1,394.68</td></tr>
<tr><td>ATP</td><td>6006</td><td>Flotillin 1</td><td>gi|115305033,gi|116004001,gi|118572320,gi|75775078</td><td>47,334.80</td><td>100.00%</td><td>6</td><td>6</td><td>7</td><td>0.07%</td><td>21.50%</td><td>VASSDLVNMGISVVSYTLKDIHDDQDYLHSLGK</td><td>2.97</td><td>3,635.79</td></tr>
<tr><td>ATP</td><td>6006</td><td>Flotillin 1</td><td>gi|115305033,gi|116004001,gi|118572320,gi|75775078</td><td>47,334.80</td><td>100.00%</td><td>6</td><td>6</td><td>7</td><td>0.07%</td><td>21.50%</td><td>VTGEVLDILSR</td><td>3.21</td><td>1,201.68</td></tr>
</table>

ATP	6006	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	6	6	7	0.07%	21.50%	VTGEVLDILSRLPESVER	3.61	2,012.10
ATP	6006	glutathione peroxidase 8	gi|114052907,gi|122143886,gi|84708688	23,965.80	99.80%	2	3	3	0.03%	11.00%	ILGSEAEPAFR	2.88	1,189.62
ATP	6006	glutathione peroxidase 8	gi|114052907,gi|122143886,gi|84708688	23,965.80	99.80%	2	3	3	0.03%	11.00%	NNFGVTFPIFHK	3.39	1,420.74
ATP	6006	PREDICTED: similar to Neuroblast differentiation-associated protein AHNAK (Desmoyokin), partial	gi|194687805	140,614.00	99.80%	2	2	2	0.02%	2.54%	FSMPGFKGEGPEVDVNLPK	2.52	2,064.01
ATP	6006	PREDICTED: similar to Neuroblast differentiation-associated protein AHNAK (Desmoyokin), partial	gi|194687805	140,614.00	99.80%	2	2	2	0.02%	2.54%	ISMPDVDLNLKGPK	2.91	1,542.82
ATP	6006	ANXA6 protein	gi|154426044,gi|157151716,gi|160332337	75,893.80	100.00%	8	8	8	0.08%	15.90%	EMSGDVRDVFVAIVQSVK	3.54	1,995.02
ATP	6006	ANXA6 protein	gi|154426044,gi|157151716,gi|160332337	75,893.80	100.00%	8	8	8	0.08%	15.90%	GLGTDEDTIIDIIAHR	2.82	1,738.90
ATP	6006	ANXA6 protein	gi|154426044,gi|157151716,gi|160332337	75,893.80	100.00%	8	8	8	0.08%	15.90%	GTVRPAGDFNPDADAK	3.18	1,630.78
ATP	6006	ANXA6 protein	gi|154426044,gi|157151716,gi|160332337	75,893.80	100.00%	8	8	8	0.08%	15.90%	ILISLATGNREEGGEDRER	3.72	2,115.08
ATP	6006	ANXA6 protein	gi|154426044,gi|157151716,gi|160332337	75,893.80	100.00%	8	8	8	0.08%	15.90%	NKPLFFADKLYK	3.98	1,483.83
ATP	6006	ANXA6 protein	gi|154426044,gi|157151716,gi|160332337	75,893.80	100.00%	8	8	8	0.08%	15.90%	SEIDLLNIR	2.42	1,072.60
ATP	6006	ANXA6 protein	gi|154426044,gi|157151716,gi|160332337	75,893.80	100.00%	8	8	8	0.08%	15.90%	SEIDLLNIRR	1.74	1,228.70

ATP	6006	ANXA6 protein	gi|154426044,gi|157151716,gi|160332337	75,893.80	100.00%	8	8	8	0.08%	15.90%	SLHQAIEGDTSGHFLK	3.36	1,739.87
ATP	6006	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	7	10	0.11%	20.50%	GFVLTFK	2.05	811.4713
ATP	6006	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	7	10	0.11%	20.50%	GVGMVADPDNPLVLDILTGSSTSYSFFPDKPITQYPHAVGK	5.52	4,350.16
ATP	6006	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	7	10	0.11%	20.50%	LPDVYGVFQFK	2.98	1,312.69
ATP	6006	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	7	10	0.11%	20.50%	SSLNPILFR	2.8	1,046.60
ATP	6006	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	7	10	0.11%	20.50%	TADDPSLSLIK	2.91	1,159.62
ATP	6006	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	7	10	0.11%	20.50%	TLVLLDNLNLR	3.15	1,283.77
ATP	6006	reticulon 4 isoform 2	gi|164259354,gi|92096636	40,940.20	100.00%	3	4	5	0.05%	7.92%	GPLPAAPLAAPER	3.33	1,259.71
ATP	6006	reticulon 4 isoform 2	gi|164259354,gi|92096636	40,940.20	100.00%	3	4	5	0.05%	7.92%	HQAQIDHYLGLANK	3.97	1,607.83
ATP	6006	reticulon 4 isoform 2	gi|164259354,gi|92096636	40,940.20	100.00%	3	4	5	0.05%	7.92%	HQAQIDHYLGLANKNVK	3.95	1,949.04
ATP	6006	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	3	6	7	0.07%	8.32%	IYQGEDLPHPK	3.2	1,296.66
ATP	6006	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	3	6	7	0.07%	8.32%	LQVKEHQHEEIQNVR	3.39	1,886.98
ATP	6006	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	3	6	7	0.07%	8.32%	SMLQATAEANNLAAAASAK	5.18	1,848.91

ATP	6006	Poliovirus receptor-related 2 (herpesvirus entry mediator B)	gi|109658349,gi|115497936	43,243.10	100.00%	3	3	3	0.03%	9.68%	ETQGSGPLPGTVTVTSR	3.67	1,686.87
ATP	6006	Poliovirus receptor-related 2 (herpesvirus entry mediator B)	gi|109658349,gi|115497936	43,243.10	100.00%	3	3	3	0.03%	9.68%	LLPVILSVR	2.15	1,009.68
ATP	6006	Poliovirus receptor-related 2 (herpesvirus entry mediator B)	gi|109658349,gi|115497936	43,243.10	100.00%	3	3	3	0.03%	9.68%	YTVTPLSEADGVK	2.93	1,379.71
ATP	6006	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	3	3	3	0.03%	6.64%	IRIDSLSAQLSQLQK	2.92	1,699.97
ATP	6006	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	3	3	3	0.03%	6.64%	LADALQELR	2.43	1,028.57
ATP	6006	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	3	3	3	0.03%	6.64%	VAVEEVDEEGKFVR	2.29	1,605.81
ATP	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	19	0.20%	42.60%	AVAISLPK	2.53	798.5084
ATP	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	19	0.20%	42.60%	AVLSAEQLRDDEVHAGLGELLR	5.64	2,391.26

ATP	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	19	0.20%	42.60%	DQAVENILLSPVVVASSLGLVSLGGK	4.67	2,565.45
ATP	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	19	0.20%	42.60%	DTQSGSLLFIGR	2.06	1,293.68
ATP	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	19	0.20%	42.60%	GVVEVTHDLQK	3.82	1,224.66
ATP	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	19	0.20%	42.60%	HLAGLGLTEAIDKNK	5.22	1,579.88

ATP	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	19	0.20%	42.60%	HLAGLGLTEAIDKNKADLSR	5.59	2,122.16
ATP	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	19	0.20%	42.60%	KPAAAAAPGTAEKLSPK	3.93	1,607.91
ATP	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	19	0.20%	42.60%	LFYADHPFIFLVR	1.77	1,637.88
ATP	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	19	0.20%	42.60%	LSSLIIIMPHHVEPLER	2.62	2,000.10

ATP	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	19	0.20%	42.60%	LSSLIIMPHHVEPLERLEK	3.45	2,370.32
ATP	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	19	0.20%	42.60%	LYGPSSVSFAEDFVR	4.1	1,673.82
ATP	6006	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	13	16	19	0.20%	42.60%	SAGLAFSLYQAMAK	4.3	1,473.74
ATP	6006	PREDICTED: transmembrane emp24 protein transport domain containing 4	gi|194666384	37,465.50	100.00%	2	3	3	0.03%	5.07%	QLLDQVEQIQK	2.86	1,341.74
ATP	6006	PREDICTED: transmembrane emp24 protein transport domain containing 4	gi|194666384	37,465.50	100.00%	2	3	3	0.03%	5.07%	QLLDQVEQIQKEQDYQR	3.4	2,161.09

ATP	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	9	12	15	0.16%	14.00%	AVVLAANHFGR	2.71	1,154.64
ATP	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	9	12	15	0.16%	14.00%	GITHIGYTDLPSR	3.01	1,429.74
ATP	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	9	12	15	0.16%	14.00%	GTVVMKDGQVIFPAPTPK	3.79	1,901.02
ATP	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	9	12	15	0.16%	14.00%	MATQASTLYSNNITK	4.39	1,658.81
ATP	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	9	12	15	0.16%	14.00%	QLTVGVPKEIFQNEKR	2.96	1,886.05
ATP	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	9	12	15	0.16%	14.00%	SLGVGYAAVDNPIFYKPNTAMLLGDAKK	4.4	2,969.54
ATP	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	9	12	15	0.16%	14.00%	TVAELEAEKAATITPFRK	3.38	1,975.09
ATP	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	9	12	15	0.16%	14.00%	VALSPAGVQALVK	5.4	1,252.76
ATP	6006	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	9	12	15	0.16%	14.00%	VTIAQGYDALSSMANIAGYK	4.7	2,089.03
ATP	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	10	14	19	0.20%	35.20%	GTGRIPDQLVILDMK	3.74	1,655.92
ATP	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	10	14	19	0.20%	35.20%	IPDQLVILDMK	3.65	1,300.72

ATP	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	10	14	19	0.20%	35.20%	IPDQLVILDMKHGVEAK	3.09	1,922.04
ATP	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	10	14	19	0.20%	35.20%	ITDSAGHILYSK	4.6	1,304.68
ATP	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	10	14	19	0.20%	35.20%	ITDSAGHILYSKEDATK	4.48	1,848.93
ATP	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	10	14	19	0.20%	35.20%	ITDSAGHILYSKEDATKGK	4.45	2,034.05
ATP	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	10	14	19	0.20%	35.20%	LKPLEVELR	3.6	1,096.67
ATP	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	10	14	19	0.20%	35.20%	NYEEIAKVEK	3.09	1,222.63
ATP	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	10	14	19	0.20%	35.20%	RLEDLSESIVNDFAYMK	5.08	2,045.99
ATP	6006	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	10	14	19	0.20%	35.20%	RLEDLSESIVNDFAYMKK	4.91	2,174.08
ATP	6006	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	99.80%	2	2	2	0.02%	4.23%	NQGFDVVLVDTAGR	4.2	1,490.76

ATP	6006	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	99.80%	2	2	2	0.02%	4.23%	VMGTFSTVTSTVK	2.75	1,373.70
ATP	6006	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	6	6	6	0.06%	9.11%	FLFLLLGPAGK	3.35	1,175.72
ATP	6006	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	6	6	6	0.06%	9.11%	GPDEEAVVDLGK	3.47	1,228.61
ATP	6006	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	6	6	6	0.06%	9.11%	KIPSGAEASNVLVGEVDFLERPIIAFVR	3.05	3,026.67
ATP	6006	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	6	6	6	0.06%	9.11%	LAPAVLLSGLTEVPVPTR	3.76	1,833.08
ATP	6006	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	6	6	6	0.06%	9.11%	MLQAGEDTVHLPFEGGSLLQIPVK	2.77	2,595.35
ATP	6006	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	6	6	6	0.06%	9.11%	TSSTVNTKFEKEELESHR	3.21	2,122.04
ATP	6006	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	4	6	6	0.06%	23.00%	FSDLDSASVDSDMYDLPK	2.59	2,020.87

ATP	6006	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	4	6	6	0.06%	23.00%	FSDLDSASVDSDMYDLPKKEDALLYQSK	4.71	3,196.49
ATP	6006	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	4	6	6	0.06%	23.00%	GFRQPSASLSDADPFHR	4.93	1,887.91
ATP	6006	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	4	6	6	0.06%	23.00%	GYNDDYYEESYLTTR	3.33	1,888.79
ATP	6006	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	5	5	6	0.06%	24.20%	ATIGADFLTK	2.54	1,036.57
ATP	6006	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	5	5	6	0.06%	24.20%	DPENFPFVVLGNK	4.25	1,475.75
ATP	6006	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	5	5	6	0.06%	24.20%	DPENFPFVVLGNKIDLENR	3.79	2,216.13
ATP	6006	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	5	5	6	0.06%	24.20%	FQSLGVAFYR	2.91	1,187.62
ATP	6006	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	5	5	6	0.06%	24.20%	VIILGDSGVGK	2.65	1,057.63
ATP	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	8	11	11	0.12%	16.80%	ARFEELNADLFR	4.26	1,480.75
ATP	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	8	11	11	0.12%	16.80%	ARFEELNADLFRGTLDPVEK	2.87	2,320.19
ATP	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	8	11	11	0.12%	16.80%	FEELNADLFR	2.44	1,253.62
ATP	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	8	11	11	0.12%	16.80%	IINEPTAAAIAYGLDK	4.01	1,659.90
ATP	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	8	11	11	0.12%	16.80%	MKEIAEAYLGKTVTNAVVTVPAYFNDSQR	3.76	3,231.64
ATP	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	8	11	11	0.12%	16.80%	NQVAMNPTNTVFDAK	3.38	1,665.79

ATP	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	8	11	11	0.12%	16.80%	STAGDTHLGGEDFDNR	2.93	1,691.73
ATP	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	8	11	11	0.12%	16.80%	TTPSYVAFTDTER	3.39	1,487.70
ATP	6006	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	8	11	11	0.12%	16.80%	TVTNAVVTVPAYFNDSQR	2.68	1,982.00
ATP	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	15	24	0.25%	26.80%	AAYFGIYDTAK	2.86	1,219.60
ATP	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	15	24	0.25%	26.80%	DFLAGGIAAAISK	4.9	1,233.68
ATP	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	15	24	0.25%	26.80%	GMGGAFVLVLYDELK	2.91	1,627.84
ATP	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	15	24	0.25%	26.80%	GMGGAFVLVLYDELKK	2.88	1,755.94
ATP	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	15	24	0.25%	26.80%	GMGGAFVLVLYDELKKVI	2.47	1,968.09
ATP	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	15	24	0.25%	26.80%	QIFLGGVDKR	2.46	1,132.65
ATP	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	15	24	0.25%	26.80%	VKLLLQVQHASK	3.83	1,363.84
ATP	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	15	24	0.25%	26.80%	YFPTQALNFAFK	4.71	1,446.74
ATP	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	15	24	0.25%	26.80%	YFPTQALNFAFKDK	3.09	1,689.86

ATP	6006	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	10	15	24	0.25%	26.80%	YFPTQALNFAFKDKYK	3.89	1,981.02
ATP	6006	PREDICTED: insulin-like growth factor 1 receptor	gi|119913553	135,693.80	100.00%	3	4	4	0.04%	3.90%	AVTLTMVENDHIR	2.42	1,514.76
ATP	6006	PREDICTED: insulin-like growth factor 1 receptor	gi|119913553	135,693.80	100.00%	3	4	4	0.04%	3.90%	SLRPEMENNPVLAPPSLSK	3.29	2,095.09
ATP	6006	PREDICTED: insulin-like growth factor 1 receptor	gi|119913553	135,693.80	100.00%	3	4	4	0.04%	3.90%	TEAEKQAEKEEAEYR	3.34	1,810.85
ATP	6006	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	8	8	8	0.08%	4.07%	FADEHVPGSPFTVK	2.45	1,530.76
ATP	6006	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	8	8	8	0.08%	4.07%	IVGPGLGSGVR	2.54	1,011.59
ATP	6006	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	8	8	8	0.08%	4.07%	LIALLEVLSQK	2.79	1,226.77
ATP	6006	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	8	8	8	0.08%	4.07%	SPFTVGVAAPLDLSR	3.81	1,529.83

ATP	6006	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	8	8	8	0.08%	4.07%	VSFAGDTIPK	2.64	1,034.55
ATP	6006	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	8	8	8	0.08%	4.07%	VTEAEIVPVGK	2.82	1,141.65
ATP	6006	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	8	8	8	0.08%	4.07%	VTVLFAGQHISK	2.17	1,299.74
ATP	6006	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	8	8	8	0.08%	4.07%	YTPTQQGNMQVLVTYGGDPIPK	4.61	2,423.19
ATP	6006	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	3	3	3	0.03%	7.62%	EAGHGTQKEEIPEEELAEDVEEIDHAER	3.52	3,189.45
ATP	6006	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	3	3	3	0.03%	7.62%	IDESSLTGESDHVK	2.32	1,516.71
ATP	6006	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	3	3	3	0.03%	7.62%	QVVAVTGDGTNDGPALK	3.35	1,641.84
ATP	6006	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	3	3	3	0.03%	7.62%	QVVAVTGDGTNDGPALKK	2.17	1,769.94
ATP	6006	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	3	3	3	0.03%	7.62%	SLDKDPLLLSGTHVMEGSGR	3.91	2,128.07

ATP	6006	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	3	3	3	0.03%	7.62%	SSLYEGLEKPESR	3.4	1,494.74
ATP	6006	UNC84B protein	gi|151553917,gi|156121283	81,429.80	99.80%	2	3	5	0.05%	3.43%	EAVASLGLTLQR	2.81	1,257.72
ATP	6006	UNC84B protein	gi|151553917,gi|156121283	81,429.80	99.80%	2	3	5	0.05%	3.43%	IRPTAVTLEHVPK	2.82	1,460.86
ATP	6006	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	6	7	7	0.07%	8.75%	DQAVMISGESGAGKTEATKR	1.93	2,052.00
ATP	6006	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	6	7	7	0.07%	8.75%	HLGYKPEEYKMGR	2.49	1,623.80
ATP	6006	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	6	7	7	0.07%	8.75%	LLGVEGSTLR	2.22	1,044.60
ATP	6006	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	6	7	7	0.07%	8.75%	LLQSNPVLEAFGNAK	3.46	1,600.87
ATP	6006	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	6	7	7	0.07%	8.75%	MSLLELVEILK	3.14	1,303.75
ATP	6006	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	6	7	7	0.07%	8.75%	VLQALGSEPIQYAVPVVKYDR	2.53	2,345.29
ATP	6006	PREDICTED: similar to Ras-interacting protein 1 isoform 2	gi|76642189	103,383.20	99.80%	2	2	2	0.02%	4.26%	AASGGAALASPGPGSGSGTPAGSGKER	4.09	2,312.12
ATP	6006	PREDICTED: similar to Ras-interacting protein 1 isoform 2	gi|76642189	103,383.20	99.80%	2	2	2	0.02%	4.26%	IFGAGLASGANYK	3.43	1,268.66
ATP	6006	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	4	4	4	0.04%	4.83%	GQPLGPAGVQVSLR	3.26	1,378.78
ATP	6006	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	4	4	4	0.04%	4.83%	SQYDFVLPQVSFTAAGYHK	2.83	2,158.06

ATP	6006	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	4	4	4	0.04%	4.83%	SSIDSEPALVLGPLK	3.31	1,525.85
ATP	6006	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	4	4	4	0.04%	4.83%	VQVMVPEAETR	2.74	1,274.64
ATP	6006	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	7	12	15	0.16%	51.00%	ADALQAGASQFETSAAK	4.12	1,665.81
ATP	6006	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	7	12	15	0.16%	51.00%	DQKLSELDDRADALQAGASQFETSAAK	4.38	2,865.39
ATP	6006	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	7	12	15	0.16%	51.00%	LQQTQNQVDEVVDIMR	4.44	1,931.95
ATP	6006	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	7	12	15	0.16%	51.00%	LSELDDRADALQAGASQFETSAAK	5.63	2,494.21
ATP	6006	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	7	12	15	0.16%	51.00%	RLQQTQNQVDEVVDIMR	4.24	2,088.05
ATP	6006	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	7	12	15	0.16%	51.00%	VNVDKVLER	3.51	1,071.62
ATP	6006	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	7	12	15	0.16%	51.00%	VNVDKVLERDQK	2.63	1,442.80
ATP	6006	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	10	15	0.16%	16.20%	DKLSELQLR	2.7	1,101.63
ATP	6006	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	10	15	0.16%	16.20%	FSLFAGGMLR	3.07	1,114.57

ATP	6006	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	10	15	0.16%	16.20%	QLVEQVEQIQK	3.22	1,341.74
ATP	6006	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	10	15	0.16%	16.20%	QLVEQVEQIQKEQNYQR	3.94	2,160.10
ATP	6006	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	10	15	0.16%	16.20%	VRQLVEQVEQIQK	2.79	1,596.91
ATP	6006	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	10	15	0.16%	16.20%	VRQLVEQVEQIQKEQNYQR	5.22	2,415.27
ATP	6006	PCDH1 protein	gi|134025143,gi|139947544	114,931.40	100.00%	3	3	3	0.03%	4.81%	GLFTISPETGEIR	2.66	1,419.75
ATP	6006	PCDH1 protein	gi|134025143,gi|139947544	114,931.40	100.00%	3	3	3	0.03%	4.81%	NTGLITVQGPVDREDLSTLR	2.73	2,184.16
ATP	6006	PCDH1 protein	gi|134025143,gi|139947544	114,931.40	100.00%	3	3	3	0.03%	4.81%	SPKPVKPVEDEDETGLQK	4.04	1,996.02
ATP	6006	KRT4 protein	gi|134024768	58,029.30	100.00%	4	4	9	0.09%	9.47%	FASFIDKVR	2.12	1,082.60
ATP	6006	KRT4 protein	gi|134024768	58,029.30	100.00%	4	4	9	0.09%	9.47%	LALDIEIATYR	4.64	1,277.71
ATP	6006	KRT4 protein	gi|134024768	58,029.30	100.00%	4	4	9	0.09%	9.47%	NEISELNR	3.4	974.4901
ATP	6006	KRT4 protein	gi|134024768	58,029.30	100.00%	4	4	9	0.09%	9.47%	NLDLDSIIAEVR	3.57	1,357.73
ATP	6006	KRT4 protein	gi|134024768	58,029.30	100.00%	4	4	9	0.09%	9.47%	RTELEAALQKAK	3.43	1,357.78
ATP	6006	PREDICTED: similar to solute carrier family 30 (zinc transporter), member 1 isoform 1	gi|76638149	55,359.70	99.80%	2	2	2	0.02%	7.51%	ESALILLQTVPK	3.14	1,311.79

ATP	6006	PREDICTED: similar to solute carrier family 30 (zinc transporter), member 1 isoform 1	gi|76638149	55,359.70	99.80%	2	2	2	0.02%	7.51%	IIKDVFHNHGIHATTIQPEFASVGSK	2.18	2,846.50
ATP	6006	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	5	7	12	0.13%	25.90%	EFADSLGIPFLETSAK	4	1,724.87
ATP	6006	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	5	7	12	0.13%	25.90%	KVVDYTTAKEFADSLGIPFLETSAK	4.82	2,730.42
ATP	6006	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	5	7	12	0.13%	25.90%	LLLIGDSGVGK	3.14	1,071.64
ATP	6006	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	5	7	12	0.13%	25.90%	NATNVEQSFMTMAAEIK	3.19	1,900.88
ATP	6006	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	5	7	12	0.13%	25.90%	VVDYTTAKEFADSLGIPFLETSAK	3.31	2,602.33
ATP	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	26	0.27%	32.40%	ALYETELADAR	3.06	1,251.62
ATP	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	26	0.27%	32.40%	IESLSSQLSNLQK	3.2	1,446.78
ATP	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	26	0.27%	32.40%	IQELEDLLAK	2.91	1,171.66
ATP	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	26	0.27%	32.40%	IQELEDLLAKER	2.44	1,456.80
ATP	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	26	0.27%	32.40%	LALDMEISAYRK	2.46	1,425.74
ATP	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	26	0.27%	32.40%	LAQALHEMREQHDAQVK	3.35	2,020.00
ATP	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	26	0.27%	32.40%	LAVYIDKVR	2.46	1,076.65
ATP	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	26	0.27%	32.40%	LLEGEEERLK	3.1	1,215.66
ATP	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	26	0.27%	32.40%	LREYEAALNSK	3.36	1,293.68
ATP	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	26	0.27%	32.40%	LVEVDSGRQIEYEYK	2.44	1,827.91

ATP	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	26	0.27%	32.40%	LYKEELEQTYHAK	4.41	1,651.83
ATP	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	26	0.27%	32.40%	MRIESLSSQLSNLQK	3.01	1,749.92
ATP	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	26	0.27%	32.40%	NMYEEEINETR	3.08	1,443.61
ATP	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	26	0.27%	32.40%	SLESDLEDLKDQIAQLEASLAAAK	5.09	2,558.32
ATP	6006	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	15	22	26	0.27%	32.40%	TTIPEEEEEEEEAAEVAVEEELFHQQGAPR	4.15	3,425.55
ATP	6006	RecName: Full=40S ribosomal protein S27	gi|108860958,gi|148231402,gi|85812223,gi|86827527	9,442.90	99.80%	2	2	2	0.02%	31.00%	DLLHPSPEEEKRK	2.47	1,577.83
ATP	6006	RecName: Full=40S ribosomal protein S27	gi|108860958,gi|148231402,gi|85812223,gi|86827527	9,442.90	99.80%	2	2	2	0.02%	31.00%	LVQSPNSYFMDVK	2.34	1,543.75
ATP	6006	CALM3 protein	gi|111308539,gi|114053089,gi|115305083,gi|157831834,gi|157879669,gi|194671098,gi|28189857,gi|49037473,gi|86822265	19,973.60	99.80%	2	2	2	0.02%	17.00%	MKDTDSEEEIREAFR	2.65	1,871.84
ATP	6006	CALM3 protein	gi|111308539,gi|114053089,gi|115305083,gi|157831834,gi|157879669,gi|194671098,gi|28189857,gi|49037473,gi|86822265	19,973.60	99.80%	2	2	2	0.02%	17.00%	VFDKDGNGYISAELR	3.1	1,754.87

ATP	6006	RecName: Full=Cytochrome c oxidase polypeptide 7A2, mitochondrial; AltName: Full=Cytochrome c oxidase polypeptide VIIa-liver/heart; Short=Cytochrome c oxidase subunit VIIa-L; Short=VIIC; Flags: Precursor	gi|117120,gi|28461241,gi|488158,gi|74354141	9,305.40	99.80%	2	2	2	0.02%	27.70%	GGIADALLYR	3.17	1,048.58
ATP	6006	RecName: Full=Cytochrome c oxidase polypeptide 7A2, mitochondrial; AltName: Full=Cytochrome c oxidase polypeptide VIIa-liver/heart; Short=Cytochrome c oxidase subunit VIIa-L; Short=VIIC; Flags: Precursor	gi|117120,gi|28461241,gi|488158,gi|74354141	9,305.40	99.80%	2	2	2	0.02%	27.70%	LFQEDNGIPVHLK	2.34	1,509.81
ATP	6006	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	6	6	6	0.06%	13.70%	ATTPVIMVGPGTGVAPFIGFIQER	4.68	2,474.31

ATP	6006	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	6	6	6	0.06%	13.70%	GMAADPEEYDLADLSSLPEIEK	2.55	2,409.10
ATP	6006	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	6	6	6	0.06%	13.70%	HLMHLELDISDSK	3.02	1,553.76
ATP	6006	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	6	6	6	0.06%	13.70%	NPFLAVVTTNR	3.95	1,231.68
ATP	6006	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	6	6	6	0.06%	13.70%	TALTYYLDITNPPR	2.08	1,637.85
ATP	6006	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	6	6	6	0.06%	13.70%	YAVFALGNK	2.52	982.5356
ATP	6006	TXNDC10 protein	gi|151554048,gi|156121223	51,713.50	100.00%	2	2	2	0.02%	6.61%	LLKGDLAYNYRGPR	2.64	1,635.90
ATP	6006	TXNDC10 protein	gi|151554048,gi|156121223	51,713.50	100.00%	2	2	2	0.02%	6.61%	MDATSYSSIASEFGVR	3.8	1,736.78
ATP	6006	MTCH1 protein	gi|154426180,gi|157074126	41,499.70	100.00%	3	3	3	0.03%	8.74%	KVLYLPSFFTYAK	3.03	1,576.88

ATP	6006	MTCH1 protein	gi|154426180,gi|157074126	41,499.70	100.00%	3	3	3	0.03%	8.74%	LMSNALSTVTR	3.05	1,208.63
ATP	6006	MTCH1 protein	gi|154426180,gi|157074126	41,499.70	100.00%	3	3	3	0.03%	8.74%	YSGVLSSIGK	2.05	1,010.55
ATP	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	8	10	10	0.11%	16.60%	ALEEAMEQKAELER	3.45	1,662.80
ATP	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	8	10	10	0.11%	16.60%	ANLQIDQLNTDLNLER	3.98	1,869.97
ATP	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	8	10	10	0.11%	16.60%	ELEDATETADAMNR	2.82	1,581.67
ATP	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	8	10	10	0.11%	16.60%	ELEDATETADAMNREVSSLK	2.46	2,225.02
ATP	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	8	10	10	0.11%	16.60%	IAQLEEQLDNETKER	4.72	1,815.91
ATP	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	8	10	10	0.11%	16.60%	KFDQLLAEEK	2.69	1,220.65
ATP	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	8	10	10	0.11%	16.60%	QISTLHAQVTDMR	2.2	1,515.76
ATP	6006	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	8	10	10	0.11%	16.60%	QLEEAEEEAQRANASR	2.94	1,830.86
ATP	6006	PREDICTED: similar to keratin 2 (epidermal ichthyosis bullosa of Siemens)	gi|119892108	64,293.10	99.80%	2	3	5	0.05%	3.89%	FLEQQNQVLQTK	4.12	1,475.79
ATP	6006	PREDICTED: similar to keratin 2 (epidermal ichthyosis bullosa of Siemens)	gi|119892108	64,293.10	99.80%	2	3	5	0.05%	3.89%	TAAENEFVTLKK	3.04	1,350.73
ATP	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	18	25	0.26%	31.70%	AASFLLALEPELEAR	4.03	1,629.88

ATP	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	18	25	0.26%	31.70%	DTYIENEKLISGK	2.82	1,509.78
ATP	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	18	25	0.26%	31.70%	FFTVKLPVALDPGAK	3.24	1,602.93
ATP	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	18	25	0.26%	31.70%	HFDETVNRYK	3.15	1,308.63
ATP	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	18	25	0.26%	31.70%	IDHILDAL	2.26	909.5042
ATP	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	18	25	0.26%	31.70%	ISVIVEAVYTHVLQPYPTQITQSEK	3.17	2,843.52
ATP	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	18	25	0.26%	31.70%	LPVALDPGAK	2.09	980.5777
ATP	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	18	25	0.26%	31.70%	LVDHVFDEQVIDSLTVK	3.06	1,957.03
ATP	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	18	25	0.26%	31.70%	NIQVDSPYEISR	3.37	1,420.71
ATP	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	18	25	0.26%	31.70%	QFVVFEGNHYFYSPYPTK	3.13	2,223.05
ATP	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	18	25	0.26%	31.70%	SEDLLDYGPFR	3.51	1,311.62
ATP	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	18	25	0.26%	31.70%	VHSENNSPFLTITSMTR	4.5	1,949.94
ATP	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	18	25	0.26%	31.70%	VTAEVVLAHAGSGSSPR	5.85	1,637.86
ATP	6006	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	14	18	25	0.26%	31.70%	YDYQRQPDSGVSSVR	2.58	1,756.82
ATP	6006	PREDICTED: similar to tetraspanin 9	gi|119893128	26,633.40	99.80%	2	2	2	0.02%	23.80%	DLKEGLLLYNSENNVGLK	3.3	2,019.08
ATP	6006	PREDICTED: similar to tetraspanin 9	gi|119893128	26,633.40	99.80%	2	2	2	0.02%	23.80%	VTQWFADNKHVLGTVGMCLLITQILGMAFSMTLFQHIHR	2.77	4,473.29
ATP	6006	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	6	7	7	0.07%	8.32%	ALTLGALTLPLAR	2.92	1,309.82

ATP	6006	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	6	7	7	0.07%	8.32%	GNKEPNPMVQLSIQDVTQESK	5.01	2,358.16
ATP	6006	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	6	7	7	0.07%	8.32%	LHVLEAQDLIAK	3.64	1,349.78
ATP	6006	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	6	7	7	0.07%	8.32%	LLAETVAPAVR	2.79	1,139.68
ATP	6006	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	6	7	7	0.07%	8.32%	LLVPLVPDLQDVAQLR	2.79	1,789.06
ATP	6006	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	6	7	7	0.07%	8.32%	LTHSDSPPEAPAGPLGQVK	3.45	1,900.98
ATP	6006	CD9 molecule	gi|151556398,gi|162821,gi|27806911,gi|399217	25,240.80	99.80%	2	2	4	0.04%	6.19%	EVQKFYEDTYNKLK	2.6	1,804.91
ATP	6006	CD9 molecule	gi|151556398,gi|162821,gi|27806911,gi|399217	25,240.80	99.80%	2	2	4	0.04%	6.19%	FYEDTYNKLK	2.49	1,320.65
ATP	6006	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	2	2	2	0.02%	3.31%	LSFQHDPETSVLILR	4.21	1,754.94
ATP	6006	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	2	2	2	0.02%	3.31%	VVIIGAGKPATVVLQTK	3.33	1,694.06
ATP	6006	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	4	4	4	0.04%	4.97%	DVIDKQHTEQEASYGR	3.81	1,875.88

ATP	6006	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	4	4	4	0.04%	4.97%	LNQPQPDFTK	2.6	1,187.61
ATP	6006	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	4	4	4	0.04%	4.97%	SFHSFYQLLQGGSDQMLR	4.31	2,130.01
ATP	6006	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	4	4	4	0.04%	4.97%	TVATGRDVIDKQHTEQEASYGR	3.1	2,461.21
ATP	6006	Chromosome 20 open reading frame 3 ortholog	gi|74268319,gi|78369434	46,074.40	99.80%	2	2	2	0.02%	7.28%	GGADVFVENLPGFPDNIR	2.55	1,916.95
ATP	6006	Chromosome 20 open reading frame 3 ortholog	gi|74268319,gi|78369434	46,074.40	99.80%	2	2	2	0.02%	7.28%	LLLSSETPIEGR	3.93	1,314.73
ATP	6006	PREDICTED: similar to Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A	gi|119896006	130,855.40	100.00%	2	2	2	0.02%	1.48%	TTVVLAPLGDDFR	3.37	1,403.75

ATP	6006	PREDICTED: similar to Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A	gi|119896006	130,855.40	100.00%	2	2	2	0.02%	1.48%	TTVVLAPLGDDFRYTER	2.91	1,953.01
ATP	6006	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	5	6	7	0.07%	24.30%	AHGSVVKSEDYALPSYVDRR	3.68	2,249.13

ATP	6006	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	5	6	7	0.07%	24.30%	DYPLPDVAHVK	1.8	1,253.65
ATP	6006	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	5	6	7	0.07%	24.30%	FKESFAEMNR	2.37	1,274.58

ATP	6006	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	5	6	7	0.07%	24.30%	SEDYALPSYVDR	3.26	1,414.65
ATP	6006	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	5	6	7	0.07%	24.30%	SEDYALPSYVDRR	2.05	1,570.75
ATP	6006	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	9	13	18	0.19%	15.00%	APVPTGEVYFADSFDR	3.2	1,770.83
ATP	6006	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	9	13	18	0.19%	15.00%	IPNPDFFEDLEPFK	2.35	1,707.83
ATP	6006	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	9	13	18	0.19%	15.00%	KIPNPDFFEDLEPFK	4.69	1,835.92
ATP	6006	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	9	13	18	0.19%	15.00%	LPGDKGLVLMSR	3.6	1,301.72
ATP	6006	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	9	13	18	0.19%	15.00%	TDAPQPDVKEDEEEKEEEK	3.49	2,245.00

ATP	6006	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	9	13	18	0.19%	15.00%	TPELNLDQFHDK	4.23	1,456.71
ATP	6006	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	9	13	18	0.19%	15.00%	TPELNLDQFHDKTPYTIMFGPDK	4.03	2,723.30
ATP	6006	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	9	13	18	0.19%	15.00%	TPYTIMFGPDK	3.47	1,285.61
ATP	6006	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	9	13	18	0.19%	15.00%	VTYKAPVPTGEVYFADSFDR	4.13	2,262.11
ATP	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	14	19	23	0.24%	11.00%	GATYNIIVEAVK	2.61	1,277.71
ATP	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	14	19	23	0.24%	11.00%	GDSPASSKPVSINYR	2.8	1,577.79
ATP	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	14	19	23	0.24%	11.00%	GLRPGVVYEGQLISVQHYGQR	5.36	2,356.25
ATP	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	14	19	23	0.24%	11.00%	NLQPGSEYAVSLVAVK	3.16	1,674.91
ATP	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	14	19	23	0.24%	11.00%	NTFAEVTGLSPGVTYHFK	3.82	1,967.99
ATP	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	14	19	23	0.24%	11.00%	QYNVGPAASQYPLR	3.44	1,563.79
ATP	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	14	19	23	0.24%	11.00%	RPGAEPGNEGSTAHSYNQYSQR	5.56	2,406.08
ATP	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	14	19	23	0.24%	11.00%	SSPVVIDASTAIDAPSNLR	3.87	1,913.00
ATP	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	14	19	23	0.24%	11.00%	SYTITGLQPGTDYK	3.67	1,543.76

ATP	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	14	19	23	0.24%	11.00%	SYTITGLQPGTDYKIHLYTLNDNAR	4.39	2,854.44
ATP	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	14	19	23	0.24%	11.00%	TEIDKPSQMQVTDVQDNSISVR	6.14	2,506.21
ATP	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	14	19	23	0.24%	11.00%	TKTETITGFQVDAIPANGQTPIQR	3.59	2,586.35
ATP	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	14	19	23	0.24%	11.00%	TPFITNPGYDTGNGIQLPGTSGQQPSLGQQMIFEEHGFRR	3.16	4,392.11
ATP	6006	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	14	19	23	0.24%	11.00%	VPGTSASATLTGLTR	4.51	1,431.78
ATP	6006	nicalin	gi|115494944,gi|94534903	63,091.10	100.00%	3	5	5	0.05%	8.72%	AAQLVDKDGTFLSTLEHYLSR	4.31	2,364.22
ATP	6006	nicalin	gi|115494944,gi|94534903	63,091.10	100.00%	3	5	5	0.05%	8.72%	MQQYDLQGQPYGTR	3.8	1,700.77
ATP	6006	nicalin	gi|115494944,gi|94534903	63,091.10	100.00%	3	5	5	0.05%	8.72%	RLPAFTLSHLQSHR	3.47	1,662.92
ATP	6006	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	4	5	6	0.06%	18.60%	KLPPLPLTLALGAFLNHR	2.43	1,971.19
ATP	6006	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	4	5	6	0.06%	18.60%	KLPPLPLTLALGAFLNHRK	2.95	2,099.29
ATP	6006	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	4	5	6	0.06%	18.60%	QLSPTEAFPVLVGDMDNSGSLNAQVIHQLGPGLR	3.71	3,576.81
ATP	6006	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	4	5	6	0.06%	18.60%	RPGEEGAVMSLAGK	2.81	1,417.71

ATP	6006	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	10	10	10	0.11%	10.90%	AFHSSLHESIQKPK	2.76	1,608.85
ATP	6006	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	10	10	10	0.11%	10.90%	GIIDSTVGDQR	3.18	1,160.59
ATP	6006	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	10	10	10	0.11%	10.90%	IDESSLTGESDHVK	2.32	1,516.71
ATP	6006	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	10	10	10	0.11%	10.90%	LKTNPVEGLSGNPADLEK	5.01	1,881.99
ATP	6006	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	10	10	10	0.11%	10.90%	QVVAVTGDGTNDGPALK	3.35	1,641.84
ATP	6006	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	10	10	10	0.11%	10.90%	QVVAVTGDGTNDGPALKK	2.17	1,769.94
ATP	6006	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	10	10	10	0.11%	10.90%	RAPLHSPPSQHYTIIFNTFVLMQLFNEINSR	3.62	3,686.89

ATP	6006	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	10	10	10	0.11%	10.90%	TNPVEGLSGNPADLEK	3.31	1,640.81
ATP	6006	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	10	10	10	0.11%	10.90%	TQDGVALEIQPLNSQEGIDSEEKEK	3	2,757.34
ATP	6006	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	10	10	10	0.11%	10.90%	TQDGVALEIQPLNSQEGIDSEEKEKK	4.56	2,885.44
ATP	6006	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	3	4	9	0.09%	26.90%	AGLQFPVGR	3.16	944.5313
ATP	6006	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	3	4	9	0.09%	26.90%	HLQLAIR	2.43	850.5258
ATP	6006	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	3	4	9	0.09%	26.90%	VTIAQGGVLPNIQAVLLPK	5.02	1,931.17
ATP	6006	phosphatidic acid phosphatase type 2A	gi|122692411,gi|81674095	32,253.70	99.80%	2	4	5	0.05%	10.20%	KEEDSHTTLHETPTTGNHYR	4.37	2,353.08
ATP	6006	phosphatidic acid phosphatase type 2A	gi|122692411,gi|81674095	32,253.70	99.80%	2	4	5	0.05%	10.20%	NNYIATIYK	2.41	1,099.58

ATP	6006	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	99.80%	2	2	2	0.02%	5.08%	VGLSDAFVVVHR	3.76	1,298.72
ATP	6006	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	99.80%	2	2	2	0.02%	5.08%	VNLSFDFPFYGHFLR	2.59	1,858.93
ATP	6006	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	gi|28461259,gi|400648,gi|560,gi|73586733	9,307.30	99.80%	2	2	2	0.02%	22.00%	FYSVNVDYSK	2.92	1,221.58
ATP	6006	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	gi|28461259,gi|400648,gi|560,gi|73586733	9,307.30	99.80%	2	2	2	0.02%	22.00%	LGPNDQYKFYSVNVDYSK	2.84	2,137.02
ATP	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	17	23	0.24%	30.90%	ASLDRPFTSLESAFYSIVGLSSLGAQVPDVK	2.46	3,254.69

ATP	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	17	23	0.24%	30.90%	ISTEVGITNVDLSTVDKDQSIAPK	2.65	2,530.33
ATP	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	17	23	0.24%	30.90%	LMDHVGTEPSIKEDQVIQLMNAIFSK	4.01	2,959.49

ATP	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	17	23	0.24%	30.90%	LQVTNVLSQPLTQATVK	5.68	1,840.05
ATP	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	17	23	0.24%	30.90%	LQVTNVLSQPLTQATVKLEHAK	3.38	2,418.37

ATP	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	17	23	0.24%	30.90%	LSKEETVLATVQALQTASYLSQQADLR	4.57	2,963.57
ATP	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	17	23	0.24%	30.90%	NFESLSEAFSVASAAAALSENR	3.27	2,271.09

ATP	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	17	23	0.24%	30.90%	SIVEEIEDLVAR	4.01	1,372.73
ATP	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	17	23	0.24%	30.90%	TGQEVVFVAEPDSK	3.07	1,505.75

ATP	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	17	23	0.24%	30.90%	VEGDNRYIANTVELR	3.92	1,748.89
ATP	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	17	23	0.24%	30.90%	VKISTEVGITNVDLSTVDKDQSIAPK	3.62	2,757.49

ATP	6006	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	12	17	23	0.24%	30.90%	YIANTVELR	2.87	1,078.59
ATP	6006	PREDICTED: integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	gi|119913150	148,911.70	99.80%	2	2	2	0.02%	1.98%	ALSESQEENMADNSVNLK	2.32	1,994.90
ATP	6006	PREDICTED: integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	gi|119913150	148,911.70	99.80%	2	2	2	0.02%	1.98%	VVFNLNTFK	2.47	1,081.60
ATP	6006	STT3B protein	gi|146186621,gi|148235371	93,202.50	100.00%	3	3	4	0.04%	4.99%	ENPPVEDSSDEDDKRNPGNLYDK	2.64	2,633.16
ATP	6006	STT3B protein	gi|146186621,gi|148235371	93,202.50	100.00%	3	3	4	0.04%	4.99%	HVTEQEKTEEGLGPNIK	4.17	1,908.97
ATP	6006	STT3B protein	gi|146186621,gi|148235371	93,202.50	100.00%	3	3	4	0.04%	4.99%	KHVTEQEKTEEGLGPNIK	3.38	2,037.06
ATP	6006	Synaptojanin 2 binding protein	gi|74354054,gi|78369420	15,792.00	99.80%	2	2	2	0.02%	19.30%	LQEGDKILSVNGQDLK	3.46	1,756.94
ATP	6006	Synaptojanin 2 binding protein	gi|74354054,gi|78369420	15,792.00	99.80%	2	2	2	0.02%	19.30%	NLLHQDAVDLFR	3	1,440.76

ATP	6006	ADPGK protein	gi|126010731,gi|126722892,gi|205686178	54,066.80	99.80%	2	2	2	0.02%	9.66%	FFSDKETFHDIAQVASEFPEAQHYVGGNAALIGQK	3.23	3,851.87
ATP	6006	ADPGK protein	gi|126010731,gi|126722892,gi|205686178	54,066.80	99.80%	2	2	2	0.02%	9.66%	NDLEEAFVHFMGK	2.28	1,552.71
ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	AGTQLLAGLR	3.3	999.5947
ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	AQNQGEGAYEAELIVSIPLQADFIGVVR	3.03	2,987.55
ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	ASGDFQTIKLNGFEVFAR	2.92	2,000.02
ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	ENPETEEDVGPVVQHIYELR	2.98	2,353.13
ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	FDLQIQSSNLFDK	2.79	1,554.78
ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	FGSAIAPLGDLDQDGFNDIAIAAPYGGEDKK	4.39	3,165.54
ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	FSVHQQSEMDTSVK	4.45	1,638.74
ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	GALPTKLDFQVELLLDKLK	4.52	2,141.26
ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	GATDIDKNGYPDLIVGAFGVDR	4.67	2,293.15
ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	GIVYIFNGRPTGLNAVPSQILEGK	4.48	2,543.40
ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	IYIGDDNPLTLIVK	3.32	1,573.88
ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	LNGFEVFAR	2.67	1,052.55
ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	MFLLVGAPK	3.55	991.5647
ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	SSASFNVIEFPYK	3.21	1,488.74
ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	TLGMVYIYDGK	2.8	1,275.63
ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	VRPPQEEQEREQLQPHENGEGNSET	2.34	2,917.33

ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	VYSIKYNNQLATR	3.59	1,569.84
ATP	6006	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	18	21	35	0.37%	27.30%	YKENPETEEDVGPVVQHIYELR	4.11	2,644.29
ATP	6006	PREDICTED: similar to 60S ribosomal protein L9	gi|119904384,gi|119905715,gi|164420694,gi|76607197,gi|91207745	21,858.70	100.00%	3	3	3	0.03%	17.20%	FLDGIYVSEK	2.99	1,170.60
ATP	6006	PREDICTED: similar to 60S ribosomal protein L9	gi|119904384,gi|119905715,gi|164420694,gi|76607197,gi|91207745	21,858.70	100.00%	3	3	3	0.03%	17.20%	MKTILSNQTVDIPENVDINLK	2.5	2,401.26
ATP	6006	PREDICTED: similar to 60S ribosomal protein L9	gi|119904384,gi|119905715,gi|164420694,gi|76607197,gi|91207745	21,858.70	100.00%	3	3	3	0.03%	17.20%	TILSNQTVDIPENVDINLKGR	2.69	2,339.26
ATP	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	9	9	10	0.11%	22.50%	AVDSLVPIGR	2.88	1,026.59
ATP	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	9	9	10	0.11%	22.50%	FENAFLSHVISQHQALLSK	3.12	2,169.15
ATP	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	9	9	10	0.11%	22.50%	ILGADTSVDLEETGR	3.44	1,575.79

ATP	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	9	9	10	0.11%	22.50%	ISVREPMQTGIK	2.83	1,374.74
ATP	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	9	9	10	0.11%	22.50%	ITKFENAFLSHVISQHQALLSK	4.35	2,511.37
ATP	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	9	9	10	0.11%	22.50%	TGAIVDVPVGEELLGR	3.91	1,624.89
ATP	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	9	9	10	0.11%	22.50%	TSIAIDTIINQK	2.68	1,316.74
ATP	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	9	9	10	0.11%	22.50%	VLSIGDGIAR	2.52	1,000.58
ATP	6006	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	9	9	10	0.11%	22.50%	VVDALGNAIDGKGPIGSK	4.88	1,710.94

ATP	6006	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	9	10	0.11%	41.80%	IMVANIEEVLQR	3.69	1,430.77
ATP	6006	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	9	10	0.11%	41.80%	IMVANIEEVLQRGEALSALDSK	2.32	2,402.26
ATP	6006	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	9	10	0.11%	41.80%	KLAFAYLEDLHSEFDEQHGK	3.38	2,377.15
ATP	6006	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	9	10	0.11%	41.80%	KVPTVSRPYSFIEFDTYIQK	3.01	2,418.27
ATP	6006	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	9	10	0.11%	41.80%	NLGSINTELQDVQR	4.19	1,586.81
ATP	6006	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	9	10	0.11%	41.80%	VADGLPLAASMQEDEQSGR	3.39	1,989.92
ATP	6006	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	9	10	0.11%	41.80%	VADGLPLAASMQEDEQSGRDLQQYQSQAK	5.48	3,179.49
ATP	6006	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	4	6	8	0.08%	19.60%	INVNEIFYDLVR	3.32	1,494.80
ATP	6006	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	4	6	8	0.08%	19.60%	LVVLGSGGVGK	2.84	985.6042
ATP	6006	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	4	6	8	0.08%	19.60%	SKINVNEIFYDLVR	3.95	1,709.92
ATP	6006	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	4	6	8	0.08%	19.60%	YDPTIEDSYRK	2.55	1,386.65
ATP	6006	metadherin	gi|114051299,gi|89994114	64,037.90	99.80%	2	2	2	0.02%	5.83%	KREEAAAAPAPAADDQGVLK	3.01	2,079.08
ATP	6006	metadherin	gi|114051299,gi|89994114	64,037.90	99.80%	2	2	2	0.02%	5.83%	TISTSDPADALIK	2.66	1,331.71

ATP	6006	RecName: Full=ATP synthase subunit g, mitochondrial; Short=ATPase subunit g	gi|2493093,gi|74354012,gi|7579922,gi|94400870	11,604.00	99.80%	2	4	6	0.06%	19.20%	APALVNAAVTYSKPR	3.8	1,557.87
ATP	6006	RecName: Full=ATP synthase subunit g, mitochondrial; Short=ATPase subunit g	gi|2493093,gi|74354012,gi|7579922,gi|94400870	11,604.00	99.80%	2	4	6	0.06%	19.20%	NLAEKAPALVNAAVTYSKPR	6.46	2,113.18
ATP	6006	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	99.90%	2	2	3	0.03%	15.30%	LLLLGTGESGK	3.43	1,087.64
ATP	6006	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	99.90%	2	2	3	0.03%	15.30%	VRVPTTGIIEYPFDLQSVIFR	5.37	2,450.34
ATP	6006	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	99.90%	2	2	3	0.03%	15.30%	YYLNDLDRVADPAYLPTQQDVLR	3.27	2,738.38
ATP	6006	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	99.80%	2	2	2	0.02%	4.73%	LPVPASAPIPFFHR	3.68	1,548.87
ATP	6006	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	99.80%	2	2	2	0.02%	4.73%	NAELEAIPNSGMDHTHR	2.9	1,907.87

ATP	6006	PREDICTED: similar to CAAX prenyl protease 1 homolog (Prenyl protein-specific endoprotease 1) (Farnesylated proteins-converting enzyme 1) (FACE-1) (Zinc metalloproteinase Ste24 homolog) isoform 1	gi|76614153	54,663.70	99.80%	2	2	3	0.03%	9.26%	DIQEESGMEPRNDGEGDSEEIKAK	3.56	2,679.17
ATP	6006	PREDICTED: similar to CAAX prenyl protease 1 homolog (Prenyl protein-specific endoprotease 1) (Farnesylated proteins-converting enzyme 1) (FACE-1) (Zinc metalloproteinase Ste24 homolog) isoform 1	gi|76614153	54,663.70	99.80%	2	2	3	0.03%	9.26%	TTTHVPLELGQIMDSETFEK	5.48	2,292.11
ATP	6006	RecName: Full=60S ribosomal protein L7a	gi|108860939,gi|146231828,gi|83638795,gi|94966839	30,008.40	99.80%	2	2	3	0.03%	10.20%	LKVPPAINQFTQALDR	4.79	1,811.02
ATP	6006	RecName: Full=60S ribosomal protein L7a	gi|108860939,gi|146231828,gi|83638795,gi|94966839	30,008.40	99.80%	2	2	3	0.03%	10.20%	NFGIGQDIQPK	2.51	1,216.63

ATP	6006	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	3	3	3	0.03%	9.11%	GFKDQIYDIFQK	2.87	1,501.77
ATP	6006	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	3	3	3	0.03%	9.11%	LQMEAPHIIVGTPGR	2.64	1,634.87
ATP	6006	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	3	3	3	0.03%	9.11%	VLITTDLLAR	2.93	1,114.68
ATP	6006	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	5	6	7	0.07%	23.80%	DVYVQLYLQHLTAR	3.25	1,718.92
ATP	6006	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	5	6	7	0.07%	23.80%	GPPDFSSDEEREPTPVLGSGAAVAGR	5.12	2,598.24
ATP	6006	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	5	6	7	0.07%	23.80%	HAAPILPITEFSDIPR	3.49	1,776.96

ATP	6006	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	5	6	7	0.07%	23.80%	LKSELVANNVTLPAGEQRK	3.95	2,067.16
ATP	6006	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	5	6	7	0.07%	23.80%	SSTPLPTISSSVENTR	2.5	1,675.85
ATP	6006	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	8	8	8	0.08%	5.47%	GVGAAATAVTQALNELLQHVR	4.2	2,119.16
ATP	6006	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	8	8	8	0.08%	5.47%	LAQAAQSSVATITR	4.19	1,416.78
ATP	6006	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	8	8	8	0.08%	5.47%	LLAALLEDEGGSGRPLLQAAK	2.95	2,122.19
ATP	6006	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	8	8	8	0.08%	5.47%	LNEAAAGLNQAATELVQASR	3.4	2,027.05
ATP	6006	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	8	8	8	0.08%	5.47%	MTKGITMATAKAVAAGNSCR	2.53	1,982.00
ATP	6006	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	8	8	8	0.08%	5.47%	TLSHPQQMALLDQTK	3.2	1,726.88
ATP	6006	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	8	8	8	0.08%	5.47%	TMLESAGGLIQTAR	2.93	1,463.75
ATP	6006	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	8	8	8	0.08%	5.47%	VLGEAMTGISQNAK	3.09	1,434.73
ATP	6006	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	5	5	6	0.06%	11.30%	FKPPSVAVVQPK	2.95	1,296.77
ATP	6006	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	5	5	6	0.06%	11.30%	GLIPQLIGVAPEK	2.2	1,334.80
ATP	6006	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	5	5	6	0.06%	11.30%	HLNYTEFTQFLQELQLEHAR	3.36	2,517.25
ATP	6006	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	5	5	6	0.06%	11.30%	IAPLAEGALPYNLAELQR	4.71	1,939.06
ATP	6006	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	5	5	6	0.06%	11.30%	YLGLYNDPNSNPK	3.83	1,494.72
ATP	6006	IKK interacting protein	gi|126010633,gi|126165284,gi|193806036	39,199.60	99.80%	2	2	2	0.02%	6.88%	METSEFQGLQSK	3.62	1,400.64
ATP	6006	IKK interacting protein	gi|126010633,gi|126165284,gi|193806036	39,199.60	99.80%	2	2	2	0.02%	6.88%	NIGDLLSSSIDR	3.72	1,289.67
ATP	6006	ALDH3A2 protein	gi|151557095,gi|156120617	54,059.30	99.80%	2	2	2	0.02%	4.95%	IAFGGEMDEATR	2.95	1,312.58
ATP	6006	ALDH3A2 protein	gi|151557095,gi|156120617	54,059.30	99.80%	2	2	2	0.02%	4.95%	NADEAIQFINER	2.3	1,419.69

ATP	6006	defender against cell death 1	gi|59858361,gi|73918963,gi|74354770,gi|77736467,gi|83286811	12,477.50	99.80%	2	3	4	0.04%	19.50%	ADFQGISPER	3.01	1,119.54
ATP	6006	defender against cell death 1	gi|59858361,gi|73918963,gi|74354770,gi|77736467,gi|83286811	12,477.50	99.80%	2	3	4	0.04%	19.50%	FLEEYLSATPQR	2.41	1,453.73
ATP	6006	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	5	5	5	0.05%	13.40%	AFITNIPFDVK	2.77	1,264.69
ATP	6006	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	5	5	5	0.05%	13.40%	GDFFPPERPQQLPHGLGGIGMGLGPGGQPIDANHLNK	4.46	3,834.91
ATP	6006	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	5	5	5	0.05%	13.40%	GGNRFEPYANPTKR	4.37	1,606.81
ATP	6006	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	5	5	5	0.05%	13.40%	GNFGGSFAGSFGGAGGHAPGVAR	4.36	2,034.95
ATP	6006	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	5	5	5	0.05%	13.40%	LKEVFSMAGVVVR	3.87	1,450.81
ATP	6006	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	5	7	8	0.08%	15.20%	ELQALTDAMYTNLR	2.55	1,654.81
ATP	6006	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	5	7	8	0.08%	15.20%	EVVADLALPMADGREFSLR	2.74	2,105.07

ATP	6006	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	5	7	8	0.08%	15.20%	LLLFPFLSPQKDPEIYTDPEVFK	3.64	2,736.45
ATP	6006	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	5	7	8	0.08%	15.20%	LLLFPFLSPQKDPEIYTDPEVFKYNR	4.07	3,169.66
ATP	6006	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	5	7	8	0.08%	15.20%	VLDSMPVLDSVLSESLR	3.88	1,875.97
ATP	6006	metalloproteinase	gi|1044811,gi|157742933,gi|27806209,gi|29839751	84,171.20	100.00%	4	5	5	0.05%	7.35%	AIDTIYQTTDFSGIR	3.42	1,700.85
ATP	6006	metalloproteinase	gi|1044811,gi|157742933,gi|27806209,gi|29839751	84,171.20	100.00%	4	5	5	0.05%	7.35%	EAVIAQISSHVK	2.33	1,281.72
ATP	6006	metalloproteinase	gi|1044811,gi|157742933,gi|27806209,gi|29839751	84,171.20	100.00%	4	5	5	0.05%	7.35%	HYEGLSYDVDSLHQK	4.9	1,790.83
ATP	6006	metalloproteinase	gi|1044811,gi|157742933,gi|27806209,gi|29839751	84,171.20	100.00%	4	5	5	0.05%	7.35%	LPPPKPLPGTLKR	1.74	1,413.89
ATP	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	4	0.04%	32.70%	AILVDLEPGTMDSVR	3.25	1,631.83
ATP	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	4	0.04%	32.70%	ALTVPELTQQVFDAK	3.55	1,659.90
ATP	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	4	0.04%	32.70%	GHYTEGAELVDSVLDVVRK	3.22	2,087.08
ATP	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	4	0.04%	32.70%	IMNTFSVVPSPK	3	1,335.70
ATP	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	4	0.04%	32.70%	ISVYYNEATGGK	3.28	1,301.64
ATP	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	4	0.04%	32.70%	LAVNMVPFPR	3.84	1,159.63
ATP	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	4	0.04%	32.70%	LHFFMPGFAPLTSR	3.49	1,636.83
ATP	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	4	0.04%	32.70%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	3.15	4,479.06

ATP	6006	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	4	0.04%	32.70%	YLTVAAVFR	2.35	1,039.59
ATP	6006	melanoma cell adhesion molecule	gi|2323281	9,468.30	99.80%	2	3	5	0.05%	38.40%	APGDQGEKYIDLRH	2.69	1,598.79
ATP	6006	melanoma cell adhesion molecule	gi|2323281	9,468.30	99.80%	2	3	5	0.05%	38.40%	SDKLPEEMGLLQGSSGDKR	4.9	2,063.01
ATP	6006	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	5	6	369	3.88%	47.60%	AAVTSLFAK	2.47	907.5247
ATP	6006	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	5	6	369	3.88%	47.60%	FFESFGDLSSADAILGNPK	3.97	2,014.98
ATP	6006	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	5	6	369	3.88%	47.60%	LLGNVLVVVLAR	4.93	1,265.83
ATP	6006	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	5	6	369	3.88%	47.60%	RFGSEFSPELQASFQK	2.74	1,857.91
ATP	6006	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	5	6	369	3.88%	47.60%	VKVDEVGGEALGR	4.16	1,328.72
ATP	6006	Ribosomal protein L6	gi|126717393,gi|58760432,gi|61553343,gi|61553350,gi|67461090,gi|72534798	32,672.90	99.80%	2	2	2	0.02%	10.50%	AVPQLQGYLR	2.17	1,144.65
ATP	6006	Ribosomal protein L6	gi|126717393,gi|58760432,gi|61553343,gi|61553350,gi|67461090,gi|72534798	32,672.90	99.80%	2	2	2	0.02%	10.50%	HQEGEIFDTEREKYEITEQR	3.13	2,537.19
ATP	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	12	12	12	0.13%	7.95%	AFGPGLQGGSAGSPAR	4.36	1,429.72
ATP	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	12	12	12	0.13%	7.95%	ANLPQSFQVDTSK	2.86	1,434.72

ATP	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	12	12	12	0.13%	7.95%	AYGPGIEPTGNMVK	3.06	1,449.70
ATP	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	12	12	12	0.13%	7.95%	FNEEHIPDSPFVVPVASPSGDAR	3.05	2,467.19
ATP	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	12	12	12	0.13%	7.95%	GAGTGGLGLAVEGPSEAK	3.78	1,570.81
ATP	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	12	12	12	0.13%	7.95%	IANLQTDLSDGLR	2.82	1,415.75
ATP	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	12	12	12	0.13%	7.95%	LIALLEVLSQK	2.79	1,226.77
ATP	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	12	12	12	0.13%	7.95%	LTVSSLQESGLK	3.08	1,261.70
ATP	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	12	12	12	0.13%	7.95%	SPFEVYVDKSQGDASK	3	1,756.84
ATP	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	12	12	12	0.13%	7.95%	SPFSVGVSPSLDLSK	3.43	1,519.80

ATP	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	12	12	12	0.13%	7.95%	VAQPAITDNKDGTVTVR	2.38	1,784.95
ATP	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	12	12	12	0.13%	7.95%	VTAQGPGLEPSGNIANK	4.63	1,652.86
ATP	6006	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	12	12	12	0.13%	7.95%	YTPVQQGPVGINVTYGGDAIPK	3.23	2,274.18
ATP	6006	NRAS protein	gi|146186548,gi|148226664	21,211.30	100.00%	3	3	3	0.03%	25.90%	SALTIQLIQNHFVDEYDPTIEDSYRK	2.76	3,095.53
ATP	6006	NRAS protein	gi|146186548,gi|148226664	21,211.30	100.00%	3	3	3	0.03%	25.90%	SFADINLYR	2.65	1,098.56
ATP	6006	NRAS protein	gi|146186548,gi|148226664	21,211.30	100.00%	3	3	3	0.03%	25.90%	TRQGVEDAFYTLVR	3.18	1,654.85
ATP	6006	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	7	12	17	0.18%	29.90%	ANQVTDESLESTR	3.16	1,449.68
ATP	6006	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	7	12	17	0.18%	29.90%	ANQVTDESLESTRR	2.8	1,605.78
ATP	6006	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	7	12	17	0.18%	29.90%	ILGLAIESQDAGIK	3.58	1,427.81
ATP	6006	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	7	12	17	0.18%	29.90%	TITMLDEQGEQLK	3.14	1,521.75
ATP	6006	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	7	12	17	0.18%	29.90%	TITMLDEQGEQLKR	2.54	1,677.85
ATP	6006	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	7	12	17	0.18%	29.90%	VTNGQPQQATAGAASGGYIK	3.21	1,918.96
ATP	6006	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	7	12	17	0.18%	29.90%	VTNGQPQQATAGAASGGYIKR	2.94	2,075.06

ATP	6006	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	gi|124828540,gi|126158903,gi|145566947	55,991.00	99.80%	2	2	2	0.02%	7.55%	NLFPSNLVVAAFR	3.06	1,447.81
ATP	6006	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	gi|124828540,gi|126158903,gi|145566947	55,991.00	99.80%	2	2	2	0.02%	7.55%	SSETNGYLDSAQEGPAAGPGEPGTTAR	3.63	2,620.18
ATP	6006	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	6	10	16	0.17%	7.97%	ESTLHLVLR	2.74	1,067.62
ATP	6006	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	6	10	16	0.17%	7.97%	IQDKEGIPPDQQR	2.6	1,523.78
ATP	6006	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	6	10	16	0.17%	7.97%	QLEDGRTLSDYNIQK	3.27	1,779.89
ATP	6006	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	6	10	16	0.17%	7.97%	TITLEVEPSDTIENVK	3.04	1,787.93
ATP	6006	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	6	10	16	0.17%	7.97%	TITLEVEPSDTIENVKAK	3.74	1,987.06
ATP	6006	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	6	10	16	0.17%	7.97%	TLSDYNIQKESTLHLVLR	4.17	2,130.16
ATP	6006	TPA: predicted NADPH oxidase-5	gi|151427572,gi|155372001	86,454.40	99.90%	2	3	5	0.05%	3.71%	AIGLQMALDLLAK	3.39	1,372.79
ATP	6006	TPA: predicted NADPH oxidase-5	gi|151427572,gi|155372001	86,454.40	99.90%	2	3	5	0.05%	3.71%	MAALHIVEVNLLPSK	3.92	1,650.92

ATP	6006	RecName: Full=Small nuclear ribonucleoprotein Sm D1; Short=Sm-D1; AltName: Full=snRNP core protein D1	gi|109894869,gi|73586929,gi|78050059	13,263.90	99.80%	2	3	4	0.04%	27.70%	NREPVQLETLSIR	3.32	1,554.86
ATP	6006	RecName: Full=Small nuclear ribonucleoprotein Sm D1; Short=Sm-D1; AltName: Full=snRNP core protein D1	gi|109894869,gi|73586929,gi|78050059	13,263.90	99.80%	2	3	4	0.04%	27.70%	YFILPDSLPLDTLLVDVEPK	4.18	2,287.25
ATP	6006	RecName: Full=Syntaxin-4	gi|122140085,gi|74356383,gi|78050061	34,382.50	99.90%	2	2	2	0.02%	10.10%	AIEPQKEEADENYNSVNTR	3.9	2,207.02
ATP	6006	RecName: Full=Syntaxin-4	gi|122140085,gi|74356383,gi|78050061	34,382.50	99.90%	2	2	2	0.02%	10.10%	NILSSADYVER	3.15	1,266.63
ATP	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	21	0.22%	18.40%	AFTGREFDELSPSAQR	3.72	1,810.87
ATP	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	21	0.22%	18.40%	AKDIVPGDIVEIAVGDKVPADIR	3.23	2,390.33

ATP	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	21	0.22%	18.40%	AMGVVVATGVNTEIGK	4.18	1,561.83
ATP	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	21	0.22%	18.40%	EEMNLEDSANFIK	2.86	1,555.69
ATP	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	21	0.22%	18.40%	EFTLEFSR	1.99	1,028.50
ATP	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	21	0.22%	18.40%	KSEIGIAMGSGTAVAK	4.79	1,535.81
ATP	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	21	0.22%	18.40%	MNVFDTELK	2.49	1,112.53
ATP	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	21	0.22%	18.40%	NAENAIEALKEYEPEMGK	2.94	2,051.96

ATP	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	21	0.22%	18.40%	NMLFSGTNIAAGK	2.73	1,339.67
ATP	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	21	0.22%	18.40%	SEIGIAMGSGTAVAK	4.25	1,407.72
ATP	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	21	0.22%	18.40%	TASEMVLADDNFSTIVAAVEEGR	3.48	2,441.15
ATP	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	21	0.22%	18.40%	VDQSILTGESVSVIK	4.38	1,574.86
ATP	6006	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	13	15	21	0.22%	18.40%	VGSTKVPMTPGVK	2.97	1,316.72
ATP	6006	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	100.00%	3	5	5	0.05%	7.75%	HSLEGNPRDEEDDDEDMYSDNINAATEEK	6.05	3,354.35

ATP	6006	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	100.00%	3	5	5	0.05%	7.75%	IVTLDSLEDTK	3.09	1,233.66
ATP	6006	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	100.00%	3	5	5	0.05%	7.75%	NLSLPFIFHEK	2.42	1,344.73
ATP	6006	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	99.80%	2	2	2	0.02%	4.20%	ILEVVNQVQDEER	4.22	1,570.81
ATP	6006	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	99.80%	2	2	2	0.02%	4.20%	IPVYSAFR	2.12	952.525
ATP	6006	PREDICTED: similar to hCG1980844	gi|194674945	298,419.90	100.00%	3	3	3	0.03%	1.29%	LDLKDIPNAIR	3.52	1,267.74
ATP	6006	PREDICTED: similar to hCG1980844	gi|194674945	298,419.90	100.00%	3	3	3	0.03%	1.29%	QLQPNEEADYLGVR	3.49	1,631.80
ATP	6006	PREDICTED: similar to hCG1980844	gi|194674945	298,419.90	100.00%	3	3	3	0.03%	1.29%	YLLTQELLR	2.95	1,148.67
ATP	6006	PREDICTED: similar to karyopherin beta 1 isoform 2	gi|76644624	97,210.30	100.00%	2	2	2	0.02%	3.54%	AAVENLPTFLVELSR	3.63	1,658.91
ATP	6006	PREDICTED: similar to karyopherin beta 1 isoform 2	gi|76644624	97,210.30	100.00%	2	2	2	0.02%	3.54%	LLETTDRPDGHQNNLR	2.35	1,878.94

ATP	6006	PREDICTED: similar to potassium-chloride cotransporter-1 isoform 2	gi|194675074	120,598.40	99.90%	2	2	2	0.02%	1.75%	DNIIPFLR	2.12	987.5623
ATP	6006	PREDICTED: similar to potassium-chloride cotransporter-1 isoform 2	gi|194675074	120,598.40	99.90%	2	2	2	0.02%	1.75%	LVLLNMPGPPK	2.92	1,194.69
ATP	6006	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	9	9	10	0.11%	10.80%	EKDGEFSVLQLVGMLR	3.46	1,836.95
ATP	6006	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	9	9	10	0.11%	10.80%	EVVLLDFAAAK	2.76	1,175.67
ATP	6006	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	9	9	10	0.11%	10.80%	FADIVSILDK	3.73	1,120.63
ATP	6006	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	9	9	10	0.11%	10.80%	FADIVSILDKLIR	3.33	1,502.89
ATP	6006	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	9	9	10	0.11%	10.80%	IDTIAPDEITGSSDFEAR	4.12	1,936.91
ATP	6006	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	9	9	10	0.11%	10.80%	TLADFDPR	2.44	934.463
ATP	6006	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	9	9	10	0.11%	10.80%	TYVDPHTYEDPNQAVLK	1.96	1,989.96
ATP	6006	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	9	9	10	0.11%	10.80%	VIGAGEFGEVYK	2.58	1,268.65

ATP	6006	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	9	9	10	0.11%	10.80%	YSEPPLGLTR	2.51	1,132.60
ATP	6006	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	4	4	5	0.05%	23.20%	DFTPAELR	2.05	948.4786
ATP	6006	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	4	4	5	0.05%	23.20%	FYGPEGPYGVFAGR	2.63	1,516.72
ATP	6006	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	4	4	5	0.05%	23.20%	IVRGDQPAASDSDDDEPPPLPR	4.48	2,347.12
ATP	6006	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	4	4	5	0.05%	23.20%	KFYGPEGPYGVFAGR	4.51	1,644.82
ATP	6006	PTPN1 protein	gi|151556032,gi|154152077	49,019.80	100.00%	3	3	3	0.03%	8.24%	FSYLAVIEGAK	3.78	1,197.65
ATP	6006	PTPN1 protein	gi|151556032,gi|154152077	49,019.80	100.00%	3	3	3	0.03%	8.24%	QLELENLMSRETR	2.68	1,634.82
ATP	6006	PTPN1 protein	gi|151556032,gi|154152077	49,019.80	100.00%	3	3	3	0.03%	8.24%	YRDVSPFDHSR	3.64	1,378.65
ATP	6006	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	99.90%	2	3	3	0.03%	5.12%	LVQDVANNTNEEAGDGTTTATVLAR	5.17	2,560.25
ATP	6006	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	99.90%	2	3	3	0.03%	5.12%	TLKIPAMTIAK	2.18	1,202.72
ATP	6006	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	15	23	0.24%	35.70%	DILLRPELEELR	2.55	1,495.85
ATP	6006	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	15	23	0.24%	35.70%	GPNGLLVYQGK	3.78	1,145.63

ATP	6006	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	15	23	0.24%	35.70%	IDGNLVIRPYTPVSSDDDKGFVDLVIK	2.87	2,975.57
ATP	6006	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	15	23	0.24%	35.70%	IGDTIEFR	2.57	950.4943
ATP	6006	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	15	23	0.24%	35.70%	IGDTIEFRGPNGLLVYQGK	2.85	2,077.11
ATP	6006	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	15	23	0.24%	35.70%	LIDKEVISHDTR	3.89	1,425.77
ATP	6006	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	15	23	0.24%	35.70%	LIDKEVISHDTRR	2.91	1,581.87
ATP	6006	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	15	23	0.24%	35.70%	STPAITLENPDIKYPLR	4.42	1,928.05
ATP	6006	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	15	23	0.24%	35.70%	SVGMIAGGTGITPMLQVIR	5.11	1,917.03
ATP	6006	endothelial cell adhesion molecule	gi|118151218,gi|119919027,gi|86823868	41,779.80	100.00%	3	5	5	0.05%	9.34%	ALEEPANDIKEDAIAPR	3.53	1,851.94
ATP	6006	endothelial cell adhesion molecule	gi|118151218,gi|119919027,gi|86823868	41,779.80	100.00%	3	5	5	0.05%	9.34%	GKALEEPANDIKEDAIAPR	4.35	2,037.06
ATP	6006	endothelial cell adhesion molecule	gi|118151218,gi|119919027,gi|86823868	41,779.80	100.00%	3	5	5	0.05%	9.34%	GSDTISKNGTLSSVTSAR	3.22	1,780.90
ATP	6006	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	5	5	5	0.05%	1.94%	GTLEPVQRPDVVLVGAGHR	3.25	2,000.10
ATP	6006	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	5	5	5	0.05%	1.94%	HPTPLALGQFHTVTLLR	3.14	1,901.08
ATP	6006	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	5	5	5	0.05%	1.94%	LRPGIVQSGGIVR	3.72	1,351.82

ATP	6006	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	5	5	5	0.05%	1.94%	LRSPVISIDPPSSTVQQGQDASFK	6.08	2,557.33
ATP	6006	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	5	5	5	0.05%	1.94%	SVVPQGGPHSLR	2.25	1,233.67
ATP	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	13	15	17	0.18%	28.10%	ALEEANADLEVK	2.73	1,301.66
ATP	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	13	15	17	0.18%	28.10%	ASLENSLEETKGR	3.15	1,433.72
ATP	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	13	15	17	0.18%	28.10%	ILNEMRDQYEK	3.05	1,438.70
ATP	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	13	15	17	0.18%	28.10%	ILNEMRDQYEKMAEK	3.56	1,913.91
ATP	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	13	15	17	0.18%	28.10%	LASYLDKVR	3.06	1,064.61
ATP	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	13	15	17	0.18%	28.10%	LLEGEDAHLSSSQFSSGSQSSR	5.06	2,309.06
ATP	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	13	15	17	0.18%	28.10%	QRPAEIKDYSPYFK	3.12	1,741.89
ATP	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	13	15	17	0.18%	28.10%	TEELNREVATNSELVQSGK	3.77	2,104.05
ATP	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	13	15	17	0.18%	28.10%	TRLEQEIATYR	3.86	1,379.73
ATP	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	13	15	17	0.18%	28.10%	TRLEQEIATYRR	3.97	1,535.83
ATP	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	13	15	17	0.18%	28.10%	VLDELTLAR	4	1,029.59

ATP	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	13	15	17	0.18%	28.10%	VTMQNLNDRLASYLDK	2.46	1,896.95
ATP	6006	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	13	15	17	0.18%	28.10%	VTMQNLNDRLASYLDKVR	2.2	2,152.12
ATP	6006	Transmembrane protein 49	gi|111307060,gi|115496266,gi|122133514	46,165.40	99.80%	2	2	2	0.02%	12.60%	LSGAEPDDEEYQEFEEMLEHAETAQDFASR	4.73	3,489.46
ATP	6006	Transmembrane protein 49	gi|111307060,gi|115496266,gi|122133514	46,165.40	99.80%	2	2	2	0.02%	12.60%	VAMNKEQYNGNFTDPSSVNEK	4.59	2,388.08
ATP	6006	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	6	10	15	0.16%	11.60%	FASFIDKVR	2.12	1,082.60
ATP	6006	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	6	10	15	0.16%	11.60%	NKYEDEINKR	2.84	1,308.65
ATP	6006	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	6	10	15	0.16%	11.60%	SFSTASAITPSVSR	3.93	1,410.72
ATP	6006	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	6	10	15	0.16%	11.60%	SLDLDSIIAEVK	4.84	1,302.72
ATP	6006	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	6	10	15	0.16%	11.60%	TEAESWYQTKYEELQQTAGR	4.58	2,418.12
ATP	6006	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	6	10	15	0.16%	11.60%	TLNNKFASFIDKVR	4.1	1,652.91
ATP	6006	CLPTM1L protein	gi|126010733,gi|126723356,gi|187470818	62,084.20	99.80%	2	2	2	0.02%	6.69%	MTVIWRGLWPTFQFGTYSESERR	2.25	2,847.40
ATP	6006	CLPTM1L protein	gi|126010733,gi|126723356,gi|187470818	62,084.20	99.80%	2	2	2	0.02%	6.69%	SSTELPLTVSYDK	2.71	1,439.73
ATP	6006	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	4	4	4	0.04%	7.92%	ALVQTEDHLLLFLQQLAGR	3.96	2,165.21
ATP	6006	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	4	4	4	0.04%	7.92%	HLLVGLPSGAILSLPK	4.54	1,614.99
ATP	6006	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	4	4	4	0.04%	7.92%	QLHELAPSIFFYLVDADQGR	2.67	2,319.18
ATP	6006	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	4	4	4	0.04%	7.92%	RPEIPTEQSREENLIPYSPDVQIHAER	3.29	3,203.61

ATP	6006	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	100.00%	3	4	5	0.05%	14.00%	AQIQEQNPSIEVVYYNK	3.91	2,023.01
ATP	6006	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	100.00%	3	4	5	0.05%	14.00%	ELQVGIPVTNEQGQR	2.49	1,667.87
ATP	6006	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	100.00%	3	4	5	0.05%	14.00%	NLLLSGAQLEASR	4.7	1,371.76
ATP	6006	RecName: Full=CD81 antigen; AltName: CD_antigen=CD81	gi|122140914,gi|73586978,gi|78042548	25,835.90	99.80%	2	3	3	0.03%	9.75%	DVKQFYDQALQQAIVDDDANNAK	4.59	2,609.25
ATP	6006	RecName: Full=CD81 antigen; AltName: CD_antigen=CD81	gi|122140914,gi|73586978,gi|78042548	25,835.90	99.80%	2	3	3	0.03%	9.75%	QFYDQALQQAIVDDDANNAK	5.18	2,267.06
ATP	6006	RAB21, member RAS oncogene family	gi|109658186,gi|115496760,gi|122144675	24,128.60	99.80%	2	2	2	0.02%	12.20%	FHALGPIYYR	2.89	1,236.65
ATP	6006	RAB21, member RAS oncogene family	gi|109658186,gi|115496760,gi|122144675	24,128.60	99.80%	2	2	2	0.02%	12.20%	HVSIQEAESYAESVGAK	3.87	1,804.87
ATP	6006	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	100.00%	4	5	6	0.06%	12.90%	ALSFVLR	1.9	805.493
ATP	6006	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	100.00%	4	5	6	0.06%	12.90%	LNQAVEFDVLPAFDALGQLTK	5.06	2,289.21
ATP	6006	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	100.00%	4	5	6	0.06%	12.90%	PRPVILDPADPTGNVAGK	3.65	1,816.99
ATP	6006	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	100.00%	4	5	6	0.06%	12.90%	QLAKPRPVILDPADPTGNVAGK	2.38	2,257.27

ATP	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	16	26	52	0.55%	48.80%	AVFPSIVGRPR	3.17	1,198.71
ATP	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	16	26	52	0.55%	48.80%	DLTDYLMK	2.38	1,014.48
ATP	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	16	26	52	0.55%	48.80%	DLYANTVLSGGTTMYPGIADR	4.71	2,231.07
ATP	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	16	26	52	0.55%	48.80%	EITALAPSTMK	2.81	1,161.62
ATP	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	16	26	52	0.55%	48.80%	GYSFTTTAER	3.24	1,132.53
ATP	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	16	26	52	0.55%	48.80%	GYSFTTTAEREIVR	1.81	1,629.82
ATP	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	16	26	52	0.55%	48.80%	HQGVMVGMGQKDSYVGDEAQSKR	3.13	2,507.18
ATP	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	16	26	52	0.55%	48.80%	IKIIAPPER	2.89	1,036.65
ATP	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	16	26	52	0.55%	48.80%	IKIIAPPERK	2.84	1,164.75
ATP	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	16	26	52	0.55%	48.80%	KDLYANTVLSGGTTMYPGIADR	5.18	2,359.16
ATP	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	16	26	52	0.55%	48.80%	LDLAGRDLTDYLMK	3.45	1,639.84
ATP	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	16	26	52	0.55%	48.80%	QEYDESGPSIVHR	2.88	1,516.70
ATP	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	16	26	52	0.55%	48.80%	QEYDESGPSIVHRK	2.52	1,644.80
ATP	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	16	26	52	0.55%	48.80%	SYELPDGQVITIGNER	4	1,790.89
ATP	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	16	26	52	0.55%	48.80%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	5.71	3,199.61
ATP	6006	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	16	26	52	0.55%	48.80%	VAPEEHPVLLTEAPLNPK	4.32	1,954.06
ATP	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	14	16	18	0.19%	30.90%	EATNPPVIQEEKPK	3.26	1,579.83

ATP	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	14	16	18	0.19%	30.90%	ELSDFISYLK	2.1	1,214.63
ATP	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	14	16	18	0.19%	30.90%	ELSDFISYLKR	1.49	1,370.73
ATP	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	14	16	18	0.19%	30.90%	FLEDYFDGNLKR	3.45	1,516.74
ATP	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	14	16	18	0.19%	30.90%	FVMQEEFSR	2.71	1,188.54
ATP	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	14	16	18	0.19%	30.90%	GFPTIYFSPANKK	3.06	1,469.78
ATP	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	14	16	18	0.19%	30.90%	IFRDGEESGAYDGPR	5.02	1,668.76
ATP	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	14	16	18	0.19%	30.90%	KLHFAVASR	2.23	1,028.60
ATP	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	14	16	18	0.19%	30.90%	KTFSHELSDFGLESTTGEIPVVAVR	3.66	2,719.39
ATP	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	14	16	18	0.19%	30.90%	LRKDPNIVIAK	3.31	1,266.79
ATP	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	14	16	18	0.19%	30.90%	MDATANDVPSPYEVR	4.38	1,680.75
ATP	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	14	16	18	0.19%	30.90%	TFSHELSDFGLESTGEIPVVAVR	3.21	2,591.30
ATP	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	14	16	18	0.19%	30.90%	VDCTANTNTCNKYGVSGYPTLK	2.76	2,349.09
ATP	6006	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	14	16	18	0.19%	30.90%	YGVSGYPTLK	2.34	1,084.57
ATP	6006	PECAM1 protein	gi|111308531	82,597.50	100.00%	8	11	20	0.21%	10.60%	APVHFTIEK	2.52	1,041.57
ATP	6006	PECAM1 protein	gi|111308531	82,597.50	100.00%	8	11	20	0.21%	10.60%	APVHFTIEKFELNIR	2.48	1,814.00
ATP	6006	PECAM1 protein	gi|111308531	82,597.50	100.00%	8	11	20	0.21%	10.60%	FHIIPEGK	2.56	940.5252
ATP	6006	PECAM1 protein	gi|111308531	82,597.50	100.00%	8	11	20	0.21%	10.60%	GTETVYSEIR	2.85	1,154.57
ATP	6006	PECAM1 protein	gi|111308531	82,597.50	100.00%	8	11	20	0.21%	10.60%	KADPDFVENRYSR	2.22	1,596.78
ATP	6006	PECAM1 protein	gi|111308531	82,597.50	100.00%	8	11	20	0.21%	10.60%	PAVPLLNSNNEK	2.6	1,295.70
ATP	6006	PECAM1 protein	gi|111308531	82,597.50	100.00%	8	11	20	0.21%	10.60%	QMPVEMSRPAVPLLNSNNEK	3.32	2,270.13
ATP	6006	PECAM1 protein	gi|111308531	82,597.50	100.00%	8	11	20	0.21%	10.60%	RNTESYLIPHVR	3.69	1,484.80
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	DGQVINETSQHHDDLE	2.55	1,836.80
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	EEAESTLQSFR	2.92	1,296.61

ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	EEAESTLQSFRQDVDNASLAR	3.44	2,366.12
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	ETNLDSLPLVDTHSK	3.24	1,668.84
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	ETNLDSLPLVDTHSKR	3.32	1,824.95
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	EYQDLLNVK	2.15	1,121.58
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	FADLSEAANR	3.99	1,093.53
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	FADLSEAANRNNDALR	3.45	1,776.86
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	FANYIDKVR	2.63	1,125.61
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	HLREYQDLLNVK	4.95	1,527.83
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	ILLAELEQLK	3.48	1,169.71
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	ILLAELEQLKGQGK	4.36	1,539.91
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	ISLPLPNFSSLNLR	4.99	1,570.90
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	ISLPLPNFSSLNLRETNLDSLPLVDTHSKR	4.09	3,376.82
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	KLHDEEIQELQAQIQEQHVQIDMDVSKPDLTAALR	4.59	4,085.06
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	KVESLQEEIAFLK	4.56	1,533.85
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	KVESLQEEIAFLKK	4.81	1,661.95
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	LHDEEIQELQAQIQEQHVQIDMDVSKPDLTAALR	3.33	3,956.97
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	LQEEMLQREEAESTLQSFR	3.05	2,340.11
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	LQEEMLQREEAESTLQSFRQDVDNASLAR	4.14	3,409.63
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	MALDIEIATYR	2.54	1,311.66
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	TLYTSSPGGVYATR	4.06	1,472.74
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	TNEKVELQELNDR	4.31	1,587.80

ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	TNEKVELQELNDRFANYIDK	3.72	2,439.22
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	VELQELNDR	3.27	1,115.57
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	VESLQEEIAFLK	3.1	1,405.76
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	VEVERDNLAEDIMR	3.31	1,704.82
ATP	6006	vimentin	gi|110347570	53,710.80	100.00%	28	37	49	0.52%	48.90%	VEVERDNLAEDIMRLR	2.33	1,974.01
ATP	6006	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	5	8	13	0.14%	20.60%	DKLDGNELDLSLSDLNEVPVK	3.03	2,313.18
ATP	6006	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	5	8	13	0.14%	20.60%	DKLDGNELDLSLSDLNEVPVKELAALPK	6.32	3,035.62
ATP	6006	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	5	8	13	0.14%	20.60%	LRQLPADFGR	2.52	1,172.65
ATP	6006	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	5	8	13	0.14%	20.60%	LVNLQHLDLLNNR	3.67	1,561.88
ATP	6006	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	5	8	13	0.14%	20.60%	LVTLPVSFAQLK	4.69	1,315.80
ATP	6006	17,000 dalton myosin light chain	gi|578,gi|74268209	16,942.80	99.80%	2	2	2	0.02%	19.20%	ALGQNPTNAEVLK	3.09	1,354.73
ATP	6006	17,000 dalton myosin light chain	gi|578,gi|74268209	16,942.80	99.80%	2	2	2	0.02%	19.20%	VLDFEHFLPMLQTVAK	2.91	1,904.00

ATP	6006	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	4	4	4	0.04%	7.66%	DAGQISGLNVLR	3.47	1,242.68
ATP	6006	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	4	4	4	0.04%	7.66%	ETGVDLTKDNMALQR	2.59	1,706.84

ATP	6006	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	4	4	4	0.04%	7.66%	TTPSVVAFTADGER	3.45	1,450.72
ATP	6006	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	4	4	4	0.04%	7.66%	VQQTVQDLFGR	2.86	1,290.68
ATP	6006	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	8	10	11	0.12%	53.50%	ADLEAQRDVTYEEAK	2.84	1,737.83
ATP	6006	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	8	10	11	0.12%	53.50%	ADLEAQRDVTYEEAKQFAEENGLLFLEASAK	4.12	3,485.71
ATP	6006	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	8	10	11	0.12%	53.50%	GAAGALMVYDITR	2.98	1,353.68
ATP	6006	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	8	10	11	0.12%	53.50%	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	4.46	3,150.56

ATP	6006	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	8	10	11	0.12%	53.50%	KIYQNIQDGSLDLNAAESGVQHKPSAPQGGR	6.03	3,278.65
ATP	6006	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	8	10	11	0.12%	53.50%	NLTNPNTVIILIGNK	4.59	1,623.94
ATP	6006	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	8	10	11	0.12%	53.50%	TGENVEDAFLEAAK	2.17	1,493.71
ATP	6006	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	8	10	11	0.12%	53.50%	YIIIGDMGVGK	3.01	1,181.62
ATP	6006	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	4	5	6	0.06%	27.50%	EHGLIFMETSAK	2.83	1,378.67
ATP	6006	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	4	5	6	0.06%	27.50%	FQPVHDLTIGVEFGAR	4.07	1,785.93
ATP	6006	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	4	5	6	0.06%	27.50%	GAAGALLVYDITR	2.76	1,319.73
ATP	6006	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	4	5	6	0.06%	27.50%	YIIIGDTGVGK	2.24	1,135.64
ATP	6006	RAB5A, member RAS oncogene family	gi|113911876,gi|115495947,gi|122144200	23,670.90	100.00%	2	3	3	0.03%	21.90%	GVDLTEPTQPTR	2.52	1,313.67
ATP	6006	RAB5A, member RAS oncogene family	gi|113911876,gi|115495947,gi|122144200	23,670.90	100.00%	2	3	3	0.03%	21.90%	LVLLGESAVGK	2.87	1,085.66
ATP	6006	RAB5A, member RAS oncogene family	gi|113911876,gi|115495947,gi|122144200	23,670.90	100.00%	2	3	3	0.03%	21.90%	TSMNVNEIFMAIAK	4.25	1,584.78
ATP	6006	RAB5A, member RAS oncogene family	gi|113911876,gi|115495947,gi|122144200	23,670.90	100.00%	2	3	3	0.03%	21.90%	YHSLAPMYYR	2.55	1,316.61
ATP	6006	Chain R, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Reduced State	gi|149241523,gi|149241540,gi|149241553,gi|149241570,gi|149241583,gi|149241600,gi|149241613,gi|42564216,gi|50872151,gi|60391934,gi|81674705	16,717.40	99.80%	2	3	4	0.04%	29.60%	EIYPYVIQELRPTLNELGISTPEELGLDKV	2.5	3,428.82

ATP	6006	Chain R, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Reduced State	gi|149241523,gi|149241540,gi|149241553,gi|149241570,gi|149241583,gi|149241600,gi|149241613,gi|42564216,gi|50872151,gi|60391934,gi|81674705	16,717.40	99.80%	2	3	4	0.04%	29.60%	GMNTLVGYDLVPEPK	4.11	1,648.83
ATP	6006	apolipoprotein E	gi|110225417,gi|157279088,gi|27806739,gi|312893,gi|416629,gi|59858471,gi|74355004,gi|81	35,961.60	99.80%	2	2	2	0.02%	10.80%	AYKEELEGQLGPMAQETQAR	4.72	2,265.08
ATP	6006	apolipoprotein E	gi|110225417,gi|157279088,gi|27806739,gi|312893,gi|416629,gi|59858471,gi|74355004,gi|81	35,961.60	99.80%	2	2	2	0.02%	10.80%	LAVYQAGASEGAER	3.11	1,421.70
ATP	6006	RecName: Full=Vesicle-associated membrane protein 8; Short=VAMP-8	gi|122140420,gi|74353894,gi|77735533	11,339.40	99.80%	2	2	2	0.02%	33.00%	NKTEDLEATSEHFK	4.92	1,648.78
ATP	6006	RecName: Full=Vesicle-associated membrane protein 8; Short=VAMP-8	gi|122140420,gi|74353894,gi|77735533	11,339.40	99.80%	2	2	2	0.02%	33.00%	NLRDEVEGVKNIMTQNVER	3.21	2,260.14
ATP	6006	ANXA11 protein	gi|111306940,gi|113969,gi|162674,gi|27806221,gi|78	54,002.00	99.80%	2	2	2	0.02%	8.75%	GTITDASGFDPLRDAEVLR	2.78	2,033.03
ATP	6006	ANXA11 protein	gi|111306940,gi|113969,gi|162674,gi|27806221,gi|78	54,002.00	99.80%	2	2	2	0.02%	8.75%	SEIDLLDIR	2.95	1,073.58
ATP	6006	ANXA11 protein	gi|111306940,gi|113969,gi|162674,gi|27806221,gi|78	54,002.00	99.80%	2	2	2	0.02%	8.75%	SLYHDITGDTSGDYRK	3.98	1,827.85

ATP	6006	RecName: Full=Annexin A1; AltName: Full=Annexin-1; AltName: Full=Annexin I; AltName: Full=Lipocortin I; AltName: Full=Calpactin II; AltName: Full=Chromobindin-9; AltName: Full=p35; AltName: Full=Phospholipase A2	gi|118597373,gi|264182,gi|61553085,gi|73587269,gi|73853762,gi|74	38,935.40	100.00%	3	3	3	0.03%	17.10%	GDRSEELAVNDDLADSDAR	5.37	2,047.92
ATP	6006	RecName: Full=Annexin A1; AltName: Full=Annexin-1; AltName: Full=Annexin I; AltName: Full=Lipocortin I; AltName: Full=Calpactin II; AltName: Full=Chromobindin-9; AltName: Full=p35; AltName: Full=Phospholipase A2	gi|118597373,gi|264182,gi|61553085,gi|73587269,gi|73853762,gi|74	38,935.40	100.00%	3	3	3	0.03%	17.10%	GGPGSAVSPYPTFNPSSDVEALHK	2.85	2,414.16

ATP	6006	RecName: Full=Annexin A1; AltName: Full=Annexin-1; AltName: Full=Annexin I; AltName: Full=Lipocortin I; AltName: Full=Calpactin II; AltName: Full=Chromobindin-9; AltName: Full=p35; AltName: Full=Phospholipase A2	gi|118597373,gi|264182,gi|61553085,gi|73587269,gi|73853762,gi|74	38,935.40	100.00%	3	3	3	0.03%	17.10%	GLGTDEDTLNEILASR	3.5	1,703.84
ATP	6006	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	7	8	0.08%	10.10%	IHSAALSFLKENLK	2.48	1,570.90
ATP	6006	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	7	8	0.08%	10.10%	IPQAVVDVSSHLQK	3.25	1,520.84
ATP	6006	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	7	8	0.08%	10.10%	QETGIDDIPDVK	2.31	1,329.65
ATP	6006	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	7	8	0.08%	10.10%	SIEEIVSFQHLR	3.53	1,457.77
ATP	6006	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	7	8	0.08%	10.10%	SNTTQSGPEGSLVNSQSLK	3.49	1,933.95
ATP	6006	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	6	7	8	0.08%	10.10%	YLDLSYNDIR	2.45	1,271.63
ATP	6006	PREDICTED: similar to MYB binding protein 1a	gi|119911777	151,796.60	100.00%	2	2	2	0.02%	1.85%	DLAALELLNTLFR	2.39	1,488.84
ATP	6006	PREDICTED: similar to MYB binding protein 1a	gi|119911777	151,796.60	100.00%	2	2	2	0.02%	1.85%	TAGDRVETLYAR	2.88	1,351.70
ATP	6006	Chain A, Structure Of Mammalian C3 With An Intact Thioester At 3a Resolution	gi|110590846,gi|110590847,gi|124056491,gi|83764016,gi|86438252,gi|99028969	187,214.10	99.80%	2	2	2	0.02%	2.05%	LYNVEATSYALLALAR	2.91	1,881.05

ATP	6006	Chain A, Structure Of Mammalian C3 With An Intact Thioester At 3a Resolution	gi|110590846,gi|110590847,gi|124056491,gi|83764016,gi|86438252,gi|99028969	187,214.10	99.80%	2	2	2	0.02%	2.05%	RPYTVAIAAYALALLGK	5.47	1,791.05
ATP	6006	MGAT1 protein	gi|154426138,gi|59858237,gi|62751783	51,684.70	100.00%	3	3	3	0.03%	8.05%	GIVSFLYR	2.68	954.5407
ATP	6006	MGAT1 protein	gi|154426138,gi|59858237,gi|62751783	51,684.70	100.00%	3	3	3	0.03%	8.05%	LNQHFVPFTQLDLSYLR	4.31	2,091.10
ATP	6006	MGAT1 protein	gi|154426138,gi|59858237,gi|62751783	51,684.70	100.00%	3	3	3	0.03%	8.05%	VYGAPLLQVEK	2.35	1,216.69
ATP	6006	PREDICTED: similar to Thioredoxin domain-containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein ERp46) isoform 1	gi|119915902	45,792.10	99.80%	2	2	2	0.02%	4.55%	FFKPGQEAVK	2.86	1,150.63
ATP	6006	PREDICTED: similar to Thioredoxin domain-containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein ERp46) isoform 1	gi|119915902	45,792.10	99.80%	2	2	2	0.02%	4.55%	GYPTLLLFR	2.03	1,079.62

ATP	6006	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	6	9	13	0.14%	29.70%	FFDEESYSLLR	3.42	1,405.66
ATP	6006	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	6	9	13	0.14%	29.70%	NNEDVSVIPPLFTVSVDHR	3.64	2,138.09

ATP	6006	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	6	9	13	0.14%	29.70%	NRVQNMALYADVSGK	3.73	1,681.83
ATP	6006	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	6	9	13	0.14%	29.70%	NRVQNMALYADVSGKQFPVTR	2.74	2,410.23

ATP	6006	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	6	9	13	0.14%	29.70%	VQNMALYADVSGK	4.34	1,411.69
ATP	6006	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	6	9	13	0.14%	29.70%	VQNMALYADVSGKQFPVTR	3.5	2,140.09
ATP	6006	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	3	4	4	0.04%	7.72%	ASPAPGSGHPDGPGTHLEMNSLDR	3.26	2,416.10

ATP	6006	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	3	4	4	0.04%	7.72%	LRPESALAQAQK	3.56	1,311.74
ATP	6006	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	3	4	4	0.04%	7.72%	NVDLSTFYQNR	3.15	1,356.65
ATP	6006	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	3	4	7	0.07%	5.16%	IPLNDIFR	3.07	987.5623
ATP	6006	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	3	4	7	0.07%	5.16%	VALKIPLNDIFR	3.91	1,398.85
ATP	6006	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	3	4	7	0.07%	5.16%	YLDFVFAVK	2.38	1,101.60
ATP	6006	Nicastrin	gi|74267600,gi|77735901	79,055.00	99.80%	2	2	3	0.03%	3.63%	ALAGVATVLAR	3.21	1,041.64
ATP	6006	Nicastrin	gi|74267600,gi|77735901	79,055.00	99.80%	2	2	3	0.03%	3.63%	MATAGGGCVADPGSR	3.32	1,349.59
ATP	6006	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	4	9	0.09%	18.80%	DFSLEQLR	2.4	1,007.52
ATP	6006	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	4	9	0.09%	18.80%	FYGPAGPYGIFAGR	3.04	1,472.73
ATP	6006	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	4	9	0.09%	18.80%	GLGAGAGAGEESPAASLPR	4.48	1,667.83
ATP	6006	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	4	9	0.09%	18.80%	RGLGAGAGAGEESPAASLPR	4.18	1,823.94

ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	DQLKPTQLLQNVAR	3.59	1,623.92
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	EYTGFPDPYDELNSGKGEGVAYR	2.18	2,564.16
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	FKGFPPPVLSEDGSSIR	4.81	1,832.95
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	GNNPFFDELFFYNVHLTPSELMDEIISIR	4.3	3,473.67
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	HKDGSNLPILPSQR	2.91	1,561.84
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	ILHQHLGPPEER	3.71	1,425.76
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	ILVELSTLLEK	3.56	1,257.77
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	IPAHQVLYSTSGGDASGK	3.94	1,787.89
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	ISVYDYDTFTR	3.13	1,379.65
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	ISVYDYDTFTRDEK	2.46	1,751.81
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	ISVYDYDTFTRDEKVGETIIDLENR	2.6	2,991.46

ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	IYRAEDIPQMDDAFSQTVK	3.04	2,243.07
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	LQSNIEALK	2.7	1,015.58
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	NDVVGTTYLHLSK	3.26	1,446.76
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	NLGPPGPPFNITPR	3.02	1,476.80
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	NLMALDKDSFSDPYAHVSFLHR	3.31	2,579.23
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	NLVDPFVEVSFAGK	3.53	1,521.79
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	SDENEDPSVVGEFK	3.4	1,551.68
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	SLLTEADAGHTEFTDEVYQNESR	4.32	2,612.17
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	SRALSQIHEAAVR	2.4	1,437.79
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	TLHSSFQPNISQGR	3.55	1,571.79
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	TQGLVPEHVETR	2.51	1,365.71

ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	VEMTLEVLNEK	2.14	1,320.67
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	VEMTLEVLNEKEADERPAGK	2.87	2,274.13
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	VFLPKEELYMPPLVIK	3.71	1,932.09
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	VGETIIDLENRFLSR	2.32	1,761.95
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	VIEDRDNYIPNTLNPVFGR	4.35	2,232.14
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	VIIELFDNDQVGKDEFLGR	2.96	2,207.13
ATP	6006	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	29	35	39	0.41%	20.30%	VIVESASNIPK	2.93	1,156.66
ATP	6006	TXNDC13 protein	gi|148878448,gi|149642897	38,865.40	100.00%	3	3	3	0.03%	12.10%	FFVTTLPAFFHAK	2.62	1,525.82
ATP	6006	TXNDC13 protein	gi|148878448,gi|149642897	38,865.40	100.00%	3	3	3	0.03%	12.10%	VDVIQEPGLSGR	3.2	1,269.68
ATP	6006	TXNDC13 protein	gi|148878448,gi|149642897	38,865.40	100.00%	3	3	3	0.03%	12.10%	YRGPGVYEDLQNYILEK	2.81	2,057.03
ATP	6006	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	3	3	3	0.03%	17.80%	FKNLENSPLGEALR	3.23	1,587.85
ATP	6006	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	3	3	3	0.03%	17.80%	NRESYEVTLTHK	3.15	1,476.74
ATP	6006	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	3	3	3	0.03%	17.80%	SVPLAATSMLITQGLISK	2.81	1,846.04

ATP	6006	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	3	3	3	0.03%	10.80%	GSYGDLGGPIITTQVTIPK	4.06	1,917.03
ATP	6006	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	3	3	3	0.03%	10.80%	IILDLISESPIKGR	2.84	1,553.93
ATP	6006	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	3	3	3	0.03%	10.80%	TDYNASVSVPDSSGPER	3.54	1,780.80
ATP	6006	myristoylated alanine-rich protein kinase C substrate	gi|115495497,gi|148872484,gi|163340,gi|94534743	31,960.80	99.80%	2	2	2	0.02%	6.87%	GEATAERPGEAAVASSPSK	4.04	1,814.89
ATP	6006	myristoylated alanine-rich protein kinase C substrate	gi|115495497,gi|148872484,gi|163340,gi|94534743	31,960.80	99.80%	2	2	2	0.02%	6.87%	TAAKGEATAERPGEAAVASSPSK	4.12	2,186.10
ATP	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	10	13	16	0.17%	11.40%	KPLIGSVLAK	2.27	1,025.67
ATP	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	10	13	16	0.17%	11.40%	NLESPSSFTIK	2.37	1,222.63
ATP	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	10	13	16	0.17%	11.40%	RTSDKGQFFGITK	2.57	1,484.79

ATP	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	10	13	16	0.17%	11.40%	TSDKGQFFGITK	2.83	1,328.68
ATP	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	10	13	16	0.17%	11.40%	VDKNTGDVYALER	3.97	1,479.74
ATP	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	10	13	16	0.17%	11.40%	VFRVDKNTGDVYALER	2.45	1,881.98
ATP	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	10	13	16	0.17%	11.40%	VGSPLGSLFVEDPDEPQNR	3.35	2,056.00
ATP	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	10	13	16	0.17%	11.40%	VGSPLGSLFVEDPDEPQNRK	2.63	2,184.09
ATP	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	10	13	16	0.17%	11.40%	YSFVQGEYR	2.78	1,148.54
ATP	6006	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	10	13	16	0.17%	11.40%	YTFSVPEDIR	2.69	1,226.61
ATP	6006	EH-domain containing 1	gi|110331767,gi|158455084,gi|59858079,gi|62751751,gi|75070053	60,666.10	99.80%	2	2	2	0.02%	9.36%	IGPEPTTDSFIAVMHGPTEGVVPGNALVVDPR	3.56	3,288.66
ATP	6006	EH-domain containing 1	gi|110331767,gi|158455084,gi|59858079,gi|62751751,gi|75070053	60,666.10	99.80%	2	2	2	0.02%	9.36%	LFEAEEQDLFKDIQSLPR	3.07	2,178.11
ATP	6006	LOC515309 protein	gi|148878460,gi|149773584	31,548.40	100.00%	3	4	4	0.04%	15.20%	ASDYGMKLPILR	2.54	1,379.74
ATP	6006	LOC515309 protein	gi|148878460,gi|149773584	31,548.40	100.00%	3	4	4	0.04%	15.20%	KEEEEEEEEYDEGSNLKR	4.27	2,241.96
ATP	6006	LOC515309 protein	gi|148878460,gi|149773584	31,548.40	100.00%	3	4	4	0.04%	15.20%	SNPEDQILYQTER	2.84	1,592.76
ATP	6006	PREDICTED: lamin B2	gi|194668843	70,532.10	100.00%	3	3	3	0.03%	12.10%	ALELENDRLQLK	3.15	1,441.80

ATP	6006	PREDICTED: lamin B2	gi|194668843	70,532.10	100.00%	3	3	3	0.03%	12.10%	ETENGEEGEDEAAEFGEEDLFHQQGDPR	3.32	3,164.28
ATP	6006	PREDICTED: lamin B2	gi|194668843	70,532.10	100.00%	3	3	3	0.03%	12.10%	LALDMEISAYRK	2.46	1,425.74
ATP	6006	PREDICTED: lamin B2	gi|194668843	70,532.10	100.00%	3	3	3	0.03%	12.10%	LLEGEEERLK	3.1	1,215.66
ATP	6006	PREDICTED: lamin B2	gi|194668843	70,532.10	100.00%	3	3	3	0.03%	12.10%	TTLVNADGEEVAMR	3.41	1,521.72
ATP	6006	acyl-CoA synthetase long-chain family member 5	gi|115497154,gi|152941112,gi|94534758	76,013.10	100.00%	3	3	3	0.03%	5.86%	ALVLISNVEK	2.63	1,085.66
ATP	6006	acyl-CoA synthetase long-chain family member 5	gi|115497154,gi|152941112,gi|94534758	76,013.10	100.00%	3	3	3	0.03%	5.86%	GAMLTHANIVSNASGFLK	3.17	1,846.95
ATP	6006	acyl-CoA synthetase long-chain family member 5	gi|115497154,gi|152941112,gi|94534758	76,013.10	100.00%	3	3	3	0.03%	5.86%	TLKPTLFPTVPR	2.44	1,369.82
ATP	6006	PREDICTED: thrombomodulin	gi|119905421	60,710.90	99.80%	2	2	2	0.02%	4.84%	GPATFLAASR	2.66	990.5367
ATP	6006	PREDICTED: thrombomodulin	gi|119905421	60,710.90	99.80%	2	2	2	0.02%	4.84%	SSVAEDVISLLLSGDGPR	2.71	1,814.95
ATP	6006	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	100.00%	2	2	2	0.02%	4.31%	LQTVQSADQVLVLR	3.6	1,569.90
ATP	6006	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	100.00%	2	2	2	0.02%	4.31%	QVVLVGQEPVLFSGSVR	4.34	1,814.02
ATP	6006	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	gi|165973956,gi|2493087,gi|81294315	10,254.50	99.80%	2	3	3	0.03%	25.00%	DFTPSGIAGAFQR	2.35	1,366.68

ATP	6006	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	gi|165973956,gi|2493087,gi|81294315	10,254.50	99.80%	2	3	3	0.03%	25.00%	YYNKYVNVK	2.42	1,190.62
ATP	6006	glutaminyl-peptide cyclotransferase-like	gi|110331975,gi|110331977,gi|112362220,gi|115495265,gi|122146335,gi|95768579,gi|95769160	41,828.70	99.80%	2	2	2	0.02%	10.70%	ELRGPLIGSLPEAR	4.01	1,507.86
ATP	6006	glutaminyl-peptide cyclotransferase-like	gi|110331975,gi|110331977,gi|112362220,gi|115495265,gi|122146335,gi|95768579,gi|95769160	41,828.70	99.80%	2	2	2	0.02%	10.70%	IQAIELFMLLDLLGAPNPTFYSHFPR	3.15	3,019.58
ATP	6006	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	6	6	6	0.06%	29.90%	AGAGSATLSMAYAGAR	3.36	1,470.70
ATP	6006	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	6	6	6	0.06%	29.90%	ANAFVAELKDLDPAR	4.19	1,629.86
ATP	6006	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	6	6	6	0.06%	29.90%	LTLYDIAHTPGVAADLSHIETR	2.8	2,393.25

ATP	6006	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	6	6	6	0.06%	29.90%	VAVLGASGGIGQPLSLLLK	2.31	1,793.09
ATP	6006	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	6	6	6	0.06%	29.90%	VNVPVIGGHAGK	3.33	1,147.66
ATP	6006	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	6	6	6	0.06%	29.90%	VSPFEEKMIAEAIPELK	2.85	1,947.01
ATP	6006	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	6	8	15	0.16%	31.30%	FGLIPEEFFQFLYPK	2.15	1,874.97
ATP	6006	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	6	8	15	0.16%	31.30%	HYLFDVQR	2.75	1,077.55
ATP	6006	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	6	8	15	0.16%	31.30%	IAQLEEVKQASIK	4.52	1,456.84

ATP	6006	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	6	8	15	0.16%	31.30%	NNIAMALEVTYR	3.63	1,410.70
ATP	6006	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	6	8	15	0.16%	31.30%	QIQDAIDMEKSQQALVQK	3.67	2,089.06
ATP	6006	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	6	8	15	0.16%	31.30%	QIQDAIDMEKSQQALVQKR	2.71	2,245.16
ATP	6006	PREDICTED: similar to oxysterol 7alpha-hydroxylase	gi|194672764	90,479.20	99.90%	2	2	3	0.03%	4.47%	FLFGIPYPDSDVLFR	2.27	1,785.92
ATP	6006	PREDICTED: similar to oxysterol 7alpha-hydroxylase	gi|194672764	90,479.20	99.90%	2	2	3	0.03%	4.47%	MLTDSDLIDEIHSTYQFLQGK	3.95	2,470.18
ATP	6006	p33/41 (annexin IV)	gi|1063258,gi|113956,gi|14278334,gi|157829985,gi|157830000,gi|163030,gi|216,gi|48374083,gi|74353976	35,872.70	100.00%	3	3	3	0.03%	11.90%	GLGTDDDTLIR	2.76	1,175.59
ATP	6006	p33/41 (annexin IV)	gi|1063258,gi|113956,gi|14278334,gi|157829985,gi|157830000,gi|163030,gi|216,gi|48374083,gi|74353976	35,872.70	100.00%	3	3	3	0.03%	11.90%	GLGTDEDAIINVLAYR	2.92	1,719.89

ATP	6006	p33/41 (annexin IV)	gi|1063258,gi|113956,gi|14278334,gi|157829985,gi|157830000,gi|163030,gi|216,gi|48374083,gi|74353976	35,872.70	100.00%	3	3	3	0.03%	11.90%	INQTYQLQYGR	2.71	1,383.70
ATP	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	8	11	13	0.14%	26.40%	AVFVDLEPTVIDEVR	3.75	1,701.91
ATP	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	8	11	13	0.14%	26.40%	DVNAAIATIK	3.07	1,015.58
ATP	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	8	11	13	0.14%	26.40%	EIIDLVLDR	2.43	1,085.62
ATP	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	8	11	13	0.14%	26.40%	IHFPLATYAPVISAEK	3.24	1,756.96
ATP	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	8	11	13	0.14%	26.40%	LISQIVSSITASLR	4.07	1,487.88
ATP	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	8	11	13	0.14%	26.40%	NLDIERPTYTNLNR	2.5	1,718.88
ATP	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	8	11	13	0.14%	26.40%	QLFHPEQLITGKEDAANNYAR	3.41	2,415.21
ATP	6006	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	8	11	13	0.14%	26.40%	TIGGGDDSFNTFFSETGAGK	2.6	2,007.89
ATP	6006	PREDICTED: similar to transmembrane protein 165	gi|76619924	34,667.10	99.80%	2	2	3	0.03%	13.30%	MSPDEGQEELEEVQAELK	3.25	2,076.93
ATP	6006	PREDICTED: similar to transmembrane protein 165	gi|76619924	34,667.10	99.80%	2	2	3	0.03%	13.30%	NKEPPAPAQQLQPQPAAVQGPEPAR	5.13	2,619.36

ATP	6006	RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8; AltName: Full=NADH-ubiquinone oxidoreductase 19 kDa subunit; AltName: Full=Complex I-19kD;	gi|1171870, gi|28461275,gi|5996815,gi|86827664	20,073.10	99.80%	2	2	2	0.02%	18.60%	ARPEPNPEVEGDLKPAR	6.5	1,874.97
ATP	6006	RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8; AltName: Full=NADH-ubiquinone oxidoreductase 19 kDa subunit; AltName: Full=Complex I-19kD;	gi|1171870, gi|28461275,gi|5996815,gi|86827664	20,073.10	99.80%	2	2	2	0.02%	18.60%	VKTDRPLPENPYHSR	4.31	1,808.94

ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	AAAQDIFSPK	2.4	1,047.55
ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	ATILYASETGR	3.7	1,181.62

ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	AVDTRLEELGGER	3.03	1,444.74
ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	DFINQYYSSIK	3.17	1,377.67

ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	DFINQYYSSIKR	3.08	1,533.77
ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	ESSNTDSAGALGTLR	3.9	1,478.71

ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	KESSNTDSAGALGTLR	3.16	1,606.80
ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	KLQTRPSPGPPPAEQLLSQAR	4.83	2,271.26

ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	KMFQATVLSVENLQSSK	3.29	1,926.00
ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	LLSTLAEEPSEQQELETLSQDPR	4.32	2,613.29

ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	LLSTLAEEPSEQQELETLSQDPRR	3.56	2,769.39
ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	LSTQAEGLQLLPGLIHVHR	4.97	2,082.18

ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	MFQATVLSVENLQSSK	3.35	1,797.91
ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	QALTFFLDITSPPSPR	2.39	1,789.95

ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	RKESSNTDSAGALGTLR	3.4	1,762.90
ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	SAITVFPQR	2.62	1,018.57

ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	SAITVFPQRAPGR	3.44	1,399.78
ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	TYVQDILR	2.41	1,007.55

ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	VEDPPPPTESVAVEQLEK	4.12	1,963.99
ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	VLTAFSREPDSPK	3.77	1,446.76

ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	VLTAFSREPDSPKTYVQDILR	3.48	2,435.29
ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	YHEDIFGLTLR	2.98	1,363.70

ATP	6006	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	23	30	38	0.40%	18.70%	YRLSTQAEGLQLLPGLIHVHR	2.56	2,401.35
ATP	6006	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	gi|209447036,gi|88954020	67,875.80	99.80%	2	2	2	0.02%	4.29%	VIYAMAEDGLLFK	2.85	1,485.77
ATP	6006	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	gi|209447036,gi|88954020	67,875.80	99.80%	2	2	2	0.02%	4.29%	YQPEQPNTVYQMAR	2.13	1,740.80
ATP	6006	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	7	8	9	0.09%	19.30%	DMRQTVAVGVIK	3.1	1,332.73
ATP	6006	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	7	8	9	0.09%	19.30%	EHALLAYTLGVK	3.57	1,314.74

ATP	6006	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	7	8	9	0.09%	19.30%	IGGIGTVPVGR	3.58	1,025.61
ATP	6006	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	7	8	9	0.09%	19.30%	TIEKFEKEAAEMGK	2.71	1,626.80
ATP	6006	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	7	8	9	0.09%	19.30%	VETGVLKPGMVVTFAPVNVTTEVK	5.06	2,531.38
ATP	6006	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	7	8	9	0.09%	19.30%	YYVTIIDAPGHR	2.56	1,404.73
ATP	6006	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	7	8	9	0.09%	19.30%	YYVTIIDAPGHRDFIK	2.35	1,908.00
ATP	6006	cell division cycle 42 (GTP binding protein, 25kDa)	gi|114052486,gi|122063301,gi|86821687	21,240.70	100.00%	3	3	5	0.05%	21.50%	GLKNVFDEAILAALEPPEPK	3.44	2,151.17
ATP	6006	cell division cycle 42 (GTP binding protein, 25kDa)	gi|114052486,gi|122063301,gi|86821687	21,240.70	100.00%	3	3	5	0.05%	21.50%	NVFDEAILAALEPPEPK	4.19	1,852.97

ATP	6006	cell division cycle 42 (GTP binding protein, 25kDa)	gi|114052486,gi|122063301,gi|86821687	21,240.70	100.00%	3	3	5	0.05%	21.50%	TPFLLVGTQIDLRDDPSTIEK	3.59	2,358.26
ATP	6006	RecName: Full=Golgi SNAP receptor complex member 1	gi|108935998,gi|83638559,gi|84370083	28,524.90	99.80%	2	2	3	0.03%	11.60%	ENMTSQRGMLKSIQSK	3.91	1,837.93
ATP	6006	RecName: Full=Golgi SNAP receptor complex member 1	gi|108935998,gi|83638559,gi|84370083	28,524.90	99.80%	2	2	3	0.03%	11.60%	RTELFLKEHDHLR	2.8	1,693.91
ATP	6006	minor histocompatibility antigen 13	gi|164448616	41,537.10	100.00%	3	3	4	0.04%	10.90%	GEVTEMFSYEESNPKDPAAVTETR	3.27	2,703.21
ATP	6006	minor histocompatibility antigen 13	gi|164448616	41,537.10	100.00%	3	3	4	0.04%	10.90%	LVFPQDLLEK	2.22	1,201.68
ATP	6006	minor histocompatibility antigen 13	gi|164448616	41,537.10	100.00%	3	3	4	0.04%	10.90%	SFEAPIKLVFPQDLLEK	3	1,974.09
ATP	6006	PREDICTED: similar to vesicle amine transport protein 1 isoform 1	gi|76671278	42,822.00	100.00%	4	4	4	0.04%	14.70%	GVDIVMDPLGGSDTAK	4.24	1,590.77
ATP	6006	PREDICTED: similar to vesicle amine transport protein 1 isoform 1	gi|76671278	42,822.00	100.00%	4	4	4	0.04%	14.70%	LLALYNQGHIKPR	1.94	1,522.89
ATP	6006	PREDICTED: similar to vesicle amine transport protein 1 isoform 1	gi|76671278	42,822.00	100.00%	4	4	4	0.04%	14.70%	LQTRPAAPPAPGTGQLTLR	3.24	1,945.10
ATP	6006	PREDICTED: similar to vesicle amine transport protein 1 isoform 1	gi|76671278	42,822.00	100.00%	4	4	4	0.04%	14.70%	VLLVPGPEKEN	2.82	1,194.67

ATP	6006	PREDICTED: similar to Feline leukemia virus subgroup C receptor-related protein 1 (Feline leukemia virus subgroup C receptor) (hFLVCR)	gi|194674242	59,731.10	100.00%	3	3	3	0.03%	7.73%	ATASGTPDGPKTPLAPEEETQAR	4.06	2,324.14
ATP	6006	PREDICTED: similar to Feline leukemia virus subgroup C receptor-related protein 1 (Feline leukemia virus subgroup C receptor) (hFLVCR)	gi|194674242	59,731.10	100.00%	3	3	3	0.03%	7.73%	DPGEETPGGEGTLVPR	3.45	1,610.77
ATP	6006	PREDICTED: similar to Feline leukemia virus subgroup C receptor-related protein 1 (Feline leukemia virus subgroup C receptor) (hFLVCR)	gi|194674242	59,731.10	100.00%	3	3	3	0.03%	7.73%	LLPKDPGEETPGGEGTLVPR	3.37	2,062.08

ATP	6006	RecName: Full=Hemoglobin subunit beta; AltName: Full=Hemoglobin beta chain; AltName: Full=Beta-globin	gi|122572,gi|27819608,gi|395	15,936.20	99.80%	2	3	9	0.09%	28.30%	LLGNVLVVVLAR	4.93	1,265.83
ATP	6006	RecName: Full=Hemoglobin subunit beta; AltName: Full=Hemoglobin beta chain; AltName: Full=Beta-globin	gi|122572,gi|27819608,gi|395	15,936.20	99.80%	2	3	9	0.09%	28.30%	LLGNVLVVVLARNFGKEFTPVLQADFQK	2.86	3,115.77
ATP	6006	RecName: Full=Hemoglobin subunit beta; AltName: Full=Hemoglobin beta chain; AltName: Full=Beta-globin	gi|122572,gi|27819608,gi|395	15,936.20	99.80%	2	3	9	0.09%	28.30%	NFGKEFTPVLQADFQK	3.19	1,868.95
ATP	6006	RecName: Full=Hemoglobin subunit beta; AltName: Full=Hemoglobin beta chain; AltName: Full=Beta-globin	gi|122572,gi|27819608,gi|395	15,936.20	99.80%	2	3	9	0.09%	28.30%	VKVDEVGGEALGR	4.16	1,328.72
ATP	6006	H3 histone, family 3A	gi|59858289,gi|62177168,gi|95769331	15,310.70	99.90%	2	2	5	0.05%	16.90%	EIAQDFKTDLR	3.05	1,335.69

ATP	6006	H3 histone, family 3A	gi|59858289,gi|62177168,gi|95769331	15,310.70	99.90%	2	2	5	0.05%	16.90%	YRPGTVALREIR	2.4	1,430.82
ATP	6006	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	99.80%	2	2	2	0.02%	5.57%	FTSLGLLPR	2.84	1,003.59
ATP	6006	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	99.80%	2	2	2	0.02%	5.57%	VFRLPEDQAIINR	2.97	1,570.87
ATP	6006	calpactin I light chain	gi|162785,gi|27807173,gi|46397705,gi|58760382,gi|74353914	11,185.50	99.80%	2	2	2	0.02%	37.10%	FAGDKGYLTKEDLR	1.7	1,612.83
ATP	6006	calpactin I light chain	gi|162785,gi|27807173,gi|46397705,gi|58760382,gi|74353914	11,185.50	99.80%	2	2	2	0.02%	37.10%	VLMEKEFPGFLENQKDPLAVDK	3.01	2,563.31
ATP	6006	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	3	4	4	0.04%	7.01%	AENLGEVLRGDR	2.47	1,328.69
ATP	6006	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	3	4	4	0.04%	7.01%	ISEDYYVHLIADNLPVATR	4.51	2,189.12
ATP	6006	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	3	4	4	0.04%	7.01%	IVNTPFQVLMNSEK	3.66	1,635.84
ATP	6006	PREDICTED: plexin A2	gi|194674254	210,938.30	100.00%	5	5	5	0.05%	3.85%	FVDDLFETLFSTVHR	3.18	1,825.91
ATP	6006	PREDICTED: plexin A2	gi|194674254	210,938.30	100.00%	5	5	5	0.05%	3.85%	LEVHPSSISVSEHSR	2.62	1,663.84
ATP	6006	PREDICTED: plexin A2	gi|194674254	210,938.30	100.00%	5	5	5	0.05%	3.85%	LLQAAYLAKPGDALAR	2.57	1,670.96
ATP	6006	PREDICTED: plexin A2	gi|194674254	210,938.30	100.00%	5	5	5	0.05%	3.85%	LNTLMHYQVSDR	2.7	1,492.72
ATP	6006	PREDICTED: plexin A2	gi|194674254	210,938.30	100.00%	5	5	5	0.05%	3.85%	QTSSYNIPASASISR	3.28	1,581.79

ATP	6006	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	99.80%	2	2	4	0.04%	11.70%	GAAQNIIPASTGAAK	3.22	1,369.74
ATP	6006	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	99.80%	2	2	4	0.04%	11.70%	VIHDHFGIVEGLMTTVHAITATQK	5.4	2,634.37
ATP	6006	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	100.00%	3	3	3	0.03%	12.70%	FFLSAGLIDKVDNFK	2.15	1,713.92
ATP	6006	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	100.00%	3	3	3	0.03%	12.70%	LEDPHVDIIR	2.32	1,206.65
ATP	6006	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	100.00%	3	3	3	0.03%	12.70%	VSFSYAGLSSDDPDLGPAHVVTVIAR	3.22	2,673.35
ATP	6006	intergral membrane protein 1	gi|114051696,gi|122136222,gi|152941168,gi|86823970	80,641.10	100.00%	3	3	3	0.03%	3.83%	FLAEEGFYK	2.49	1,103.54
ATP	6006	intergral membrane protein 1	gi|114051696,gi|122136222,gi|152941168,gi|86823970	80,641.10	100.00%	3	3	3	0.03%	3.83%	FYSLLDPSYAK	2.3	1,303.66
ATP	6006	intergral membrane protein 1	gi|114051696,gi|122136222,gi|152941168,gi|86823970	80,641.10	100.00%	3	3	3	0.03%	3.83%	IIFDDFR	2.02	925.4779
ATP	6006	Myeloid-associated differentiation marker	gi|111308557,gi|115497460	35,291.10	100.00%	3	6	12	0.13%	14.60%	ARPGEITGYMATVPGLLK	4.38	1,890.02
ATP	6006	Myeloid-associated differentiation marker	gi|111308557,gi|115497460	35,291.10	100.00%	3	6	12	0.13%	14.60%	LVFVRV	2.05	732.4766
ATP	6006	Myeloid-associated differentiation marker	gi|111308557,gi|115497460	35,291.10	100.00%	3	6	12	0.13%	14.60%	TTVTTTMSSSGLGSPTIVGSPR	4.86	2,240.11

ATP	6006	ribosomal protein L24	gi|27806129,gi|28189314,gi|28189753,gi|28189757,gi|28189765,gi|3132823,gi|41019240,gi|74267598	17,630.30	99.80%	2	2	2	0.02%	16.00%	AITGASLADIMAK	3.31	1,277.68
ATP	6006	ribosomal protein L24	gi|27806129,gi|28189314,gi|28189753,gi|28189757,gi|28189765,gi|3132823,gi|41019240,gi|74267598	17,630.30	99.80%	2	2	2	0.02%	16.00%	TDGKVFQFLNAK	3.96	1,367.73
ATP	6006	PREDICTED: similar to Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A) (Guanylate cyclase) (NPR-A) (Atrial natriuretic peptide A-type receptor)	gi|194665089	119,021.60	99.80%	2	2	2	0.02%	2.63%	IITYKEPDNPEYLEFLQK	3.42	2,240.15
ATP	6006	PREDICTED: similar to Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A) (Guanylate cyclase) (NPR-A) (Atrial natriuretic peptide A-type receptor)	gi|194665089	119,021.60	99.80%	2	2	2	0.02%	2.63%	MALALLDAVR	3.18	1,088.61

ATP	6006	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	13	0.14%	12.00%	DAEAWFNEK	2.73	1,109.49
ATP	6006	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	13	0.14%	12.00%	IRLENEIQTYR	4.48	1,434.77
ATP	6006	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	13	0.14%	12.00%	LASYLDKVR	3.06	1,064.61
ATP	6006	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	13	0.14%	12.00%	LENEIQTYR	3.62	1,165.58
ATP	6006	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	13	0.14%	12.00%	QSLEASLAETEGR	4.34	1,390.68

ATP	6006	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	13	0.14%	12.00%	RVLDELTLTK	2.97	1,187.70
ATP	6006	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	13	0.14%	12.00%	SQYEQLAEKNR	3.71	1,365.68
ATP	6006	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	8	13	0.14%	12.00%	VLDELTLTK	3.84	1,031.60
ATP	6006	MATR3 protein	gi|134024643,gi|156523084	93,810.30	99.80%	2	2	2	0.02%	5.57%	DLDELSRYPEDKITPENLPQILLQLK	3.26	3,080.65
ATP	6006	MATR3 protein	gi|134024643,gi|156523084	93,810.30	99.80%	2	2	2	0.02%	5.57%	YQLLQLVEPFGVISNHLILNK	2.77	2,438.38
ATP	6006	Transferrin	gi|113911795,gi|114326282	77,721.80	99.80%	2	3	67	0.70%	8.10%	AISNNEADAVTLDGGLVYEAGLKPNNLKPVVAEFHGTK	2.7	3,952.05
ATP	6006	Transferrin	gi|113911795,gi|114326282	77,721.80	99.80%	2	3	67	0.70%	8.10%	MDFELYLGYEYVTALQNLR	4.85	2,338.14
ATP	6006	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	5	8	11	0.12%	19.70%	GVGDDQLGEESEER	3.84	1,519.65

ATP	6006	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	5	8	11	0.12%	19.70%	GVGDDQLGEESEERDDHLLPM	2.75	2,357.02
ATP	6006	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	5	8	11	0.12%	19.70%	HTLADNFNPVSEER	4.5	1,628.77
ATP	6006	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	5	8	11	0.12%	19.70%	HTLADNFNPVSEERGK	3.84	1,813.88
ATP	6006	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	5	8	11	0.12%	19.70%	SFESTVGQSPDMYSYVFR	3.7	2,115.93
ATP	6006	Plasminogen activator, urokinase receptor	gi|148745533,gi|157279223,gi|163803,gi|27806067,gi|465002,gi|545771	35,970.10	99.80%	2	2	3	0.03%	6.67%	GLRNPSYTIR	2.68	1,176.65
ATP	6006	Plasminogen activator, urokinase receptor	gi|148745533,gi|157279223,gi|163803,gi|27806067,gi|465002,gi|545771	35,970.10	99.80%	2	2	3	0.03%	6.67%	SRDQCVDVITHR	2.93	1,428.70
ATP	6006	ADP-ribosylation-like factor 6 interacting protein 5	gi|59858163,gi|62460474,gi|74354855,gi|75057806	21,648.60	99.80%	2	2	3	0.03%	13.80%	FARPDFR	1.68	908.4737
ATP	6006	ADP-ribosylation-like factor 6 interacting protein 5	gi|59858163,gi|62460474,gi|74354855,gi|75057806	21,648.60	99.80%	2	2	3	0.03%	13.80%	TPMGIVLDALEQQEETITK	3.78	2,132.08
ATP	6006	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	4	5	7	0.07%	10.30%	EKPYFPIPEDYTFIQNVPLEDR	3.67	2,710.34

ATP	6006	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	4	5	7	0.07%	10.30%	KAEVEGKDLPEHAVLK	2.86	1,762.97
ATP	6006	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	4	5	7	0.07%	10.30%	LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR	6.06	3,142.43
ATP	6006	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	4	5	7	0.07%	10.30%	NFILDQTNVSAAAQR	4.22	1,647.84
ATP	6006	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	3	3	3	0.03%	5.99%	NLHQSGFSLSGTQVDEGVR	3.31	2,030.99
ATP	6006	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	3	3	3	0.03%	5.99%	SAADLISQAR	3.02	1,031.55
ATP	6006	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	3	3	3	0.03%	5.99%	TLDFDALSVGQR	2.39	1,321.67
ATP	6006	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	6	9	39	0.41%	24.30%	AIAELGIYPAVDPLDSTSR	3.97	1,988.03
ATP	6006	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	6	9	39	0.41%	24.30%	FTQAGSEVSALLGR	3.45	1,435.75

ATP	6006	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	6	9	39	0.41%	24.30%	IVAVIGAVVDVQFDEGLPPILNALEVQGR	5.2	3,031.68
ATP	6006	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	6	9	39	0.41%	24.30%	SLQDIIAILGMDELSEEDKLTVSR	3.69	2,691.38
ATP	6006	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	6	9	39	0.41%	24.30%	TIAMDGTEGLVR	2.86	1,278.64
ATP	6006	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	6	9	39	0.41%	24.30%	VLDSGAPIRIPVGPETLGR	2.78	1,947.10
ATP	6006	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	99.80%	2	2	2	0.02%	12.10%	ILEPGLNILIPVLDR	2.54	1,675.02
ATP	6006	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	99.80%	2	2	2	0.02%	12.10%	QAQILASEAEKAEQINQAAGEASAVLAK	3.75	2,839.48
ATP	6006	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	99.80%	2	2	3	0.03%	6.64%	FLVGFTNK	2.55	925.5142

ATP	6006	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	99.80%	2	2	3	0.03%	6.64%	GEDFPANNIVK	3.52	1,203.60
ATP	6006	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	6	6	6	0.06%	17.30%	FGTFHSPALEDADFDGKPMVLVAGQYSTGK	4.38	3,201.52
ATP	6006	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	6	6	6	0.06%	17.30%	GYDFPAVLR	2.55	1,037.54
ATP	6006	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	6	6	6	0.06%	17.30%	KLNPFGNTFLNR	3.23	1,420.77
ATP	6006	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	6	6	6	0.06%	17.30%	LFELEEQDLFRDIQGLPR	3.16	2,218.15
ATP	6006	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	6	6	6	0.06%	17.30%	TSFIQYLLEQEVPGSR	3.77	1,866.96
ATP	6006	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	6	6	6	0.06%	17.30%	VVGTPEVLR	1.84	969.5728
ATP	6006	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	3	4	4	0.04%	8.87%	ALGVEQDLALPAIAVIGDQSSGK	4.72	2,252.21
ATP	6006	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	3	4	4	0.04%	8.87%	ATEELQQYGDDIPSDEGDKMFFLIEK	3.53	3,034.39
ATP	6006	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	3	4	4	0.04%	8.87%	SSVLEALSGVALPR	4.76	1,398.80
ATP	6006	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	7	11	11	0.12%	31.70%	ELDAEKAFANEQLTR	3.4	1,734.87
ATP	6006	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	7	11	11	0.12%	31.70%	KQDAFYKEQLAR	3.86	1,496.79
ATP	6006	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	7	11	11	0.12%	31.70%	LSENVIDRMKETSPSGPK	3	2,004.01

ATP	6006	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	7	11	11	0.12%	31.70%	RVAEELALEQAKK	5.07	1,484.84
ATP	6006	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	7	11	11	0.12%	31.70%	SSEFYKVTTEQYQK	3.04	1,737.83
ATP	6006	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	7	11	11	0.12%	31.70%	VAEELALEQAK	3.04	1,200.65
ATP	6006	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	7	11	11	0.12%	31.70%	VAEELALEQAKK	3.75	1,328.74
ATP	6006	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	12	17	30	0.32%	17.50%	GTAEKLQPEDITQIQPQQLVLQLR	4.88	2,746.51
ATP	6006	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	12	17	30	0.32%	17.50%	IGFGSFVEK	2.56	983.5197
ATP	6006	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	12	17	30	0.32%	17.50%	LLVFSTDAGFHFAGDGK	2.12	1,781.89
ATP	6006	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	12	17	30	0.32%	17.50%	LPEGVTINYK	3.22	1,133.62
ATP	6006	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	12	17	30	0.32%	17.50%	LQPEDITQIQPQQLVLQLR	5.67	2,260.27
ATP	6006	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	12	17	30	0.32%	17.50%	LSENNIQTIFAVTEEFQPVYK	3.3	2,470.25
ATP	6006	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	12	17	30	0.32%	17.50%	LSENNIQTIFAVTEEFQPVYKELK	3.95	2,840.47
ATP	6006	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	12	17	30	0.32%	17.50%	NVLSLTDKGEVFNELVGK	4.49	1,962.05
ATP	6006	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	12	17	30	0.32%	17.50%	SAVTTVVNPKYEGK	3.54	1,492.80
ATP	6006	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	12	17	30	0.32%	17.50%	SGEPQTFTLK	2.82	1,107.57
ATP	6006	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	12	17	30	0.32%	17.50%	SKGTAEKLQPEDITQIQPQQLVLQLR	4.09	2,961.64

ATP	6006	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	12	17	30	0.32%	17.50%	TVMPYISTTPAK	2.99	1,324.68
ATP	6006	TPM3 protein	gi|79153472	29,015.30	100.00%	3	3	3	0.03%	19.40%	HIAEEADRKYEEVAR	2.47	1,815.90
ATP	6006	TPM3 protein	gi|79153472	29,015.30	100.00%	3	3	3	0.03%	19.40%	KIQVLQQQADDAEERAER	3.01	2,127.08
ATP	6006	TPM3 protein	gi|79153472	29,015.30	100.00%	3	3	3	0.03%	19.40%	RIQLVEEELDRAQER	2.76	1,883.99
ATP	6006	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	7	11	11	0.12%	27.50%	DVFNKGYGFGMVK	1.92	1,477.71
ATP	6006	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	7	11	11	0.12%	27.50%	LSQNNFALGYK	2.92	1,254.65

ATP	6006	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	7	11	11	0.12%	27.50%	LTLDTIFVPNTGK	2.99	1,418.79
ATP	6006	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	7	11	11	0.12%	27.50%	LTLDTIFVPNTGKK	3.12	1,546.88
ATP	6006	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	7	11	11	0.12%	27.50%	LTLSALIDGK	3.09	1,030.61

ATP	6006	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	7	11	11	0.12%	27.50%	LTLSALIDGKNFNAGGHK	3.31	1,856.00
ATP	6006	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	7	11	11	0.12%	27.50%	SKLSQNNFALGYK	3.56	1,469.77
ATP	6006	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	7	11	11	0.12%	27.50%	VNNASLIGLGYTQTLRPGVK	2.93	2,101.18
ATP	6006	SLC25A3 protein	gi|151556064	39,986.50	100.00%	4	6	8	0.08%	11.10%	IQTQPGYANTLR	3.98	1,361.72
ATP	6006	SLC25A3 protein	gi|151556064	39,986.50	100.00%	4	6	8	0.08%	11.10%	LPRPPPPEMPESLK	4.19	1,603.85

ATP	6006	SLC25A3 protein	gi|151556064	39,986.50	100.00%	4	6	8	0.08%	11.10%	MYKEEGLKAFYK	3.87	1,522.76
ATP	6006	SLC25A3 protein	gi|151556064	39,986.50	100.00%	4	6	8	0.08%	11.10%	VRIQTQPGYANTLR	3.62	1,616.89
ATP	6006	Mitogen-activated protein kinase kinase 1 interacting protein 1	gi|109658269,gi|115496109,gi|122133616	13,632.00	99.80%	2	2	2	0.02%	41.10%	KLPSVEGLHAIVVSDRDGVPVIK	2.48	2,428.39
ATP	6006	Mitogen-activated protein kinase kinase 1 interacting protein 1	gi|109658269,gi|115496109,gi|122133616	13,632.00	99.80%	2	2	2	0.02%	41.10%	VANDNAPEHALRPGFLSTFALATDQGSK	3.24	2,927.46
ATP	6006	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	3	3	3	0.03%	24.10%	LAEQAERYDDMAACMK	4.23	1,860.79
ATP	6006	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	3	3	3	0.03%	24.10%	SVTEQGAELSNEER	4.08	1,548.71
ATP	6006	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	3	3	3	0.03%	24.10%	TAFDEAIAELDTLSEESYKDSTLIMQLLR	4.19	3,318.63
ATP	6006	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	4	4	4	0.04%	16.90%	IALTDNALIAR	3.75	1,170.68

ATP	6006	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	4	4	4	0.04%	16.90%	KTTHFVEGGDAGNREDQINR	2.92	2,244.08
ATP	6006	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	4	4	4	0.04%	16.90%	KVPAVPETLKK	3.13	1,209.76
ATP	6006	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	4	4	4	0.04%	16.90%	TTHFVEGGDAGNREDQINR	2.51	2,115.98
ATP	6006	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	3	3	3	0.03%	9.41%	ADLINNLGTIAK	3.2	1,242.71
ATP	6006	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	3	3	3	0.03%	9.41%	GVVDSEDLPLNISR	4.44	1,513.79
ATP	6006	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	3	3	3	0.03%	9.41%	HLEINPDHSIIETLR	2.97	1,786.94
ATP	6006	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	3	3	3	0.03%	9.41%	NPDDITNEEYGEFYK	3.2	1,833.78
ATP	6006	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	3	3	3	0.03%	9.41%	TLTIVDTGIGMTK	3.76	1,365.73
ATP	6006	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	3	3	4	0.04%	20.60%	KESYSVYVYK	2.66	1,265.64
ATP	6006	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	3	3	4	0.04%	20.60%	SRKESYSVYVYK	4.5	1,508.77
ATP	6006	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	3	3	4	0.04%	20.60%	VLKQVHPDTGISSK	3.7	1,508.84
ATP	6006	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	99.80%	2	2	2	0.02%	4.42%	IISKIENHEGVR	2.48	1,394.78

ATP	6006	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	99.80%	2	2	2	0.02%	4.42%	IYVDDGLISLLVK	3.26	1,447.84
ATP	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	13	26	0.27%	25.60%	AMGNLQIDFADPSR	3.88	1,550.73
ATP	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	13	26	0.27%	25.60%	AMGNLQIDFADPSRADDAR	3.16	2,078.96
ATP	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	13	26	0.27%	25.60%	AVVYSNTIQSIMAIVK	4.17	1,736.96
ATP	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	13	26	0.27%	25.60%	EYQLNDSAAYYLNDLER	4.09	2,076.95
ATP	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	13	26	0.27%	25.60%	IAQSDYIPTQQDVLR	3.78	1,746.90
ATP	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	13	26	0.27%	25.60%	LLLLGAGESGK	3.7	1,057.63

ATP	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	13	26	0.27%	25.60%	SREYQLNDSAAYYLNDLER	4.24	2,320.08
ATP	6006	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	13	26	0.27%	25.60%	YDEAASYIQSK	2.73	1,274.59
ATP	6006	FOLH1 protein	gi|151553958,gi|156120365	84,574.90	100.00%	4	4	4	0.04%	6.93%	AFTDPLGLPDRPFYR	1.92	1,764.91
ATP	6006	FOLH1 protein	gi|151553958,gi|156120365	84,574.90	100.00%	4	4	4	0.04%	6.93%	IPHLAGTEQNFQLAK	3.97	1,666.89
ATP	6006	FOLH1 protein	gi|151553958,gi|156120365	84,574.90	100.00%	4	4	4	0.04%	6.93%	IYNVIGTLR	3.17	1,048.62
ATP	6006	FOLH1 protein	gi|151553958,gi|156120365	84,574.90	100.00%	4	4	4	0.04%	6.93%	LQDLDKNNPILLR	2.67	1,551.89
ATP	6006	TEK tyrosine kinase, endothelial	gi|113912159,gi|27806791,gi|296578,gi|730946	125,911.60	99.80%	2	2	2	0.02%	2.13%	NILVGENYVAK	2.75	1,219.67
ATP	6006	TEK tyrosine kinase, endothelial	gi|113912159,gi|27806791,gi|296578,gi|730946	125,911.60	99.80%	2	2	2	0.02%	2.13%	YIGGNLFTSAFTR	2.68	1,446.74
ATP	6006	Na/K-ATPase beta 1 subunit [synthetic construct]	gi|22094876	35,156.20	100.00%	3	3	5	0.05%	9.54%	SYMTYVDNIDNFLK	2.35	1,738.80
ATP	6006	Na/K-ATPase beta 1 subunit [synthetic construct]	gi|22094876	35,156.20	100.00%	3	3	5	0.05%	9.54%	SYMTYVDNIDNFLKK	2.67	1,866.89
ATP	6006	Na/K-ATPase beta 1 subunit [synthetic construct]	gi|22094876	35,156.20	100.00%	3	3	5	0.05%	9.54%	VAPPGLTQIPQIQK	2.19	1,489.87
ATP	6006	plastin 3	gi|152941116	70,782.90	99.80%	2	2	2	0.02%	3.97%	AYFHLLNQIAPK	3.21	1,414.78
ATP	6006	plastin 3	gi|152941116	70,782.90	99.80%	2	2	2	0.02%	3.97%	MINLSVPDTIDER	2.88	1,518.75

ATP	6006	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	100.00%	6	7	7	0.07%	19.50%	GAGTDEFTLNR	3.38	1,180.56
ATP	6006	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	100.00%	6	7	7	0.07%	19.50%	GIGTDEKTLISILTER	4.18	1,745.96
ATP	6006	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	100.00%	6	7	7	0.07%	19.50%	LSGYSLYSAIK	3.02	1,201.65
ATP	6006	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	100.00%	6	7	7	0.07%	19.50%	SEIDLLDIR	2.95	1,073.58
ATP	6006	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	100.00%	6	7	7	0.07%	19.50%	SLGDEISETSGDFRK	2.44	1,727.81

ATP	6006	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	100.00%	6	7	7	0.07%	19.50%	TLISILTER	2.57	1,045.63
ATP	6006	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	8	9	0.09%	14.50%	GLNTIPLFVQLLYSPIENIQR	4.6	2,428.36
ATP	6006	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	8	9	0.09%	14.50%	HAVVNLINYQDDAELATR	4.61	2,042.03
ATP	6006	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	8	9	0.09%	14.50%	LHYGLPVVVK	2.91	1,124.68
ATP	6006	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	8	9	0.09%	14.50%	LIILASGGPQALVNIMR	2.75	1,782.03
ATP	6006	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	8	9	0.09%	14.50%	LLNDEDQVVVNK	2.98	1,385.73
ATP	6006	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	8	9	0.09%	14.50%	LVQLLVR	2.23	840.5666
ATP	6006	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	8	9	0.09%	14.50%	MLGSPVDSVLFYAITTLHNLLLHQEGAK	4.07	3,083.62
ATP	6006	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	5	5	5	0.05%	2.48%	GLTSSEPVSIMEK	3.26	1,393.69

ATP	6006	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	5	5	5	0.05%	2.48%	GPGDLEAPSNLVLSER	3.44	1,653.84
ATP	6006	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	5	5	5	0.05%	2.48%	IIYSPTVGDPIDEYTTVPGRR	2.67	2,349.21
ATP	6006	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	5	5	5	0.05%	2.48%	ITYQPSTGEGNEQTTTIGGR	3.22	2,110.01
ATP	6006	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	5	5	5	0.05%	2.48%	IVEVFEIGPK	2.59	1,130.65
ATP	6006	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	3	4	4	0.04%	14.10%	ANVDKVFFDLMR	4.1	1,470.74
ATP	6006	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	3	4	4	0.04%	14.10%	TRANVDKVFFDLMR	2.88	1,727.89
ATP	6006	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	3	4	4	0.04%	14.10%	VKEDENVPFLLVGNK	3.24	1,700.92
ATP	6006	ALDOA protein	gi|151554749,gi|156120479	39,418.80	99.80%	2	2	2	0.02%	7.97%	GILAADESTGSIAK	2.8	1,332.70
ATP	6006	ALDOA protein	gi|151554749,gi|156120479	39,418.80	99.80%	2	2	2	0.02%	7.97%	RLQSIGTENTEENRR	3.15	1,802.91
ATP	6006	hemoglobin alpha chain	gi|116812902,gi|126717493,gi|13634094,gi|194678485,gi|197724899,gi|197724901,gi|197724903,gi|6006421,gi|74268120	15,035.40	100.00%	5	5	7	0.07%	52.50%	AVEHLDDLPGALSELSDLHAHK	4.15	2,367.19

ATP	6006	hemoglobin alpha chain	gi|116812902,gi|126717493,gi|13634094,gi|194678485,gi|197724899,gi|197724901,gi|197724903,gi|6006421,gi|74268120	15,035.40	100.00%	5	5	7	0.07%	52.50%	FLANVSTVLTSK	3.53	1,279.73
ATP	6006	hemoglobin alpha chain	gi|116812902,gi|126717493,gi|13634094,gi|194678485,gi|197724899,gi|197724901,gi|197724903,gi|6006421,gi|74268120	15,035.40	100.00%	5	5	7	0.07%	52.50%	MFLSFPTTK	2.01	1,087.55
ATP	6006	hemoglobin alpha chain	gi|116812902,gi|126717493,gi|13634094,gi|194678485,gi|197724899,gi|197724901,gi|197724903,gi|6006421,gi|74268120	15,035.40	100.00%	5	5	7	0.07%	52.50%	TYFPHFDLSHGSAQVK	2.59	1,833.89
ATP	6006	hemoglobin alpha chain	gi|116812902,gi|126717493,gi|13634094,gi|194678485,gi|197724899,gi|197724901,gi|197724903,gi|6006421,gi|74268120	15,035.40	100.00%	5	5	7	0.07%	52.50%	VGGHAAEYGAEALER	4.21	1,529.73
ATP	6006	RecName: Full=Transmembrane emp24 domain-containing protein 1; Flags: Precursor	gi|114152289,gi|83638714,gi|84370158	25,119.90	99.80%	2	2	2	0.02%	11.50%	KADGVHTVEPTEAGDYK	3.64	1,816.87

ATP	6006	RecName: Full=Transmembrane emp24 domain-containing protein 1; Flags: Precursor	gi|114152289,gi|83638714,gi|84370158	25,119.90	99.80%	2	2	2	0.02%	11.50%	SIQVLTLLR	3.06	1,042.66
ATP	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	13	17	39	0.41%	20.30%	ATEEQLKTVMENFVAFVDK	4.06	2,215.10
ATP	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	13	17	39	0.41%	20.30%	DAFLGSFLYEYSR	2.89	1,567.74
ATP	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	13	17	39	0.41%	20.30%	FKDLGEEHFK	4.13	1,249.62
ATP	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	13	17	39	0.41%	20.30%	HLVDEPQNLIK	3.3	1,305.72
ATP	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	13	17	39	0.41%	20.30%	KQTALVELLK	4.18	1,142.71

ATP	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	13	17	39	0.41%	20.30%	KVPQVSTPTLVEVSR	4.38	1,639.94
ATP	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	13	17	39	0.41%	20.30%	LVNELTEFAK	2.93	1,163.63
ATP	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	13	17	39	0.41%	20.30%	QTALVELLK	1.94	1,014.62
ATP	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	13	17	39	0.41%	20.30%	RHPEYAVSVLLR	4.26	1,439.81
ATP	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	13	17	39	0.41%	20.30%	RHPYFYAPELLYANK	4.11	2,045.03
ATP	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	13	17	39	0.41%	20.30%	TVMENFVAFVDK	2.95	1,415.69
ATP	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	13	17	39	0.41%	20.30%	VPQVSTPTLVEVSR	2.88	1,511.84

ATP	6006	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	13	17	39	0.41%	20.30%	YLYEIAR	2.7	927.4934
ATP	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	13	0.14%	24.10%	IIGAVDQIQLTQAQLEER	4.02	2,025.10
ATP	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	13	0.14%	24.10%	IREGQVEVLK	4.09	1,170.68
ATP	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	13	0.14%	24.10%	KLEVNEAELLR	3.62	1,313.74
ATP	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	13	0.14%	24.10%	KLEVNEAELLRR	2.38	1,469.84
ATP	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	13	0.14%	24.10%	KSFTPDHVVYAR	3.21	1,419.74
ATP	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	13	0.14%	24.10%	LEVNEAELLR	3.03	1,185.65
ATP	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	13	0.14%	24.10%	NFKVMIYQDEVKLPAK	2.09	1,939.04
ATP	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	13	0.14%	24.10%	QAEMEGAVQSIQGELSK	4.49	1,820.87
ATP	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	13	0.14%	24.10%	VMIYQDEVKLPAK	3.35	1,549.83
ATP	6006	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	13	13	0.14%	24.10%	VPPFTFHVK	1.97	1,071.60

ATP	6006	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	99.80%	2	2	3	0.03%	11.00%	KYMEENDLLKK	3.52	1,426.72
ATP	6006	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	99.80%	2	2	3	0.03%	11.00%	VNLQNNPGAVEHFHMK	2.57	1,850.90
ATP	6006	ITGA3 protein	gi|151556279,gi|156120449	45,035.90	99.80%	2	2	3	0.03%	6.34%	EAGNPGSLFGYSVALHR	3.48	1,774.89
ATP	6006	ITGA3 protein	gi|151556279,gi|156120449	45,035.90	99.80%	2	2	3	0.03%	6.34%	YLLLAGAPR	3.66	973.583
ATP	6006	PREDICTED: similar to ribosomal protein S4, X-linked X	gi|119901281,gi|119930307,gi|119934106,gi|194668343,gi|76660997	29,434.70	99.80%	2	2	2	0.02%	8.75%	ERHPGSFDVVHVK	2.82	1,506.78
ATP	6006	PREDICTED: similar to ribosomal protein S4, X-linked X	gi|119901281,gi|119930307,gi|119934106,gi|194668343,gi|76660997	29,434.70	99.80%	2	2	2	0.02%	8.75%	TIRYPDPLIK	3.2	1,215.71
ATP	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	15	22	0.23%	57.50%	AKDFSLILDDVAITELSFSR	3.1	2,240.18
ATP	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	15	22	0.23%	57.50%	DLQMVNISLR	3.14	1,204.64
ATP	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	15	22	0.23%	57.50%	ESVFTVEGGHR	2.96	1,217.59
ATP	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	15	22	0.23%	57.50%	FNASQLITQR	3.86	1,177.63
ATP	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	15	22	0.23%	57.50%	IGGVQQDTILAEGLHFR	3.05	1,853.99
ATP	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	15	22	0.23%	57.50%	IVQAEGEAEAAR	3.74	1,243.63
ATP	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	15	22	0.23%	57.50%	IYLTADNLVLNLQDESFTR	4.65	2,225.15
ATP	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	15	22	0.23%	57.50%	KISSPTGSKDLQMVNISLR	2.28	2,090.13
ATP	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	15	22	0.23%	57.50%	LGLDYEER	2.75	994.4841
ATP	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	15	22	0.23%	57.50%	LLLGAGAVAYGIR	4.37	1,273.76

ATP	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	15	22	0.23%	57.50%	MLGEALSKNPGYIK	2.45	1,536.81
ATP	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	15	22	0.23%	57.50%	QKIVQAEGEAEAAR	5.54	1,499.78
ATP	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	15	22	0.23%	57.50%	VLPSIVNEVLK	2.87	1,210.74
ATP	6006	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	14	15	22	0.23%	57.50%	VLSRPNAMELPSMYQR	3.36	1,907.95
ATP	6006	TAP1 protein	gi|151557007	81,933.30	100.00%	5	8	8	0.08%	9.33%	GVVGAALGFR	3.36	946.5469
ATP	6006	TAP1 protein	gi|151557007	81,933.30	100.00%	5	8	8	0.08%	9.33%	SFANEEGEAQKFR	3.35	1,512.71
ATP	6006	TAP1 protein	gi|151557007	81,933.30	100.00%	5	8	8	0.08%	9.33%	SSQVAIEVLSAMPTVR	2.99	1,703.90
ATP	6006	TAP1 protein	gi|151557007	81,933.30	100.00%	5	8	8	0.08%	9.33%	STVAALLQNLYQPTEGQVLLDGEPLPK	4.29	2,894.55
ATP	6006	TAP1 protein	gi|151557007	81,933.30	100.00%	5	8	8	0.08%	9.33%	STVAALLQNLYQPTEGQVLLDGEPLPKYEHR	2.71	3,479.82
ATP	6006	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	100.00%	3	4	5	0.05%	9.98%	FASFIDKVR	2.12	1,082.60
ATP	6006	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	100.00%	3	4	5	0.05%	9.98%	LLKEYQELMNVK	3.27	1,507.82
ATP	6006	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	100.00%	3	4	5	0.05%	9.98%	NKYEDEINKR	2.84	1,308.65
ATP	6006	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	100.00%	3	4	5	0.05%	9.98%	NLDLDSIIAEVK	3.82	1,329.73
ATP	6006	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	100.00%	3	4	5	0.05%	9.98%	NLDLDSIIAEVKAQYEEIAQR	3.16	2,418.25

ATP	6006	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	100.00%	3	4	5	0.05%	9.98%	TLNNKFASFIDKVR	4.1	1,652.91
ATP	6006	signal sequence receptor, gamma (translocon-associated protein gamma)	gi|116004307,gi|122140189,gi|74268139	21,057.60	99.80%	2	3	5	0.05%	9.73%	GGPKQQSEEDLLLQDFSR	3.89	2,047.01
ATP	6006	signal sequence receptor, gamma (translocon-associated protein gamma)	gi|116004307,gi|122140189,gi|74268139	21,057.60	99.80%	2	3	5	0.05%	9.73%	QQSEEDLLLQDFSR	3.36	1,707.82
ATP	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	16	22	24	0.25%	50.10%	AEDGSVIDYELIDQDAR	3.14	1,908.88

ATP	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	16	22	24	0.25%	50.10%	AEDGSVIDYELIDQDARDLYDAGVKR	2.63	2,926.41
ATP	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	16	22	24	0.25%	50.10%	AYTNFDAERDALNIETAIK	4.04	2,155.07

ATP	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	16	22	24	0.25%	50.10%	GVDEVTIVNILTNR	4.9	1,542.85
ATP	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	16	22	24	0.25%	50.10%	LSLEGDHSTPPSAYGSVK	4.01	1,844.90

ATP	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	16	22	24	0.25%	50.10%	QDIAFAYQR	2.39	1,111.55
ATP	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	16	22	24	0.25%	50.10%	RAEDGSVIDYELIDQDAR	3.93	2,064.98

ATP	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	16	22	24	0.25%	50.10%	RAEDGSVIDYELIDQDARDLYDAGVK	4.01	2,926.41
ATP	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	16	22	24	0.25%	50.10%	SALSGHLETVILGLLK	3.74	1,650.98

ATP	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	16	22	24	0.25%	50.10%	SLYYYIQQDTKGDYQK	2.67	2,012.96
ATP	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	16	22	24	0.25%	50.10%	SNEQRQDIAFAYQR	5.24	1,725.83

ATP	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	16	22	24	0.25%	50.10%	SYSPYDMLESIK	2.38	1,448.66
ATP	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	16	22	24	0.25%	50.10%	TDLEKDIVSDTSGDFR	3.2	1,797.85

ATP	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	16	22	24	0.25%	50.10%	TDLEKDIVSDTSGDFRK	4.06	1,925.95
ATP	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	16	22	24	0.25%	50.10%	TKGVDEVTIVNILTNR	4.24	1,771.99

ATP	6006	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	16	22	24	0.25%	50.10%	TPAQYDASELKASMK	4.06	1,655.79
ATP	6006	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	3	3	3	0.03%	11.40%	ELIEVLQPLIAEHQAR	2.67	1,859.04
ATP	6006	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	3	3	3	0.03%	11.40%	ISFPAIQAAPSFSNSFPQIFR	3.5	2,325.20

ATP	6006	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	3	3	3	0.03%	11.40%	MSASDPNSSIFLTDTAK	3.48	1,800.83
ATP	6006	PREDICTED: similar to Transmembrane protein 16F	gi|119892265	106,290.10	99.80%	2	2	2	0.02%	3.62%	LLQVDESIIKPEQEFFTAPFEK	2.52	2,608.35
ATP	6006	PREDICTED: similar to Transmembrane protein 16F	gi|119892265	106,290.10	99.80%	2	2	2	0.02%	3.62%	SLVDDKLVFVK	2.15	1,262.74
ATP	6006	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	3	4	4	0.04%	11.50%	FRGPFTDVVTTNLK	3.19	1,594.86
ATP	6006	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	3	4	4	0.04%	11.50%	GPFTDVVTTNLK	3.76	1,291.69
ATP	6006	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	3	4	4	0.04%	11.50%	VEQVLSLEPQHELK	4.55	1,648.89
ATP	6006	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	6	7	7	0.07%	16.50%	APDFVFYAPR	3.27	1,182.59
ATP	6006	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	6	7	7	0.07%	16.50%	AQMVQEDLEKTRAELK	2.14	1,904.97
ATP	6006	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	6	7	7	0.07%	16.50%	ERQEAEEAKEALLQASQDQK	2.94	2,301.13
ATP	6006	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	6	7	7	0.07%	16.50%	FYPEDVSEELIQDITQR	2.53	2,082.00
ATP	6006	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	6	7	7	0.07%	16.50%	KAPDFVFYAPR	3.08	1,310.69
ATP	6006	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	6	7	7	0.07%	16.50%	TAMSTPHVAEPAENEQDEQDENGAEASAELR	6.63	3,342.43

ATP	6006	PREDICTED: similar to Keratin, type I cytoskeletal 24 (Cytokeratin-24) (Keratin-24) (Type I keratin-24)	gi|194676109	55,111.70	99.80%	2	3	3	0.03%	5.33%	KVLDDLTMTR	3.42	1,207.64
ATP	6006	PREDICTED: similar to Keratin, type I cytoskeletal 24 (Cytokeratin-24) (Keratin-24) (Type I keratin-24)	gi|194676109	55,111.70	99.80%	2	3	3	0.03%	5.33%	SDLEMQIESLTEELAYLK	2.79	2,112.04
ATP	6006	PREDICTED: transmembrane protein 33 isoform 2	gi|119893815,gi|119922774	27,968.00	99.80%	2	2	2	0.02%	8.10%	ALLANALTSALR	3.73	1,213.73
ATP	6006	PREDICTED: transmembrane protein 33 isoform 2	gi|119893815,gi|119922774	27,968.00	99.80%	2	2	2	0.02%	8.10%	LPHFQLSR	2.22	997.5578
ATP	6006	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	6	8	0.08%	45.00%	DSLLQDGEFTMDLR	3.21	1,655.76
ATP	6006	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	6	8	0.08%	45.00%	SSFFVNGLTLGGQK	3.8	1,454.76

ATP	6006	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	6	8	0.08%	45.00%	STGGAPTFNITVTMTAK	3.35	1,712.85
ATP	6006	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	6	8	0.08%	45.00%	TFVNITPAEVGILVGK	3.06	1,657.95
ATP	6006	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	6	8	0.08%	45.00%	TFVNITPAEVGILVGKDR	2.64	1,929.08
ATP	6006	Brain abundant, membrane attached signal protein 1	gi|115304757,gi|1930063,gi|27807507,gi|6686271	22,992.60	99.80%	2	3	3	0.03%	28.20%	AQAPAAPADEVKPAETPAANSDQTVAVKE	3.39	2,876.43
ATP	6006	Brain abundant, membrane attached signal protein 1	gi|115304757,gi|1930063,gi|27807507,gi|6686271	22,992.60	99.80%	2	3	3	0.03%	28.20%	SDGAPASDSKPSSTEAAPSSKETPAATEAPSSTPK	4.28	3,344.56
ATP	6006	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	99.80%	2	3	5	0.05%	14.90%	ALNLPSSGEGLAFFTFPNIASATK	3.84	2,453.27
ATP	6006	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	99.80%	2	3	5	0.05%	14.90%	LVMASLYHIYVALEEEIER	4.05	2,294.17

ATP	6006	annexin 5	gi|119936560,gi|120474983,gi|260137,gi|73586525	36,057.60	100.00%	3	3	3	0.03%	13.40%	DLLDDLKSELTGKFEK	2.89	1,850.98
ATP	6006	annexin 5	gi|119936560,gi|120474983,gi|260137,gi|73586525	36,057.60	100.00%	3	3	3	0.03%	13.40%	GLGTDEESILTLLTSR	2.04	1,704.90
ATP	6006	annexin 5	gi|119936560,gi|120474983,gi|260137,gi|73586525	36,057.60	100.00%	3	3	3	0.03%	13.40%	NFGTSLYSMIK	2.56	1,276.62
ATP	6006	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32, gi|59857977	33,881.70	100.00%	3	3	3	0.03%	14.80%	AVVVNAAQLASYSQSK	3.52	1,635.87
ATP	6006	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32, gi|59857977	33,881.70	100.00%	3	3	3	0.03%	14.80%	FLFGGLAGMGATVFVQPLDLVK	3.87	2,296.24

ATP	6006	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32, gi|59857977	33,881.70	100.00%	3	3	3	0.03%	14.80%	NVFNALFR	2.16	980.5311
ATP	6006	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	3	3	3	0.03%	10.10%	LTPEYLQLMK	1.94	1,251.67
ATP	6006	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	3	3	3	0.03%	10.10%	SVQTTLQTDEVK	3.19	1,348.70
ATP	6006	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	3	3	3	0.03%	10.10%	VTKPNIPEAIRR	1.93	1,393.83
ATP	6006	GLI pathogenesis-related 2	gi|111307081,gi|115497826	17,191.20	99.80%	2	2	2	0.02%	16.90%	ASASDGSSFVVAR	3.19	1,253.61
ATP	6006	GLI pathogenesis-related 2	gi|111307081,gi|115497826	17,191.20	99.80%	2	2	2	0.02%	16.90%	EAQQYSEALASTR	2.87	1,453.69
ATP	6006	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	4	5	5	0.05%	7.51%	ITVLEALR	2.84	914.567
ATP	6006	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	4	5	5	0.05%	7.51%	ITVLEALRHPIQVSR	1.7	1,732.02
ATP	6006	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	4	5	5	0.05%	7.51%	LKEYEAAVEQLKGDQIR	4.51	1,990.06
ATP	6006	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	4	5	5	0.05%	7.51%	NVLMYGPPGTGK	2.96	1,249.62
ATP	6006	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	7	7	7	0.07%	11.80%	AQAYQTGKDISTNYYASQKK	3.35	2,265.11
ATP	6006	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	7	7	7	0.07%	11.80%	ELISNASDALDKIR	2.98	1,544.83

ATP	6006	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	7	7	7	0.07%	11.80%	FAFQAEVNR	2.94	1,081.54
ATP	6006	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	7	7	7	0.07%	11.80%	FQSSHHPSDMTSLDQYVER	5.14	2,280.00
ATP	6006	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	7	7	7	0.07%	11.80%	LIINSLYK	2.48	963.5874
ATP	6006	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	7	7	7	0.07%	11.80%	NLLHVTDTGVGMTR	3.13	1,529.77
ATP	6006	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	7	7	7	0.07%	11.80%	SILFVPTSAPR	2.94	1,187.68
ATP	6006	PREDICTED: similar to FXYD domain-containing ion transport regulator 5 isoform 1	gi|76641186	18,921.80	99.80%	2	2	2	0.02%	10.40%	EDDPFFYDEDTLR	3.26	1,661.70
ATP	6006	PREDICTED: similar to FXYD domain-containing ion transport regulator 5 isoform 1	gi|76641186	18,921.80	99.80%	2	2	2	0.02%	10.40%	QPGSKEDDPFFYDEDTLR	3.05	2,158.96
ATP	6006	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	4	5	6	0.06%	6.67%	ALSAIADLLTNEHER	3.27	1,652.86
ATP	6006	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	4	5	6	0.06%	6.67%	APSRQDVYGPQPQVR	4.49	1,697.87
ATP	6006	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	4	5	6	0.06%	6.67%	HYEDGYPGSGDNYGSLSR	3.71	1,973.83

ATP	6006	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	4	5	6	0.06%	6.67%	KPTEDPTNDTVDFPKR	3.88	1,859.91
ATP	6006	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	3	5	5	0.05%	15.30%	IFDTSLTRDPLVIELGQK	5.21	2,045.13
ATP	6006	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	3	5	5	0.05%	15.30%	RVIIPSHLAYGKR	2.68	1,509.90
ATP	6006	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	3	5	5	0.05%	15.30%	VIIPSHLAYGKR	2.13	1,353.80
ATP	6006	endoglin	gi|115497110,gi|92097469	69,885.10	99.80%	2	3	5	0.05%	3.25%	FSFLLR	1.75	782.4559
ATP	6006	endoglin	gi|115497110,gi|92097469	69,885.10	99.80%	2	3	5	0.05%	3.25%	LQAPGIPLQLAYDSK	4.68	1,613.89
ATP	6006	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	3	4	4	0.04%	8.72%	AYLYLDEAHSIGALGPTGR	2.32	2,004.02
ATP	6006	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	3	4	4	0.04%	8.72%	LLKDAIVYGQPR	2.99	1,372.79
ATP	6006	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	3	4	4	0.04%	8.72%	NIGVVVVGFPATPIIESR	4.47	1,868.06
ATP	6006	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	8	0.08%	8.67%	DKLNPQSTYSEA	2.59	1,352.63
ATP	6006	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	8	0.08%	8.67%	FVTAVGTQGAISK	3.39	1,278.71
ATP	6006	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	8	0.08%	8.67%	IAPSSFVSSGPFLFIK	3.29	1,696.93
ATP	6006	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	8	0.08%	8.67%	SFEGNNNYDTPELR	3.3	1,655.73
ATP	6006	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	8	0.08%	8.67%	TGPIQDHTGDGNFIYSQADENQK	4.87	2,535.14

ATP	6006	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	6	7	8	0.08%	8.67%	TGPIQDHTGDGNFIYSQADENQKGK	3.49	2,720.26
ATP	6006	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	8	8	10	0.11%	20.60%	FGNAFLNR	2.64	938.4842
ATP	6006	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	8	8	10	0.11%	20.60%	FHEFHSPALEDADFENKPMILLVGQYSTGK	3.1	3,436.65
ATP	6006	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	8	8	10	0.11%	20.60%	GGTGADPVQTVTGGLR	3.52	1,485.77
ATP	6006	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	8	8	10	0.11%	20.60%	LFEAEAQDLFR	2.96	1,338.67
ATP	6006	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	8	8	10	0.11%	20.60%	LFEAEAQDLFRDIQSLPQK	3.81	2,248.16
ATP	6006	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	8	8	10	0.11%	20.60%	LIEAVDNMLTNK	3.33	1,376.71
ATP	6006	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	8	8	10	0.11%	20.60%	SISIIDSPGILSGEK	3.81	1,515.83
ATP	6006	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	8	8	10	0.11%	20.60%	YLLEQDFPGMR	3.31	1,384.66
ATP	6006	RRAS2 protein	gi|148743916,gi|149944707	23,381.60	99.80%	2	2	2	0.02%	13.70%	LDILDTAGQEEFGAMR	2.78	1,781.84
ATP	6006	RRAS2 protein	gi|148743916,gi|149944707	23,381.60	99.80%	2	2	2	0.02%	13.70%	MNVDQAFHELVR	2.56	1,474.71
ATP	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	26.80%	AAYFGIYDTAK	2.86	1,219.60
ATP	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	26.80%	DFLAGGVAAAISK	4.45	1,219.67
ATP	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	26.80%	GMGGAFVLVLYDEIK	2.91	1,627.84

ATP	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	26.80%	GMGGAFVLVLYDEIKK	2.88	1,755.94
ATP	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	26.80%	GMGGAFVLVLYDEIKKFT	2.87	2,004.05
ATP	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	26.80%	QIFLGGVDKR	2.46	1,132.65
ATP	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	26.80%	VKLLLQVQHASK	3.83	1,363.84
ATP	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	26.80%	YFPTQALNFAFK	4.71	1,446.74
ATP	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	26.80%	YFPTQALNFAFKDK	3.09	1,689.86
ATP	6006	adenine nucleotide translocator 2	gi|18642496,gi|32189334,gi|74355032	32,938.60	99.80%	2	3	4	0.04%	26.80%	YFPTQALNFAFKDKYK	3.89	1,981.02
ATP	6006	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	2	2	2	0.02%	6.13%	SISHYHETLGEALQGVELEFSGLDIK	4.11	2,872.44
ATP	6006	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	2	2	2	0.02%	6.13%	YLDPSFFQHR	1.79	1,309.63
ATP	6006	hypothetical protein LOC516334	gi|115496252,gi|151556904,gi|95768630	43,057.10	99.80%	2	2	2	0.02%	3.62%	ETAFEEDVQLPR	2.36	1,433.69
ATP	6006	hypothetical protein LOC516334	gi|115496252,gi|151556904,gi|95768630	43,057.10	99.80%	2	2	2	0.02%	3.62%	MRETAFEEDVQLPR	3.29	1,736.83

ATP	6006	PREDICTED: similar to Transmembrane emp24 domain-containing protein 2 precursor (Membrane protein p24A)	gi|194674620	22,715.40	99.80%	2	3	4	0.04%	12.40%	IVMFTIDIGEAPK	3.39	1,449.77
ATP	6006	PREDICTED: similar to Transmembrane emp24 domain-containing protein 2 precursor (Membrane protein p24A)	gi|194674620	22,715.40	99.80%	2	3	4	0.04%	12.40%	YTFAAHMDGTYK	3.8	1,420.62
ATP	6006	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	7	10	12	0.13%	8.16%	EATSTFTNITYR	3.05	1,403.68
ATP	6006	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	7	10	12	0.13%	8.16%	EATSTFTNITYRGT	3.3	1,561.75
ATP	6006	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	7	10	12	0.13%	8.16%	GTGDSSQITQVSPQR	3.07	1,560.76

ATP	6006	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	7	10	12	0.13%	8.16%	HVLTLTDQVTR	3.33	1,282.71
ATP	6006	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	7	10	12	0.13%	8.16%	ILEARPLSDKGTGDSSQITQVSPQR	6.21	2,683.40
ATP	6006	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	7	10	12	0.13%	8.16%	LRPDDSKIFSVQVR	3.15	1,659.92
ATP	6006	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	7	10	12	0.13%	8.16%	PLSDKGTGDSSQITQVSPQR	4.55	2,101.05
ATP	6006	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	5	7	9	0.09%	11.50%	ADLVNNLGTIAK	3.14	1,228.69
ATP	6006	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	5	7	9	0.09%	11.50%	ELISNASDALDKIR	2.98	1,544.83
ATP	6006	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	5	7	9	0.09%	11.50%	GVVDSEDLPLNISR	4.44	1,513.79
ATP	6006	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	5	7	9	0.09%	11.50%	HLEINPDHPIVETLR	2.58	1,782.95
ATP	6006	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	5	7	9	0.09%	11.50%	NPDDITQEEYGEFYK	3.35	1,847.80
ATP	6006	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	5	7	9	0.09%	11.50%	TLTLVDTGIGMTK	3.76	1,365.73

ATP	6006	Solute carrier family 1 (neutral amino acid transporter), member 5	gi|115305216,gi|15145909,gi|21541958,gi|27807087	56,431.20	99.80%	2	2	2	0.02%	4.45%	EVLDSFLDLVR	2.49	1,305.71
ATP	6006	Solute carrier family 1 (neutral amino acid transporter), member 5	gi|115305216,gi|15145909,gi|21541958,gi|27807087	56,431.20	99.80%	2	2	2	0.02%	4.45%	NIFPSNLVSAAFR	2.38	1,435.77
ATP	6006	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	6	0.06%	15.60%	ALDLFSDNAPPPELLEIINEDVAK	3.53	2,623.35
ATP	6006	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	6	0.06%	15.60%	GSFSEQGINEFLR	3.15	1,483.72
ATP	6006	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	6	0.06%	15.60%	IFQKGESPVDYDGGR	4.25	1,667.80
ATP	6006	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	6	0.06%	15.60%	LAAVDATVNQVLASR	3.08	1,527.85
ATP	6006	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	6	0.06%	15.60%	VGAVDADKHQSLGGQYGVQGFPTIK	3.11	2,572.32

ATP	6006	Deoxyribonuclease I-like 1	gi|151553571	35,175.30	99.80%	2	3	3	0.03%	7.91%	IVLHGEHLQSLLR	2.51	1,514.88
ATP	6006	Deoxyribonuclease I-like 1	gi|151553571	35,175.30	99.80%	2	3	3	0.03%	7.91%	VAREPVLDTLVK	3.57	1,339.79
ATP	6011	TIMM23 protein	gi|134025149,gi|139947578,gi|215274655	21,809.90	100.00%	3	3	5	0.05%	32.50%	NVQILNMVTR	3.56	1,203.65
ATP	6011	TIMM23 protein	gi|134025149,gi|139947578,gi|215274655	21,809.90	100.00%	3	3	5	0.05%	32.50%	TTGGLAGFFGAGGAGYSHADLAGVPLTGMNPLSPYLNVDPR	4.95	4,034.97
ATP	6011	TIMM23 protein	gi|134025149,gi|139947578,gi|215274655	21,809.90	100.00%	3	3	5	0.05%	32.50%	YLVQDTDEFILPTGANK	2.94	1,923.97
ATP	6011	Chain B, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591027,gi|110591030,gi|114686,gi|27807305,gi|599873,gi|74356487	18,544.10	100.00%	2	3	8	0.09%	19.40%	IQEYEKELEK	3.64	1,308.67
ATP	6011	Chain B, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591027,gi|110591030,gi|114686,gi|27807305,gi|599873,gi|74356487	18,544.10	100.00%	2	3	8	0.09%	19.40%	NIIPFDQMTIEDLNEVFPETK	3.64	2,509.22
ATP	6011	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	5	8	14	0.15%	8.79%	AQILLDCGEDNICVPDLQLEVFGEQNHVYLGDK	3.8	3,687.77
ATP	6011	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	5	8	14	0.15%	8.79%	DLDGNGYPDLIVGSFGVDK	3.78	1,980.96

ATP	6011	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	5	8	14	0.15%	8.79%	LAGMEPTPTLTLTGQDEFGR	5.17	2,150.04
ATP	6011	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	5	8	14	0.15%	8.79%	TIQFDFQILSK	2.64	1,339.73
ATP	6011	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	5	8	14	0.15%	8.79%	VTAPPEAEYSGLVR	3.06	1,488.77
ATP	6011	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	3	5	11	0.12%	19.70%	ASFTTFTVTK	2.93	1,102.58
ATP	6011	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	3	5	11	0.12%	19.70%	YVDSEGHLYTVPIR	3.73	1,648.83
ATP	6011	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	3	5	11	0.12%	19.70%	YVDSEGHLYTVPIREQGNIYKPNNK	4.4	2,934.47
ATP	6011	RTN3 protein	gi|115305093,gi|122132179,gi|146231798,gi|151554368,gi|32880223,gi|38327594	25,478.60	99.80%	2	4	4	0.04%	5.49%	TQIDHYVGIAR	2.67	1,272.67
ATP	6011	RTN3 protein	gi|115305093,gi|122132179,gi|146231798,gi|151554368,gi|32880223,gi|38327594	25,478.60	99.80%	2	4	4	0.04%	5.49%	YKTQIDHYVGIAR	2.99	1,563.83

ATP	6011	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	4	5	6	0.07%	17.00%	DNFHGLAIFLDTYPNDETTER	4.33	2,468.14
ATP	6011	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	4	5	6	0.07%	17.00%	DNVDDPTGNFR	2.85	1,249.54
ATP	6011	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	4	5	6	0.07%	17.00%	LPTGYYFGASAGTGDLSDNHDIISMK	5.1	2,746.27
ATP	6011	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	4	5	6	0.07%	17.00%	SPKDNVDDPTGNFR	3.83	1,561.72
ATP	6011	PREDICTED: similar to LOC512938 protein	gi|61810221	18,067.50	99.80%	2	2	2	0.02%	22.20%	MPATLLVTVHSEKWKPMTFPAHPGDR	2.19	2,962.51
ATP	6011	PREDICTED: similar to LOC512938 protein	gi|61810221	18,067.50	99.80%	2	2	2	0.02%	22.20%	SIHLTLKVVK	2.58	1,137.74
ATP	6011	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	3	3	3	0.03%	8.41%	EIILVDDYSNDPEDGALLGK	3.24	2,176.07
ATP	6011	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	3	3	3	0.03%	8.41%	NKFNQVESDKLR	2.93	1,477.78
ATP	6011	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	3	3	3	0.03%	8.41%	QHPYTFPGGSGTVFAR	3.5	1,721.84
ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	ADIGVAMGIAGSDVSK	4.57	1,506.75
ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	AVAGDASESALLK	3.79	1,231.65

ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	AVFQANQDNLPILK	4.16	1,570.86
ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	AVFQANQDNLPILKR	2.36	1,726.96
ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	DKYEPAAVSEHGDK	3.75	1,545.72
ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	EQPLDEELKDAFQNAYLELGGLGER	3.88	2,834.38
ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	GVGIISEGNETVEDIAAR	5.71	1,829.92
ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	IVEIPFNSTNK	2.38	1,261.68
ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	KADIGVAMGIAGSDVSK	5.55	1,634.84
ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	LNIPVSQVNPR	3.25	1,236.71
ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	LSLDELHR	2.64	982.5317
ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	MSINAEEVVVGDLVEVK	3	1,846.95

ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	NMVPQQALVIR	2.63	1,284.71
ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	QAADMILLDDNFASIVTGVEEGR	3.57	2,480.20
ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	QGAIVAVTGDGVNDSPALKK	2.66	1,940.05
ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	SPDFTNENPLETR	4.44	1,519.70
ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	VDNSSLTGESEPQTR	3.75	1,619.75
ATP	6011	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	18	24	46	0.50%	23.80%	VIMVTGDHPITAK	4.2	1,397.75
ATP	6011	COL18A1 protein	gi|133778103,gi|134085613,gi|157742960	135,049.70	99.80%	2	2	2	0.02%	2.33%	LFVAQAGGADPEKFQGLISELR	4.66	2,346.25
ATP	6011	COL18A1 protein	gi|133778103,gi|134085613,gi|157742960	135,049.70	99.80%	2	2	2	0.02%	2.33%	LQDLYSIVR	3.04	1,106.62
ATP	6011	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	5	6	7	0.08%	27.80%	AFDLLVDRPVTLVR	2.88	1,613.94
ATP	6011	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	5	6	7	0.08%	27.80%	DYKVDQEIVNIIQER	3.88	1,861.97
ATP	6011	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	5	6	7	0.08%	27.80%	RTPAPSPQTSLPNPITYLTK	2.97	2,182.19
ATP	6011	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	5	6	7	0.08%	27.80%	TPAPSPQTSLPNPITYLTK	4.98	2,026.09
ATP	6011	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	5	6	7	0.08%	27.80%	VDQEIVNIIQER	2.99	1,455.78

ATP	6011	ribosomal protein L18	gi|59858459,gi|62752012,gi|75060915,gi|75775560,gi|89573893	21,518.10	99.80%	2	2	3	0.03%	12.20%	ILTFDQLALDSPK	4.2	1,460.80
ATP	6011	ribosomal protein L18	gi|59858459,gi|62752012,gi|75060915,gi|75775560,gi|89573893	21,518.10	99.80%	2	2	3	0.03%	12.20%	TNRPPLSLSR	3.36	1,140.65
ATP	6011	RecName: Full=Isocitrate dehydrogenase [NADP], mitochondrial; Short=IDH; AltName: Full=Oxalosuccinate decarboxylase; AltName: Full=NADP(+)-specific ICDH; AltName: Full=IDP; AltName:	gi|109891934,gi|28461205,gi|430,gi|73587323	50,807.00	99.80%	2	2	2	0.02%	6.42%	LNEHFLNTSDFLDTIK	4.25	1,906.95
ATP	6011	RecName: Full=Isocitrate dehydrogenase [NADP], mitochondrial; Short=IDH; AltName: Full=Oxalosuccinate decarboxylase; AltName: Full=NADP(+)-specific ICDH; AltName: Full=IDP; AltName:	gi|109891934,gi|28461205,gi|430,gi|73587323	50,807.00	99.80%	2	2	2	0.02%	6.42%	TIEAEAAHGTVTR	4.09	1,355.69

ATP	6011	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	8	10	15	0.16%	15.40%	AFEESLSTLK	3.06	1,124.58
ATP	6011	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	8	10	15	0.16%	15.40%	APNRDQWSMTPPMVNAYYSPTKNEIVFPAGILQAPFYTR	2.75	4,487.20
ATP	6011	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	8	10	15	0.16%	15.40%	ELDKVFNDYTAVPDLYFENAMR	3.44	2,666.24
ATP	6011	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	8	10	15	0.16%	15.40%	HTLGENIADNGGLK	4.21	1,438.73
ATP	6011	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	8	10	15	0.16%	15.40%	NEIVFPAGILQAPFYTR	4.85	1,936.03
ATP	6011	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	8	10	15	0.16%	15.40%	TPESSHEGLITDPHSPSR	4.79	1,946.92
ATP	6011	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	8	10	15	0.16%	15.40%	VFNDYTAVPDLYFENAMR	3.45	2,181.00

ATP	6011	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	8	10	15	0.16%	15.40%	VLTGYLNYMVQLGK	3.61	1,614.86
ATP	6011	RecName: Full=60S ribosomal protein L5	gi|108862056,gi|119900687,gi|119905361,gi|61552973,gi|75775327,gi|78369655	34,262.40	99.80%	2	2	2	0.02%	8.75%	GAVDGGLSIPHSTK	2.24	1,338.70
ATP	6011	RecName: Full=60S ribosomal protein L5	gi|108862056,gi|119900687,gi|119905361,gi|61552973,gi|75775327,gi|78369655	34,262.40	99.80%	2	2	2	0.02%	8.75%	YLIEEDEDAYKK	3.08	1,515.72
ATP	6011	secretory carrier membrane protein 3 isoform 1	gi|61553277,gi|71649517,gi|73586519,gi|78369651	38,348.80	99.80%	2	2	2	0.02%	10.40%	AQQEFAAGVFSNPAVR	4.19	1,691.85
ATP	6011	secretory carrier membrane protein 3 isoform 1	gi|61553277,gi|71649517,gi|73586519,gi|78369651	38,348.80	99.80%	2	2	2	0.02%	10.40%	NYGSYSTQASTAAATAELLK	5.84	2,047.00
ATP	6011	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	5	7	14	0.15%	23.10%	GHAAPTPTPVKPPR	3.39	1,425.80
ATP	6011	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	5	7	14	0.15%	23.10%	LATMLETLR	3	1,063.58
ATP	6011	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	5	7	14	0.15%	23.10%	LEANHGLLVAR	3.11	1,192.68
ATP	6011	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	5	7	14	0.15%	23.10%	RIQSNLGALSR	3.14	1,214.70
ATP	6011	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	5	7	14	0.15%	23.10%	SHDTTSNTLAQLLAK	5.17	1,599.83
ATP	6011	vacuolar system associated protein-60	gi|1215746,gi|152941134,gi|2493459,gi|33340013,gi|41386727,gi|74356454	60,133.40	99.80%	2	3	5	0.05%	4.50%	SLEDQVEVLR	2.76	1,187.63

ATP	6011	vacuolar system associated protein-60	gi|1215746,gi|152941134,gi|2493459,gi|33340013,gi|41386727,gi|74356454	60,133.40	99.80%	2	3	5	0.05%	4.50%	TLKEEAEKPEEAAK	2.53	1,572.81
ATP	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	137	1.49%	56.30%	DAVTYTEHAK	2.35	1,134.54
ATP	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	137	1.49%	56.30%	DNIQGITKPAIR	3	1,325.75
ATP	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	137	1.49%	56.30%	ISGLIYEETR	4.17	1,180.62
ATP	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	137	1.49%	56.30%	KTVTAMDVVYALK	4.78	1,438.80
ATP	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	137	1.49%	56.30%	KTVTAMDVVYALKR	5.23	1,610.89
ATP	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	137	1.49%	56.30%	RISGLIYEETR	3.09	1,336.72

ATP	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	137	1.49%	56.30%	TVTAMDVVYALK	3.53	1,326.70
ATP	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	137	1.49%	56.30%	TVTAMDVVYALKR	3.9	1,482.80
ATP	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	137	1.49%	56.30%	VFLENVIR	3.08	989.5778
ATP	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	137	1.49%	56.30%	VFLENVIRDAVTYTEHAK	5.38	2,105.10
ATP	6011	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	17	137	1.49%	56.30%	VLRDNIQGITKPAIR	3.03	1,694.01
ATP	6011	RecName: Full=Cleft lip and palate transmembrane protein 1 homolog	gi|110278913,gi|114051439,gi|84708720	75,864.60	99.80%	2	2	2	0.02%	2.39%	NLLTGETEADPEMIK	3.09	1,676.81
ATP	6011	RecName: Full=Cleft lip and palate transmembrane protein 1 homolog	gi|110278913,gi|114051439,gi|84708720	75,864.60	99.80%	2	2	2	0.02%	2.39%	NLLTGETEADPEMIKR	3.44	1,832.91

ATP	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	16	24	0.26%	24.40%	AVDEAADALLK	2.53	1,115.59
ATP	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	16	24	0.26%	24.40%	ELDSITPEVLPGWK	3.47	1,583.83
ATP	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	16	24	0.26%	24.40%	KAVDEAADALLK	3.49	1,243.69
ATP	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	16	24	0.26%	24.40%	LAEQELQFR	2.92	1,133.60
ATP	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	16	24	0.26%	24.40%	LSQEQVDNFTLDINTAYAR	2.14	2,198.07
ATP	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	16	24	0.26%	24.40%	MKTASADLPTVPLGSAVEAIR	3.95	2,143.14
ATP	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	16	24	0.26%	24.40%	QHIALALEK	4.04	1,022.60
ATP	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	16	24	0.26%	24.40%	QKGDTSASTTAGDTLSVPAPVVQHEELIK	3.61	2,979.53
ATP	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	16	24	0.26%	24.40%	SVIENAKKEEVAGAK	3.16	1,572.86
ATP	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	16	24	0.26%	24.40%	TASADLPTVPLGSAVEAIR	4.39	1,868.01
ATP	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	16	24	0.26%	24.40%	TDHPETGEGKPKPATSEEASSTSVR	4.01	2,598.23
ATP	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	16	24	0.26%	24.40%	VQEQELKYEFEQDLSEK	3.59	2,142.02
ATP	6011	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	13	16	24	0.26%	24.40%	VVSQYHELVVQAR	4.67	1,527.83
ATP	6011	SCARB2 protein	gi|151556135,gi|156120953	53,968.70	99.80%	2	2	3	0.03%	6.49%	GQGSTDEGTADERAPLIR	2.56	1,872.90

ATP	6011	SCARB2 protein	gi|151556135,gi|156120953	53,968.70	99.80%	2	2	3	0.03%	6.49%	HDVSPYFGLFYGK	3.46	1,529.74
ATP	6011	Chromosome 1 open reading frame 77 ortholog	gi|74354304,gi|78369392,gi|85540961	26,409.90	99.80%	2	2	2	0.02%	11.70%	EQLDNQLDAYMSK	3.5	1,570.71
ATP	6011	Chromosome 1 open reading frame 77 ortholog	gi|74354304,gi|78369392,gi|85540961	26,409.90	99.80%	2	2	2	0.02%	11.70%	LAQQMENRPSVQAALK	2.76	1,799.94
ATP	6011	ATAD1 protein	gi|154426126,gi|76671592	41,750.40	99.80%	2	3	3	0.03%	11.40%	EYVNSTSEESHDEDEIRPVQQQDLHR	3.28	3,140.42
ATP	6011	ATAD1 protein	gi|154426126,gi|76671592	41,750.40	99.80%	2	3	3	0.03%	11.40%	LQPSIIFIDEIDSFLR	3.51	1,906.03
ATP	6011	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	4	6	6	0.07%	20.80%	GLFTGLTPR	2.27	961.5467
ATP	6011	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	4	6	6	0.07%	20.80%	QVCQLPGLFCYAQHIASIDGKR	2.86	2,447.23
ATP	6011	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	4	6	6	0.07%	20.80%	SAATLITHPFHVITLR	2.38	1,777.01
ATP	6011	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	4	6	6	0.07%	20.80%	VLIQVGYEPLAPTVGR	3.67	1,711.97
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	AAALRPEEDGAFRPSEAFETLQK	2.89	2,533.27
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	AEESAAHLPEEIR	2.67	1,451.71

ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	AEESAAHLPEEIR	2.84	1,607.81
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	ASVGQVESDLK	3.36	1,132.58
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	DFTSLENTVEER	2.85	1,439.66
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	DLSDGIHVVK	2.65	1,082.58
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	EAADSEHHTLQALTEK	3.64	1,779.85
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	EELGQGLQGVEQK	3.87	1,414.72
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	ELVSLKQEQQR	3.57	1,357.74
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	ERDFTSLENTVEER	4.13	1,724.81

ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	EVVKEIQTSVK	3.26	1,259.72
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	FKEAADSEHHTLQALTEK	4.28	2,055.01
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	GLGEAQLSLAGDVDELK	5.13	1,714.89
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	GLGEAQLSLAGDVDELKR	3.3	1,870.99
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	GLLEDLRNDLDR	2.32	1,428.74
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	GLLEDLRNDLDRLFVK	2.16	1,916.06
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	IETNENNLESAK	3.23	1,361.65
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	ILRAEESAAHLPEEIR	3.04	1,833.98

ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	LEEELGQLK	2.94	1,058.57
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	LQNEILKDLSDGIHVVK	5.61	1,921.08
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	LQSVEDGVQAAR	3.61	1,272.65
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	QREELGQGLQGVEQK	2.7	1,698.88
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	RLEEELGQLK	3.49	1,214.67
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	SINDNIAIFTDVQK	5.02	1,577.82
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	STIQTMESDVYTEVK	3.75	1,746.81
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	STIQTMESDVYTEVKELVSLKQEQQR	2.97	3,085.54

ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	TAVDSLVAYSVK	3.82	1,252.68
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	VQEQVHTLLGR	3.04	1,279.71
ATP	6011	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	38	80	0.87%	46.20%	VQSLQATFGTFESLVR	5.82	1,782.94
ATP	6011	similar to peptidylprolyl isomerase A (cyclophilin A)	gi|28189771,gi|58760424,gi|75948300	17,851.80	100.00%	3	4	4	0.04%	16.50%	FDDENFILK	2.56	1,140.56
ATP	6011	similar to peptidylprolyl isomerase A (cyclophilin A)	gi|28189771,gi|58760424,gi|75948300	17,851.80	100.00%	3	4	4	0.04%	16.50%	SIYGEKFDDENFILK	4.3	1,817.90
ATP	6011	similar to peptidylprolyl isomerase A (cyclophilin A)	gi|28189771,gi|58760424,gi|75948300	17,851.80	100.00%	3	4	4	0.04%	16.50%	VSFELFADKVPK	3.45	1,379.76
ATP	6011	Clusterin	gi|109939936,gi|116530,gi|146231734,gi|151555910,gi|163115,gi|27806907	51,096.70	100.00%	4	4	5	0.05%	9.11%	KLLLSSLEEAK	2.47	1,230.73
ATP	6011	Clusterin	gi|109939936,gi|116530,gi|146231734,gi|151555910,gi|163115,gi|27806907	51,096.70	100.00%	4	4	5	0.05%	9.11%	KLLLSSLEEAKK	4.26	1,358.83
ATP	6011	Clusterin	gi|109939936,gi|116530,gi|146231734,gi|151555910,gi|163115,gi|27806907	51,096.70	100.00%	4	4	5	0.05%	9.11%	LYDQLLQSYQQK	4.15	1,526.79

ATP	6011	Clusterin	gi|109939936,gi|116530,gi|146231734,gi|151555910,gi|163115,gi|27806907	51,096.70	100.00%	4	4	5	0.05%	9.11%	RPQDTQYYSPFSSFPR	3.84	1,975.93
ATP	6011	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	3	3	4	0.04%	18.70%	KQYDSYTFTASK	3.73	1,438.68
ATP	6011	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	3	3	4	0.04%	18.70%	SVIDYQTHFR	2.76	1,265.63
ATP	6011	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	3	3	4	0.04%	18.70%	TVYFDFQVGEDPPLFPSENR	3.26	2,357.11
ATP	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	23	0.25%	61.00%	AAELIANSLATAGDGLIELR	5.2	1,998.09
ATP	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	23	0.25%	61.00%	AATFGLILDDVSLTHLTFGK	2.79	2,119.14
ATP	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	23	0.25%	61.00%	DLQNVNITLR	4.09	1,185.66
ATP	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	23	0.25%	61.00%	FDAGELITQR	4.08	1,149.59
ATP	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	23	0.25%	61.00%	FGLALAVAGGVVNSALYNVDAGHR	4.75	2,371.25
ATP	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	23	0.25%	61.00%	IFTSIGEDYDER	3.43	1,444.66
ATP	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	23	0.25%	61.00%	ILFRPVASQLPR	2.8	1,396.84
ATP	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	23	0.25%	61.00%	KLEAAEDIAYQLSR	5.37	1,606.84
ATP	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	23	0.25%	61.00%	NITYLPAGQSVLLQLPQ	4.45	1,855.03
ATP	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	23	0.25%	61.00%	QVAQQEAERARFVVEK	2.98	1,888.00
ATP	6011	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	23	0.25%	61.00%	VLPSITTEILK	2.76	1,213.74
ATP	6011	ras-related C3 botulinum toxin substrate 1	gi|27806443,gi|51702785,gi|6007014,gi|73587375	21,432.60	99.90%	2	4	4	0.04%	7.81%	KLTPITYPQGLAMAK	2.53	1,647.91

ATP	6011	ras-related C3 botulinum toxin substrate 1	gi|27806443,gi|51702785,gi|6007014,gi|73587375	21,432.60	99.90%	2	4	4	0.04%	7.81%	LTPITYPQGLAMAK	3.61	1,519.82
ATP	6011	Interferon induced transmembrane protein 1 (9-27)	gi|112362418,gi|118151192,gi|118151350,gi|118151354,gi|119919513,gi|14279576,gi|14279578,gi|148744152,gi|32480628,gi|73586549,gi|73587371	13,631.00	99.80%	2	2	3	0.03%	13.70%	KMVGDITGAQSYASTAK	3.87	1,743.86
ATP	6011	Interferon induced transmembrane protein 1 (9-27)	gi|112362418,gi|118151192,gi|118151350,gi|118151354,gi|119919513,gi|14279576,gi|14279578,gi|148744152,gi|32480628,gi|73586549,gi|73587371	13,631.00	99.80%	2	2	3	0.03%	13.70%	MVGDITGAQSYASTAK	5.75	1,615.76
ATP	6011	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	6	8	8	0.09%	51.90%	ALAAAGYDVEK	3.09	1,107.57
ATP	6011	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	6	8	8	0.09%	51.90%	ALAAAGYDVEKNNSR	4.17	1,578.79
ATP	6011	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	6	8	8	0.09%	51.90%	ASGPPVSELITK	3.35	1,198.67

ATP	6011	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	6	8	8	0.09%	51.90%	KASGPPVSELITK	2.9	1,326.76
ATP	6011	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	6	8	8	0.09%	51.90%	SETAPAAPAAAPPAEK	3.42	1,478.75
ATP	6011	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	6	8	8	0.09%	51.90%	SGVSLAALKK	3.19	973.6041
ATP	6011	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	3	3	3	0.03%	14.20%	ILHVNGFNGEGGEEDPQAAR	3.76	2,110.00
ATP	6011	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	3	3	3	0.03%	14.20%	LLLLGAGESGK	3.54	1,057.63
ATP	6011	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	3	3	3	0.03%	14.20%	YFIRDEFLR	1.88	1,258.66
ATP	6011	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	3	3	3	0.03%	14.20%	YTTPEDATPEPGEDPR	2.88	1,774.78
ATP	6011	PREDICTED: similar to Transmembrane 9 superfamily member 2 precursor (p76), partial	gi|194671915	72,962.00	100.00%	3	4	5	0.05%	4.40%	IYYHVVETGSMGAR	4.22	1,598.76
ATP	6011	PREDICTED: similar to Transmembrane 9 superfamily member 2 precursor (p76), partial	gi|194671915	72,962.00	100.00%	3	4	5	0.05%	4.40%	PSENLGQVLFGER	4.25	1,445.74

ATP	6011	PREDICTED: similar to Transmembrane 9 superfamily member 2 precursor (p76), partial	gi|194671915	72,962.00	100.00%	3	4	5	0.05%	4.40%	RPSENLGQVLFGER	4.21	1,601.84
ATP	6011	interferon stimulated gene 17 [Ovis aries]	gi|12082402,gi|57619183	17,482.10	100.00%	3	3	3	0.03%	22.90%	EVLQEGVPLVHQGLK	3.96	1,645.93
ATP	6011	interferon stimulated gene 17 [Ovis aries]	gi|12082402,gi|57619183	17,482.10	100.00%	3	3	3	0.03%	22.90%	INVPAFQQR	2.79	1,072.59
ATP	6011	interferon stimulated gene 17 [Ovis aries]	gi|12082402,gi|57619183	17,482.10	100.00%	3	3	3	0.03%	22.90%	MLGGEEILVPLR	2.4	1,342.74
ATP	6011	UPF0404 protein C11orf59 homolog	gi|122140364,gi|74267677,gi|77736483	17,713.10	99.80%	2	2	2	0.02%	26.70%	LPPLPSLTSQPHQVLASEPVPFSDLQQVSR	5.1	3,267.74
ATP	6011	UPF0404 protein C11orf59 homolog	gi|122140364,gi|74267677,gi|77736483	17,713.10	99.80%	2	2	2	0.02%	26.70%	TDEQALLSSILAK	3.92	1,388.76
ATP	6011	Nucleobindin 2	gi|113912161,gi|115496067	49,171.70	99.80%	2	2	2	0.02%	8.19%	LHDVNSDGFLDEQELEALFTK	3.76	2,420.16
ATP	6011	Nucleobindin 2	gi|113912161,gi|115496067	49,171.70	99.80%	2	2	2	0.02%	8.19%	QVIDVLETDSHFR	3.39	1,558.79
ATP	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	11	11	13	0.14%	20.40%	AEVQNLGGELVVSGVDSAMSLIQAAK	4.03	2,602.34
ATP	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	11	11	13	0.14%	20.40%	AIMAQLPQEQK	3.16	1,272.66
ATP	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	11	11	13	0.14%	20.40%	ALKPEVDKLNIMAAK	2.64	1,656.94
ATP	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	11	11	13	0.14%	20.40%	ESQFLKEELVAAVEDVRK	4.26	2,090.11
ATP	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	11	11	13	0.14%	20.40%	IAEQVASFQEEK	3.31	1,378.68

ATP	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	11	11	13	0.14%	20.40%	NAGTEQDLGIQYK	3.06	1,436.70
ATP	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	11	11	13	0.14%	20.40%	NLMNAVVQTVK	3.33	1,232.67
ATP	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	11	11	13	0.14%	20.40%	QIIVDPLSFSEER	2.96	1,532.80
ATP	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	11	11	13	0.14%	20.40%	TSVQTEDDQLIAGQSAR	3.85	1,818.88
ATP	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	11	11	13	0.14%	20.40%	VIHVVTSEMDNYEPGVYTEK	4.51	2,326.09
ATP	6011	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	11	11	13	0.14%	20.40%	VLTDAVDDITSIDDFLAVSENHILEDVNK	4.51	3,200.58
ATP	6011	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	gi|111304648,gi|115496338,gi|121957506	27,838.90	99.80%	2	4	6	0.07%	11.20%	FKGPFTDVVTTNLK	4.52	1,566.85
ATP	6011	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	gi|111304648,gi|115496338,gi|121957506	27,838.90	99.80%	2	4	6	0.07%	11.20%	GPFTDVVTTNLK	4.06	1,291.69
ATP	6011	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	gi|111304648,gi|115496338,gi|121957506	27,838.90	99.80%	2	4	6	0.07%	11.20%	HEQILVLDPPTDLK	4.28	1,617.89

ATP	6011	RecName: Full=Transmembrane and coiled-coil domain-containing protein 1	gi|109895213,gi|74354058,gi|77736477	21,158.30	99.90%	2	2	2	0.02%	15.40%	LPFTPLSYIQGLSHR	4	1,728.94
ATP	6011	RecName: Full=Transmembrane and coiled-coil domain-containing protein 1	gi|109895213,gi|74354058,gi|77736477	21,158.30	99.90%	2	2	2	0.02%	15.40%	QAGGFLGPPPPSGK	2.8	1,309.69
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	AKFEELNMDLFR	4.48	1,528.75
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	DAGTIAGLNVMR	3.83	1,233.63
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	DNHLLGTFDLTGIPPAPR	2.7	1,934.01
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	ELEEIVQPIISK	4.06	1,397.79
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	FEELNMDLFR	3.3	1,329.61
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	IDTRNELESYAYSLK	3.43	1,801.90

ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	IEIESFYEGEDFSETLTR	4.27	2,164.99
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	IINEPTAAAIAYGLDK	4.5	1,659.90
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	IINEPTAAAIAYGLDKR	3.18	1,816.00
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	ITPSYVAFTPEGER	3.45	1,566.78
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	KKELEEIVQPIISK	3.93	1,653.98
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	MKETAEAYLGKK	3.66	1,384.71
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	MVNDAEKFAEEDKK	3.25	1,669.77
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	NELESYAYSLK	2.94	1,316.64

ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	NQLTSNPENTVFDAK	4.76	1,677.81
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	NQLTSNPENTVFDAKR	4.17	1,833.91
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	SDIDEIVLVGGSTR	2.84	1,460.76
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	SQIFSTASDNQPTVTIK	3.82	1,836.93
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	TFAPEEISAMVLTK	3.24	1,552.79
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	TKPYIQVDVGGGQTK	4.26	1,590.85
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	VLEDSDLKKSDIDEIVLVGGSTR	5.92	2,488.31
ATP	6011	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	22	29	45	0.49%	37.90%	VTHAVVTVPAYFNDAQR	4.03	1,887.97

ATP	6011	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	8	9	10	0.11%	18.40%	ALMGSPQLVAAVVR	3.55	1,427.80
ATP	6011	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	8	9	10	0.11%	18.40%	LLNDEDPVVVTK	2.87	1,341.73
ATP	6011	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	8	9	10	0.11%	18.40%	LNTIPLFVQLLYSSVENIQR	4.37	2,347.30
ATP	6011	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	8	9	10	0.11%	18.40%	LNYGIPAIVK	2.47	1,087.65
ATP	6011	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	8	9	10	0.11%	18.40%	MLSSPVESVLFYAITTLHNLLLYQEGAK	3.85	3,153.65
ATP	6011	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	8	9	10	0.11%	18.40%	NLSDVATKQEGLESVLK	2.87	1,830.98

ATP	6011	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	8	9	10	0.11%	18.40%	SAIVHLINYQDDAELATR	4.31	2,029.04
ATP	6011	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	8	9	10	0.11%	18.40%	TLVTQNSGVEALIHAILR	2.87	1,935.10
ATP	6011	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	23.80%	AALVDLEPGTMDSVR	3.83	1,589.78
ATP	6011	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	23.80%	GHYTEGAELVDSVLDVVR	3.5	1,958.98
ATP	6011	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	23.80%	GHYTEGAELVDSVLDVVRK	3.56	2,087.08
ATP	6011	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	23.80%	LAVNMVPFPR	3.53	1,159.63
ATP	6011	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	23.80%	LHFFMPGFAPLTAR	3.35	1,620.84
ATP	6011	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	23.80%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	4.25	4,479.06
ATP	6011	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	99.80%	2	2	2	0.02%	23.80%	YLTVAAVFR	2.56	1,039.59
ATP	6011	RecName: Full=60S ribosomal protein L11	gi|108860925,gi|115497634,gi|74268362	20,235.20	99.80%	2	2	2	0.02%	12.90%	VLEQLTGQTPVFSK	4.33	1,546.85
ATP	6011	RecName: Full=60S ribosomal protein L11	gi|108860925,gi|115497634,gi|74268362	20,235.20	99.80%	2	2	2	0.02%	12.90%	YDGIILPGK	2.54	975.5512
ATP	6011	syntaxin 7	gi|118150840,gi|122140829,gi|73586654	29,638.60	99.80%	2	2	2	0.02%	10.70%	EFGSLPTTPSDQR	2.33	1,434.69
ATP	6011	syntaxin 7	gi|118150840,gi|122140829,gi|73586654	29,638.60	99.80%	2	2	2	0.02%	10.70%	TLNQLGTPQDSPELR	4.05	1,668.86

ATP	6011	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	4	5	8	0.09%	19.60%	GDLLFLTNR	2.97	1,048.58
ATP	6011	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	4	5	8	0.09%	19.60%	GDLLFLTNRVEDPIR	3.76	1,757.95
ATP	6011	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	4	5	8	0.09%	19.60%	MLSLDFLDDVRR	2.24	1,495.76
ATP	6011	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	4	5	8	0.09%	19.60%	VGEIVVFR	2.88	918.5407
ATP	6011	PREDICTED: brain protein 44	gi|119889010,gi|194665199	14,264.40	99.80%	2	4	6	0.07%	18.90%	LRPLYNHPAGPR	3.3	1,390.77
ATP	6011	PREDICTED: brain protein 44	gi|119889010,gi|194665199	14,264.40	99.80%	2	4	6	0.07%	18.90%	VLDKVELLLPEK	3.59	1,395.85
ATP	6011	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	8	10	13	0.14%	16.60%	EDFESLLHSAK	3.29	1,275.62
ATP	6011	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	8	10	13	0.14%	16.60%	FLVVLNFGDVGQLAR	4.15	1,647.92
ATP	6011	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	8	10	13	0.14%	16.60%	FTGLSKEELLK	3.08	1,264.71
ATP	6011	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	8	10	13	0.14%	16.60%	LLIAGTDSSDLQQILR	4.52	1,742.97
ATP	6011	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	8	10	13	0.14%	16.60%	NQEDDLTETNLEQIDPIFGSK	4.78	2,406.13
ATP	6011	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	8	10	13	0.14%	16.60%	NQEDDLTETNLEQIDPIFGSKEDFESLLHSAK	3.71	3,662.73
ATP	6011	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	8	10	13	0.14%	16.60%	VDLLLSTQPGR	3.45	1,198.68

ATP	6011	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	8	10	13	0.14%	16.60%	VILDLTPNYK	3.2	1,175.67
ATP	6011	MHC class I antigen	gi|84095083	40,657.50	100.00%	6	8	59	0.64%	19.30%	DYIALNEDLR	3.77	1,221.61
ATP	6011	MHC class I antigen	gi|84095083	40,657.50	100.00%	6	8	59	0.64%	19.30%	FIAVGYVDDTQFVR	4.62	1,629.83
ATP	6011	MHC class I antigen	gi|84095083	40,657.50	100.00%	6	8	59	0.64%	19.30%	VQHEGLQEPLTLR	4.18	1,519.82
ATP	6011	MHC class I antigen	gi|84095083	40,657.50	100.00%	6	8	59	0.64%	19.30%	WAALVVPSGEEQR	3.12	1,441.74
ATP	6011	MHC class I antigen	gi|84095083	40,657.50	100.00%	6	8	59	0.64%	19.30%	YFYTAVSR	2.48	1,006.50
ATP	6011	MHC class I antigen	gi|84095083	40,657.50	100.00%	6	8	59	0.64%	19.30%	YLENGKDTLLR	3.32	1,321.71
ATP	6011	DDRGK domain containing 1	gi|115496153,gi|94534940	35,649.00	99.80%	2	2	2	0.02%	9.58%	FIYITPEELAAVANFIR	5.32	1,967.06
ATP	6011	DDRGK domain containing 1	gi|115496153,gi|94534940	35,649.00	99.80%	2	2	2	0.02%	9.58%	LRLEEEQKEEEER	2.6	1,716.84
ATP	6011	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	99.80%	2	2	2	0.02%	3.38%	ALLELQLEPEELYQTFQR	4.59	2,220.15
ATP	6011	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	99.80%	2	2	2	0.02%	3.38%	VFSGLVSTGLK	2.62	1,107.64
ATP	6011	RecName: Full=Synaptic glycoprotein SC2; AltName: Full=Trans-2,3-enoyl-CoA reductase; Short=TER	gi|122140918,gi|73586600,gi|77736441	36,056.10	99.80%	2	2	2	0.02%	7.14%	LPVGTTATLYFR	3.36	1,338.74

ATP	6011	RecName: Full=Synaptic glycoprotein SC2; AltName: Full=Trans-2,3-enoyl-CoA reductase; Short=TER	gi|122140918,gi|73586600,gi|77736441	36,056.10	99.80%	2	2	2	0.02%	7.14%	SLKDEDVLQK	2.43	1,174.63
ATP	6011	RecName: Full=Galectin-9	gi|122145068,gi|59858325,gi|62751460,gi|75775171,gi|87044899	39,329.70	99.80%	2	2	3	0.03%	9.30%	NLPAINNLEVGGDIQLTHVQT	5.39	2,246.18
ATP	6011	RecName: Full=Galectin-9	gi|122145068,gi|59858325,gi|62751460,gi|75775171,gi|87044899	39,329.70	99.80%	2	2	3	0.03%	9.30%	SGSDIAFHLNPR	2.77	1,313.66
ATP	6011	PREDICTED: similar to Calpain-5 (nCL-3) (htra-3) isoform 1	gi|76636134	72,988.00	99.80%	2	2	2	0.02%	5.16%	ANADDLQALHTLHLR	2.85	1,687.89
ATP	6011	PREDICTED: similar to Calpain-5 (nCL-3) (htra-3) isoform 1	gi|76636134	72,988.00	99.80%	2	2	2	0.02%	5.16%	VLFEDPNFPATDDSLYYK	3.95	2,134.00
ATP	6011	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	4	4	5	0.05%	28.20%	AVEFQEAQAYAEDNSLLFMETSAK	3.11	2,708.24
ATP	6011	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	4	4	5	0.05%	28.20%	GVDLQENNPASR	3.35	1,299.63
ATP	6011	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	4	4	5	0.05%	28.20%	LVLLGESAVGK	3.36	1,085.66
ATP	6011	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	4	4	5	0.05%	28.20%	QASPNIVIALAGNK	2.8	1,395.80

ATP	6011	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	7	16	0.17%	32.70%	ELNVMFIETSAK	3.68	1,397.70
ATP	6011	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	7	16	0.17%	32.70%	GSDVIIMLVGNK	3.33	1,261.68
ATP	6011	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	7	16	0.17%	32.70%	GSDVIIMLVGNKTDLADKR	2.55	2,061.10
ATP	6011	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	7	16	0.17%	32.70%	LQLWDTAGQER	2.72	1,316.66
ATP	6011	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	7	16	0.17%	32.70%	LVFLGEQSVGK	2.74	1,176.66
ATP	6011	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	7	16	0.17%	32.70%	RVAAALPGMESTQDR	2.93	1,617.80
ATP	6011	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	7	16	0.17%	32.70%	VAAALPGMESTQDR	2.68	1,461.70

ATP	6011	Chain F, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Oxidized State	gi|149241541,gi|149241554,gi|149241571,gi|149241584,gi|149241601,gi|149241614	10,651.90	100.00%	3	3	3	0.03%	30.60%	ASGGGVPTDEEQATGLER	3.78	1,773.83
ATP	6011	Chain F, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Oxidized State	gi|149241541,gi|149241554,gi|149241571,gi|149241584,gi|149241601,gi|149241614	10,651.90	100.00%	3	3	3	0.03%	30.60%	GQDPYNILAPK	3.16	1,215.64
ATP	6011	Chain F, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Oxidized State	gi|149241541,gi|149241554,gi|149241571,gi|149241584,gi|149241601,gi|149241614	10,651.90	100.00%	3	3	3	0.03%	30.60%	KGQDPYNILAPK	2.81	1,343.73
ATP	6011	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	4	0.04%	27.10%	DLTDYLMK	2.34	1,014.48
ATP	6011	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	4	0.04%	27.10%	GYSFTTTAER	3.61	1,132.53
ATP	6011	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	4	0.04%	27.10%	HQGVMVGMGQKDCYVGDEAQSK	2.8	2,383.05

ATP	6011	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	4	0.04%	27.10%	HQGVMVGMGQKDCYVGDEAQSKR	2.79	2,539.15
ATP	6011	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	4	0.04%	27.10%	IKIIAPPER	2.45	1,036.65
ATP	6011	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	4	0.04%	27.10%	LDLAGRDLTDYLMK	3	1,639.84
ATP	6011	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	4	0.04%	27.10%	SYELPDGQVITIGNER	4.26	1,790.89
ATP	6011	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	4	0.04%	27.10%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	5.42	3,183.61
ATP	6011	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	gi|27806197,gi|3676399,gi|71153779,gi|73586683	29,157.00	100.00%	2	3	6	0.07%	15.70%	AAFDDAIAELDTLSEESYKDSTLIMQLLR	4.79	3,274.60
ATP	6011	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	gi|27806197,gi|3676399,gi|71153779,gi|73586683	29,157.00	100.00%	2	3	6	0.07%	15.70%	EAAENSLVAYK	2.22	1,194.60

ATP	6011	RecName: Full=Coiled-coil domain-containing protein 56	gi|108935963,gi|74268043,gi|77736311	11,689.70	99.80%	2	2	2	0.02%	20.80%	EKLTPAQLQFMR	2.73	1,477.78
ATP	6011	RecName: Full=Coiled-coil domain-containing protein 56	gi|108935963,gi|74268043,gi|77736311	11,689.70	99.80%	2	2	2	0.02%	20.80%	FLDELEDEAK	3.13	1,208.57
ATP	6011	proteasome activator 28 alpha subunit	gi|63139650,gi|73921836,gi|86821522,gi|91680535	28,675.80	99.80%	2	2	2	0.02%	10.40%	APLDIPVPDPVKEK	2.44	1,517.86
ATP	6011	proteasome activator 28 alpha subunit	gi|63139650,gi|73921836,gi|86821522,gi|91680535	28,675.80	99.80%	2	2	2	0.02%	10.40%	QLVHELDEAEYR	2.38	1,501.73
ATP	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	13	17	0.19%	13.50%	GAAMVTAVAYR	3.27	1,125.57
ATP	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	13	17	0.19%	13.50%	GDFIALDLGGSSFR	3.29	1,454.73
ATP	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	13	17	0.19%	13.50%	GKFNTSDVSAIEK	3.99	1,395.71
ATP	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	13	17	0.19%	13.50%	LSDETLLDIMNR	4.01	1,435.71
ATP	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	13	17	0.19%	13.50%	LVDEFSLNSGK	3.01	1,208.62
ATP	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	13	17	0.19%	13.50%	QIEETLAHFSLTK	3.68	1,516.80
ATP	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	13	17	0.19%	13.50%	SANLVAATLGAILSR	4.49	1,456.85
ATP	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	13	17	0.19%	13.50%	SIPDGSEKGDFIALDLGGSSFR	3.47	2,268.11
ATP	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	13	17	0.19%	13.50%	TTVGVDGSLYK	2.73	1,139.59
ATP	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	13	17	0.19%	13.50%	YLSQIESDR	2.33	1,110.54
ATP	6011	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	13	17	0.19%	13.50%	YLSQIESDRLALLQVR	2.36	1,904.06

ATP	6011	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	3	4	5	0.05%	5.19%	DIQGSLQDIFK	3.24	1,263.66
ATP	6011	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	3	4	5	0.05%	5.19%	INENTGSVSVTR	3.43	1,276.65
ATP	6011	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	3	4	5	0.05%	5.19%	SIVVSPILIPENQR	3.85	1,564.91
ATP	6011	EGF, latrophilin and seven transmembrane domain containing 1	gi|115305144,gi|116004035	77,458.50	100.00%	3	3	5	0.05%	4.35%	HIEEPVALLR	2.38	1,176.67
ATP	6011	EGF, latrophilin and seven transmembrane domain containing 1	gi|115305144,gi|116004035	77,458.50	100.00%	3	3	5	0.05%	4.35%	LIHTAEQATLR	3.76	1,252.70
ATP	6011	EGF, latrophilin and seven transmembrane domain containing 1	gi|115305144,gi|116004035	77,458.50	100.00%	3	3	5	0.05%	4.35%	VTFTLSHIK	2.69	1,045.60
ATP	6011	PREDICTED: similar to programmed cell death 8 isoform 2	gi|76658657	66,854.50	99.80%	2	2	2	0.02%	4.89%	ISGLGLTPEEK	3.71	1,143.63
ATP	6011	PREDICTED: similar to programmed cell death 8 isoform 2	gi|76658657	66,854.50	99.80%	2	2	2	0.02%	4.89%	VLIVSEDPELPYMRPPLSK	2.78	2,199.17

ATP	6011	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	8	11	13	0.14%	19.80%	FAIQTDPNSNDGLVTVVKPIDFETNR	3.48	2,890.46
ATP	6011	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	8	11	13	0.14%	19.80%	FLEAGIYEVPIIITDSGNPPK	3.84	2,273.21
ATP	6011	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	8	11	13	0.14%	19.80%	GPFPQELVR	2.27	1,042.57

ATP	6011	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	8	11	13	0.14%	19.80%	MYVLTVAAENQVPLAK	3.31	1,762.94
ATP	6011	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	8	11	13	0.14%	19.80%	QLLIDPEDDVRDNILK	2.03	1,896.01
ATP	6011	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	8	11	13	0.14%	19.80%	SAAPHPGDIGDFINEGLK	4.6	1,837.91

ATP	6011	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	8	11	13	0.14%	19.80%	YDEEGGGEEDQDYDLSQLQQPDTVEPDAIKPVGIR	6.43	3,905.78
ATP	6011	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	8	11	13	0.14%	19.80%	YSVTGPGADQPPTGIFIINPISGQLSVTKPLDR	3.86	3,438.83
ATP	6011	mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor	gi|61553497,gi|70778822,gi|73919274,gi|83638650	31,226.90	99.80%	2	2	2	0.02%	11.70%	AQFGQPEILIGTIPGAGGTQR	4.91	2,111.12
ATP	6011	mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor	gi|61553497,gi|70778822,gi|73919274,gi|83638650	31,226.90	99.80%	2	2	2	0.02%	11.70%	NSNVGLIQLNRPK	3.74	1,452.83
ATP	6011	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	100.00%	4	5	12	0.13%	56.30%	ELAEAQEDTILK	4.28	1,359.70
ATP	6011	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	100.00%	4	5	12	0.13%	56.30%	IERELAEAQEDTILK	3.93	1,757.93

ATP	6011	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	100.00%	4	5	12	0.13%	56.30%	MVPPVQVSPLIK	2.18	1,323.77
ATP	6011	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	100.00%	4	5	12	0.13%	56.30%	YSALFLGMAYGAK	4.17	1,407.70
ATP	6011	DnaJ (Hsp40) homolog, subfamily C, member 19	gi|73587098,gi|77735867,gi|83305915	12,481.10	99.80%	2	2	2	0.02%	27.60%	EAALILGVSPTANK	3.02	1,383.78
ATP	6011	DnaJ (Hsp40) homolog, subfamily C, member 19	gi|73587098,gi|77735867,gi|83305915	12,481.10	99.80%	2	2	2	0.02%	27.60%	IMLLNHPDKGGSPYIAAK	3.58	1,941.03
ATP	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	13	15	0.16%	31.60%	FLESGGQDGAGDDDDLEDLEEAEEPDLEEDDDQK	4.81	3,739.49
ATP	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	13	15	0.16%	31.60%	FLESGGQDGAGDDDDLEDLEEAEEPDLEEDDDQKAVKDEL	6.33	4,394.84
ATP	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	13	15	0.16%	31.60%	GNFDEALAAHK	3.1	1,172.57
ATP	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	13	15	0.16%	31.60%	HNQLPLVIEFTEQTAPK	4.39	1,965.04
ATP	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	13	15	0.16%	31.60%	ILEFFGLK	1.99	966.566
ATP	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	13	15	0.16%	31.60%	ILFIFIDSDHTDNQR	1.85	1,833.91
ATP	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	13	15	0.16%	31.60%	LITLEEEMTK	2.47	1,222.62
ATP	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	13	15	0.16%	31.60%	NFEEVAFDEKK	3.72	1,355.65
ATP	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	13	15	0.16%	31.60%	QFLLAAEAIDDIPFGITSNSDVFSK	4.45	2,698.36
ATP	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	13	15	0.16%	31.60%	YKPESDELTAEK	3.7	1,409.68
ATP	6011	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	13	15	0.16%	31.60%	YQLDKDGVVLFK	2.92	1,424.78

ATP	6011	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	5	9	0.10%	23.40%	GAVGALLVYDIAK	3.98	1,289.75
ATP	6011	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	5	9	0.10%	23.40%	HLTYENVER	2.22	1,160.57
ATP	6011	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	5	9	0.10%	23.40%	NILTEIYR	2.4	1,021.57
ATP	6011	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	5	9	0.10%	23.40%	STIGVEFATR	2.78	1,080.57
ATP	6011	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	5	5	9	0.10%	23.40%	VVLIGDSGVGK	2.82	1,043.61
ATP	6011	SEPT11 protein	gi|126010811,gi|126723403,gi|162416046	48,974.60	100.00%	3	3	3	0.03%	9.88%	AAAQLLQSQAQQSGAQQTK	5.26	1,957.01
ATP	6011	SEPT11 protein	gi|126010811,gi|126723403,gi|162416046	48,974.60	100.00%	3	3	3	0.03%	9.88%	FESDPATHNEPGVR	2.61	1,555.71
ATP	6011	SEPT11 protein	gi|126010811,gi|126723403,gi|162416046	48,974.60	100.00%	3	3	3	0.03%	9.88%	VNIIPIIAK	2.26	980.6504
ATP	6011	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	4	4	4	0.04%	15.00%	IPDEFDNDPILVQQLR	4.43	1,911.98
ATP	6011	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	4	4	4	0.04%	15.00%	QNLFFSSLTSR	2.6	1,299.67
ATP	6011	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	4	4	4	0.04%	15.00%	TVLEHYALEEDPLEAFK	3.69	2,004.00

ATP	6011	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	4	4	4	0.04%	15.00%	VLLDLSAFLK	2.76	1,118.68
ATP	6011	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	4	4	4	0.04%	5.34%	GLGYAQYLPR	2.86	1,137.61
ATP	6011	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	4	4	4	0.04%	5.34%	GMGGLFSVGETTAK	3.25	1,370.66
ATP	6011	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	4	4	4	0.04%	5.34%	VGQISFDLPR	2.95	1,131.62
ATP	6011	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	4	4	4	0.04%	5.34%	VSEEIFFGR	3.14	1,083.55
ATP	6011	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	7	8	11	0.12%	45.20%	HLIIGVSSDR	2.62	1,096.61
ATP	6011	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	7	8	11	0.12%	45.20%	IIGVGDKIR	2.61	970.6046
ATP	6011	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	7	8	11	0.12%	45.20%	NASEMIDKLTLTFNR	3.11	1,768.89

ATP	6011	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	7	8	11	0.12%	45.20%	NYQEYSLANIIYYSLK	3.44	1,981.99
ATP	6011	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	7	8	11	0.12%	45.20%	RPPTFGDASVIALELLNSGYEFDEGSIIFNR	4.83	3,427.72
ATP	6011	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	7	8	11	0.12%	45.20%	TEEKPIFSLDTISSAESMSIYDDIDADVLR	5.93	3,376.60
ATP	6011	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	7	8	11	0.12%	45.20%	VYGVGSLALYEK	3.07	1,298.70
ATP	6011	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	3	4	4	0.04%	18.60%	QMEQISQFLQAAER	3.98	1,694.82
ATP	6011	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	3	4	4	0.04%	18.60%	TLMNLGGLAVAR	3.97	1,231.68
ATP	6011	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	3	4	4	0.04%	18.60%	YFSDNQLQEGK	2.73	1,328.61

ATP	6011	PREDICTED: similar to Heparan sulfate 2-O-sulfotransferase 1 (2-O-sulfotransferase) (2OST), partial	gi|119889909	37,063.70	99.80%	2	2	3	0.03%	6.69%	LVSYYYFLR	2.72	1,223.65
ATP	6011	PREDICTED: similar to Heparan sulfate 2-O-sulfotransferase 1 (2-O-sulfotransferase) (2OST), partial	gi|119889909	37,063.70	99.80%	2	2	3	0.03%	6.69%	NNPVMSLQDQVR	3.45	1,416.69
ATP	6011	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	7	8	0.09%	10.70%	IMKVEYHLLSPYVSPR	2.6	1,948.04
ATP	6011	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	7	8	0.09%	10.70%	LAADEEENVDSNMR	3.73	1,608.68
ATP	6011	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	7	8	0.09%	10.70%	MLNENSYVPR	2.79	1,238.58
ATP	6011	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	7	8	0.09%	10.70%	SAFSNLFGGEPLSYTR	4.05	1,745.85
ATP	6011	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	7	8	0.09%	10.70%	SSVGTSLLLTLAR	2.21	1,317.77
ATP	6011	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	7	8	0.09%	10.70%	VEYHLLSPYVSPR	3.52	1,559.82
ATP	6011	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	7	7	8	0.09%	10.70%	VSASPLLYSLIEK	3.58	1,419.81

ATP	6011	Caveolin 2	gi|157279219,gi|38322700,gi|51512145,gi|56119130,gi|66774044	18,142.30	100.00%	3	3	5	0.05%	27.20%	ADVQLFMDDDSYSR	2.7	1,677.71
ATP	6011	Caveolin 2	gi|157279219,gi|38322700,gi|51512145,gi|56119130,gi|66774044	18,142.30	100.00%	3	3	5	0.05%	27.20%	SFSSVSLQLSHD	2.99	1,306.63
ATP	6011	Caveolin 2	gi|157279219,gi|38322700,gi|51512145,gi|56119130,gi|66774044	18,142.30	100.00%	3	3	5	0.05%	27.20%	VGFEDVIAEPVSTHSFDK	3.88	1,976.96
ATP	6011	calcium binding protein P22	gi|115497570,gi|122142989,gi|152941188,gi|74354201	22,425.20	100.00%	2	2	2	0.02%	14.40%	IINAFFPEGEDQVNFR	3.23	1,895.93
ATP	6011	calcium binding protein P22	gi|115497570,gi|122142989,gi|152941188,gi|74354201	22,425.20	100.00%	2	2	2	0.02%	14.40%	IPELAINPLGDR	3.78	1,307.73
ATP	6011	ACTN4 protein	gi|146186472,gi|148238040,gi|162416099	104,913.30	99.80%	2	2	2	0.02%	4.50%	LSNRPAFMPSEGK	3.11	1,449.72
ATP	6011	ACTN4 protein	gi|146186472,gi|148238040,gi|162416099	104,913.30	99.80%	2	2	2	0.02%	4.50%	SIVDYKPNLDLLEQQHQLIQEALIFDNK	2.8	3,324.75
ATP	6011	Chromosome 9 open reading frame 46 ortholog	gi|74354529,gi|77735799	17,091.30	99.80%	2	3	3	0.03%	15.60%	GMITFESLEK	2.87	1,170.57
ATP	6011	Chromosome 9 open reading frame 46 ortholog	gi|74354529,gi|77735799	17,091.30	99.80%	2	3	3	0.03%	15.60%	MKGEAENILETEK	4.23	1,507.73
ATP	6011	STAT1 protein	gi|154426144	86,914.50	99.80%	2	2	2	0.02%	3.35%	ELSAVTFPDIIR	3.19	1,360.75
ATP	6011	STAT1 protein	gi|154426144	86,914.50	99.80%	2	2	2	0.02%	3.35%	VMAAENIPENPLK	3.69	1,441.74
ATP	6011	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	100.00%	4	4	14	0.15%	22.20%	DYLALNEDLR	3.77	1,221.61
ATP	6011	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	100.00%	4	4	14	0.15%	22.20%	FITVGYVDDTQFVR	3.58	1,659.84

ATP	6011	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	100.00%	4	4	14	0.15%	22.20%	NGEDQTQDMELVETRPSGDGTFQK	2.76	2,698.19
ATP	6011	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	100.00%	4	4	14	0.15%	22.20%	VQHEGLQEPLTLR	4.18	1,519.82
ATP	6011	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	100.00%	4	4	14	0.15%	22.20%	YFLTAVSR	2.55	956.5199
ATP	6011	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	100.00%	4	4	14	0.15%	22.20%	YFLTAVSRPGLGEPR	3.23	1,662.90
ATP	6011	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	3	3	3	0.03%	12.70%	DTILQLNLK	2.6	1,057.63
ATP	6011	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	3	3	3	0.03%	12.70%	IATSGYLPTQQDVLR	3.82	1,661.89

ATP	6011	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	3	3	3	0.03%	12.70%	VRVPTTGIIEYPFDLENIIFR	5.53	2,492.36
ATP	6011	RecName: Full=Hexokinase-1; AltName: Full=Hexokinase type I; Short=HK I; AltName: Full=Brain form hexokinase	gi|123891,gi|163152,gi|27805797	103,049.20	99.80%	2	2	2	0.02%	10.60%	GAAMVTAVAYR	3.27	1,125.57
ATP	6011	RecName: Full=Hexokinase-1; AltName: Full=Hexokinase type I; Short=HK I; AltName: Full=Brain form hexokinase	gi|123891,gi|163152,gi|27805797	103,049.20	99.80%	2	2	2	0.02%	10.60%	GDFIALDLGGSSFR	3.29	1,454.73

ATP	6011	RecName: Full=Hexokinase-1; AltName: Full=Hexokinase type I; Short=HK I; AltName: Full=Brain form hexokinase	gi|123891,gi|163152,gi|27805797	103,049.20	99.80%	2	2	2	0.02%	10.60%	GKFNTSDVSAIEK	3.99	1,395.71
ATP	6011	RecName: Full=Hexokinase-1; AltName: Full=Hexokinase type I; Short=HK I; AltName: Full=Brain form hexokinase	gi|123891,gi|163152,gi|27805797	103,049.20	99.80%	2	2	2	0.02%	10.60%	KETNSNATVNMLPSFLRSIPDGTEDGDFLALDLGGTNFR	2.19	4,213.05
ATP	6011	RecName: Full=Hexokinase-1; AltName: Full=Hexokinase type I; Short=HK I; AltName: Full=Brain form hexokinase	gi|123891,gi|163152,gi|27805797	103,049.20	99.80%	2	2	2	0.02%	10.60%	LSDETLLDIMNR	4.01	1,435.71

ATP	6011	RecName: Full=Hexokinase-1; AltName: Full=Hexokinase type I; Short=HK I; AltName: Full=Brain form hexokinase	gi|123891,gi|163152,gi|27805797	103,049.20	99.80%	2	2	2	0.02%	10.60%	SIPDGSEKGDFIALDLGGSSFR	3.47	2,268.11
ATP	6011	RecName: Full=Hexokinase-1; AltName: Full=Hexokinase type I; Short=HK I; AltName: Full=Brain form hexokinase	gi|123891,gi|163152,gi|27805797	103,049.20	99.80%	2	2	2	0.02%	10.60%	SIPDGTEDGDFLALDLGGTNFR	3.91	2,310.09
ATP	6011	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	3	4	5	0.05%	26.40%	IALMPLLQAEK	3.44	1,242.71
ATP	6011	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	3	4	5	0.05%	26.40%	LQIEDFEAR	2.85	1,120.56
ATP	6011	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	3	4	5	0.05%	26.40%	VKQDMPPVGGYGPIDYKR	4.08	2,036.03

ATP	6011	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	gi|111307057,gi|115432055,gi|2852383,gi|71153774	28,065.10	100.00%	3	4	5	0.05%	25.60%	AVTEQGHELSNEER	2.31	1,598.74
ATP	6011	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	gi|111307057,gi|115432055,gi|2852383,gi|71153774	28,065.10	100.00%	3	4	5	0.05%	25.60%	QTTVSNSQQAYQEAFEISKK	3.05	2,287.12
ATP	6011	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	gi|111307057,gi|115432055,gi|2852383,gi|71153774	28,065.10	100.00%	3	4	5	0.05%	25.60%	TAFDEAIAELDTLNEESYKDSTLIMQLLR	3.91	3,345.64
ATP	6011	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	4	4	5	0.05%	21.80%	FFVVSSESR	3.09	1,057.53
ATP	6011	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	4	4	5	0.05%	21.80%	RKPDEVLDDEDIGSAPLK	5.59	1,997.02
ATP	6011	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	4	4	5	0.05%	21.80%	TELHIPNVDLK	2.48	1,278.71
ATP	6011	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	4	4	5	0.05%	21.80%	VLKEDALPDLKTEYEVDSEDR	4.95	2,464.21
ATP	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	12	16	0.17%	40.40%	AVLVDLEPGTMDSVR	3.02	1,617.82

ATP	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	12	16	0.17%	40.40%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	3.88	3,213.49
ATP	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	12	16	0.17%	40.40%	EVDEQMLNVQNK	2.82	1,462.68
ATP	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	12	16	0.17%	40.40%	GHYTEGAELVDSVLDVVR	3.5	1,958.98
ATP	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	12	16	0.17%	40.40%	GHYTEGAELVDSVLDVVRK	3.56	2,087.08
ATP	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	12	16	0.17%	40.40%	IMNTFSVVPSPK	3.78	1,335.70
ATP	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	12	16	0.17%	40.40%	IREEYPDRIMNTFSVVPSPK	3.08	2,394.21
ATP	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	12	16	0.17%	40.40%	ISEQFTAMFR	3	1,245.59
ATP	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	12	16	0.17%	40.40%	LAVNMVPFPR	3.53	1,159.63
ATP	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	12	16	0.17%	40.40%	LHFFMPGFAPLTSR	3.38	1,636.83
ATP	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	12	16	0.17%	40.40%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	4.25	4,479.06
ATP	6011	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	12	12	16	0.17%	40.40%	YLTVAAVFR	2.56	1,039.59
ATP	6011	chromatin modifying protein 4C	gi|114051754,gi|87578327	26,417.80	99.80%	2	2	2	0.02%	12.30%	EALENSYTNTEVLK	3.32	1,610.79
ATP	6011	chromatin modifying protein 4C	gi|114051754,gi|87578327	26,417.80	99.80%	2	2	2	0.02%	12.30%	LPNAPSSSLPAQPDR	3.66	1,549.80

ATP	6011	RecName: Full=Peptidyl-prolyl cis-trans isomerase B; Short=PPIase; Short=Rotamase; AltName: Full=Cyclophilin B; AltName: Full=S-cyclophilin; Short=SCYLP; Flags: Precursor	gi|215274238,gi|27806469,gi|529242,gi|59858297,gi|74268324	23,726.00	99.90%	2	2	3	0.03%	12.50%	TVDNFVALATGEK	4.53	1,364.71
ATP	6011	RecName: Full=Peptidyl-prolyl cis-trans isomerase B; Short=PPIase; Short=Rotamase; AltName: Full=Cyclophilin B; AltName: Full=S-cyclophilin; Short=SCYLP; Flags: Precursor	gi|215274238,gi|27806469,gi|529242,gi|59858297,gi|74268324	23,726.00	99.90%	2	2	3	0.03%	12.50%	VIKDFMIQGGDFTR	3.25	1,642.83
ATP	6011	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	4	4	4	0.04%	10.70%	MALVLDALPR	3.44	1,114.63
ATP	6011	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	4	4	4	0.04%	10.70%	NVVLQTLEGHLR	1.94	1,378.78
ATP	6011	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	4	4	4	0.04%	10.70%	QVLLAQAEAEK	2.82	1,199.66
ATP	6011	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	4	4	4	0.04%	10.70%	VDEIVVLSGDNSK	2.85	1,374.71

ATP	6011	RecName: Full=GPI transamidase component PIG-S; AltName: Full=Phosphatidylinositol-glycan biosynthesis class S protein	gi|116248578,gi|74268100,gi|77735383	61,769.20	99.80%	2	2	2	0.02%	8.11%	APLPYSQISGLNSLK	3.83	1,587.87
ATP	6011	RecName: Full=GPI transamidase component PIG-S; AltName: Full=Phosphatidylinositol-glycan biosynthesis class S protein	gi|116248578,gi|74268100,gi|77735383	61,769.20	99.80%	2	2	2	0.02%	8.11%	LMVPVTVVFTQESVPLDDQEKLPFTVVHER	4.46	3,468.81
ATP	6011	PREDICTED: phosphoenolpyruvate carboxykinase 2 (mitochondrial) isoform 1	gi|194670361	70,632.70	99.80%	2	2	2	0.02%	3.91%	EVLAELEALEGR	2.54	1,328.71
ATP	6011	PREDICTED: phosphoenolpyruvate carboxykinase 2 (mitochondrial) isoform 1	gi|194670361	70,632.70	99.80%	2	2	2	0.02%	3.91%	SYLTEQVNQDLPK	3.26	1,534.77
ATP	6011	PREDICTED: similar to mCG10725 isoform 1	gi|119889261,gi|119912821,gi|194673249,gi|58760422,gi|70778964,gi|74354988,gi|75052080	13,725.00	99.80%	2	2	2	0.02%	15.20%	AALQELLSK	3.28	972.5725

ATP	6011	PREDICTED: similar to mCG10725 isoform 1	gi|119889261,gi|119912821,gi|194673249,gi|58760422,gi|70778964,gi|74354988,gi|75052080	13,725.00	99.80%	2	2	2	0.02%	15.20%	LITPAVVSER	2.13	1,084.64
ATP	6011	YWHAG protein	gi|157279400,gi|157744500,gi|2852385,gi|71153781	28,285.10	99.80%	2	2	2	0.02%	17.40%	NVTELNEPLSNEER	4.11	1,643.79
ATP	6011	YWHAG protein	gi|157279400,gi|157744500,gi|2852385,gi|71153781	28,285.10	99.80%	2	2	2	0.02%	17.40%	TAFDDAIAELDTLNEDSYKDSTLIMQLLR	3	3,317.61
ATP	6011	Chain C, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591028,gi|110591031,gi|114687,gi|163036,gi|27807291,gi|55670489,gi|73586602	12,514.70	100.00%	5	5	7	0.08%	44.40%	ADMNTFPNFTFEDPKFEVVEKPQS	3.25	2,833.30
ATP	6011	Chain C, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591028,gi|110591031,gi|114687,gi|163036,gi|27807291,gi|55670489,gi|73586602	12,514.70	100.00%	5	5	7	0.08%	44.40%	QTSGGPVDAGPEYQQDLDR	4.06	2,032.92
ATP	6011	Chain C, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591028,gi|110591031,gi|114687,gi|163036,gi|27807291,gi|55670489,gi|73586602	12,514.70	100.00%	5	5	7	0.08%	44.40%	QTSGGPVDAGPEYQQDLDRELFK	3.48	2,550.21
ATP	6011	Chain C, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591028,gi|110591031,gi|114687,gi|163036,gi|27807291,gi|55670489,gi|73586602	12,514.70	100.00%	5	5	7	0.08%	44.40%	RQTSGGPVDAGPEYQQDLDR	4.11	2,189.02
ATP	6011	Chain C, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591028,gi|110591031,gi|114687,gi|163036,gi|27807291,gi|55670489,gi|73586602	12,514.70	100.00%	5	5	7	0.08%	44.40%	RQTSGGPVDAGPEYQQDLDRELFK	4.99	2,706.31

ATP	6011	heterogeneous nuclear ribonucleoprotein A2/B1	gi|114051756,gi|122145945,gi|87578315	35,988.50	99.80%	2	3	3	0.03%	13.20%	GFGFVTFDDHDPVDKIVLQK	2.98	2,277.16
ATP	6011	heterogeneous nuclear ribonucleoprotein A2/B1	gi|114051756,gi|122145945,gi|87578315	35,988.50	99.80%	2	3	3	0.03%	13.20%	NMGGPYGGGNYGPGGSGGSGGYGGR	5.21	2,205.90
ATP	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	9	9	9	0.10%	9.20%	ISGETIFVTAPHEATAGIIGVNR	4.1	2,353.25
ATP	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	9	9	9	0.10%	9.20%	IYIDSNNNPER	2.66	1,334.63
ATP	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	9	9	9	0.10%	9.20%	KFDVNTSAVQVLIEHIGNLDR	4.08	2,368.26
ATP	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	9	9	9	0.10%	9.20%	LAELEEFINGPNNAHIQQVGDR	2.99	2,464.22

ATP	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	9	9	9	0.10%	9.20%	LASTLVHLGEYQAAVDGAR	2.88	1,971.03
ATP	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	9	9	9	0.10%	9.20%	NNLAGAEELFAR	3.01	1,304.66
ATP	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	9	9	9	0.10%	9.20%	RPISADSAIMNPASK	3.71	1,573.80
ATP	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	9	9	9	0.10%	9.20%	TLQIFNIEMK	2.86	1,252.66
ATP	6011	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	9	9	9	0.10%	9.20%	TSIDAYDNFDNISLAQR	2.64	1,942.91

ATP	6011	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	99.80%	2	4	4	0.04%	11.40%	NPSTSLGPTLEPEEVVNK	4.86	1,910.97
ATP	6011	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	99.80%	2	4	4	0.04%	11.40%	SVTGEIVLITGAGHGIGR	4.45	1,736.97
ATP	6011	pre-B-cell leukemia transcription factor interacting protein 1	gi|110331795,gi|115497324,gi|151554897,gi|158706093	80,239.50	99.80%	2	2	2	0.02%	3.71%	ALESELQQLR	3.01	1,186.64
ATP	6011	pre-B-cell leukemia transcription factor interacting protein 1	gi|110331795,gi|115497324,gi|151554897,gi|158706093	80,239.50	99.80%	2	2	2	0.02%	3.71%	EQGPTGQEPSPGFLEQK	3.96	1,828.87
ATP	6011	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	99.80%	2	2	2	0.02%	10.30%	AELNEFLTR	2.63	1,092.57
ATP	6011	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	99.80%	2	2	2	0.02%	10.30%	GGKPEPPAMPQPVPTA	3.26	1,589.80
ATP	6011	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	8	10	0.11%	13.50%	ADDKLIAEEGVDSLNVK	4.29	1,815.93
ATP	6011	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	8	10	0.11%	13.50%	AMYLPETLSPADQLK	2.8	1,692.85
ATP	6011	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	8	10	0.11%	13.50%	DFSVFFQK	2.32	1,017.50
ATP	6011	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	8	10	0.11%	13.50%	FLQDTIEEMALK	4.4	1,453.72

ATP	6011	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	8	10	0.11%	13.50%	IRETGERPSNEEIMR	2.62	1,832.89
ATP	6011	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	8	10	0.11%	13.50%	KLEEGGPVYSPPAQAAVR	3.69	1,868.99
ATP	6011	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	8	10	0.11%	13.50%	LLELQSIGTNNFLR	4.41	1,617.90
ATP	6011	voltage-dependent anion channel 1	gi|8810220, gi|90111863	30,723.80	100.00%	10	12	41	0.45%	41.30%	GYGFGLIK	2.08	854.4772
ATP	6011	voltage-dependent anion channel 1	gi|8810220, gi|90111863	30,723.80	100.00%	10	12	41	0.45%	41.30%	LTFDSSFSPNTGKK	3.46	1,528.76
ATP	6011	voltage-dependent anion channel 1	gi|8810220, gi|90111863	30,723.80	100.00%	10	12	41	0.45%	41.30%	LTLSALLDGK	3.27	1,030.61
ATP	6011	voltage-dependent anion channel 1	gi|8810220, gi|90111863	30,723.80	100.00%	10	12	41	0.45%	41.30%	LTLSALLDGKNVNAGGHK	2.74	1,808.00
ATP	6011	voltage-dependent anion channel 1	gi|8810220, gi|90111863	30,723.80	100.00%	10	12	41	0.45%	41.30%	SENGLEFTSSGSANTETTK	4.49	1,959.88
ATP	6011	voltage-dependent anion channel 1	gi|8810220, gi|90111863	30,723.80	100.00%	10	12	41	0.45%	41.30%	SRVTQSNFAVGYK	3.15	1,456.75
ATP	6011	voltage-dependent anion channel 1	gi|8810220, gi|90111863	30,723.80	100.00%	10	12	41	0.45%	41.30%	TDEFQLHTNVNDGTEFGGSIYQK	6.02	2,600.19
ATP	6011	voltage-dependent anion channel 1	gi|8810220, gi|90111863	30,723.80	100.00%	10	12	41	0.45%	41.30%	TKSENGLEFTSSGSANTETTK	5.07	2,189.02
ATP	6011	voltage-dependent anion channel 1	gi|8810220, gi|90111863	30,723.80	100.00%	10	12	41	0.45%	41.30%	VNNSSLIGLGYTQTLKPGIK	4.74	2,103.18
ATP	6011	voltage-dependent anion channel 1	gi|8810220, gi|90111863	30,723.80	100.00%	10	12	41	0.45%	41.30%	VTQSNFAVGYK	4.18	1,213.62

ATP	6011	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	5	6	16	0.17%	26.90%	LTFDTTFSPNTGKK	3.01	1,556.80
ATP	6011	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	5	6	16	0.17%	26.90%	LTLSALVDGK	3.54	1,016.60
ATP	6011	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	5	6	16	0.17%	26.90%	TGDFQLHTNVNDGTEFGGSIYQK	4.59	2,528.17
ATP	6011	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	5	6	16	0.17%	26.90%	VNNSSLIGVGYTQTLRPGVK	5.17	2,103.16
ATP	6011	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	5	6	16	0.17%	26.90%	YQLDPTASISAK	3.28	1,293.67
ATP	6011	Trx-like protein	gi|109726696,gi|115494922,gi|122145628,gi|126920889,gi|146231808	31,563.90	99.80%	2	2	2	0.02%	8.27%	LLPESSQPLKK	2.47	1,239.73
ATP	6011	Trx-like protein	gi|109726696,gi|115494922,gi|122145628,gi|126920889,gi|146231808	31,563.90	99.80%	2	2	2	0.02%	8.27%	VDVTEQPGLSGR	4.31	1,257.64
ATP	6011	endothelial cell-specific molecule 2	gi|114053335,gi|86438024	20,621.00	99.80%	2	3	4	0.04%	13.20%	ESEDPQKPGSSGLSESGSTANGEK	4.05	2,378.06
ATP	6011	endothelial cell-specific molecule 2	gi|114053335,gi|86438024	20,621.00	99.80%	2	3	4	0.04%	13.20%	NKESEDPQKPGSSGLSESGSTANGEK	3.01	2,620.20
ATP	6011	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	4	5	6	0.07%	4.68%	DEQYTALSNMPK	2.98	1,412.64

ATP	6011	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	4	5	6	0.07%	4.68%	GLGEHELDEDEEDYESSAK	5.15	2,151.88
ATP	6011	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	4	5	6	0.07%	4.68%	IFGELSSYEDFLDAR	3.75	1,761.83
ATP	6011	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	4	5	6	0.07%	4.68%	IKRDEQYTALSNMPK	4.23	1,809.92
ATP	6011	PREDICTED: similar to Zinc finger protein basonuclin-1	gi|76647059	111,795.20	99.70%	2	2	2	0.02%	2.48%	IEKETMETADEKR	2.66	1,595.76
ATP	6011	PREDICTED: similar to Zinc finger protein basonuclin-1	gi|76647059	111,795.20	99.70%	2	2	2	0.02%	2.48%	VEPCVPFPDYIK	2.22	1,406.70
ATP	6011	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	6	6	6	0.07%	25.50%	EQNGDSLVHAALVAESAAIGSAEANAFSVLQHVLGAGPHVK	2.94	4,065.08
ATP	6011	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	6	6	6	0.07%	25.50%	GSNATSSLYQAVAK	2.72	1,396.71

ATP	6011	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	6	6	6	0.07%	25.50%	MALIGLGVSHPVLK	3.08	1,450.85
ATP	6011	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	6	6	6	0.07%	25.50%	QVAEQFLNIR	2.57	1,217.66
ATP	6011	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	6	6	6	0.07%	25.50%	SMAASGNLGHTPFIDEL	2.36	1,775.83
ATP	6011	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	6	6	6	0.07%	25.50%	TIAQGNLSNPDVQAAK	3.92	1,626.84
ATP	6011	Chain A, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793901,gi|71042575,gi|71042585,gi|75765179,gi|75765190,gi|82407287	49,194.40	100.00%	4	4	4	0.04%	14.80%	DVILQELQENDTSMR	2.78	1,806.85

ATP	6011	Chain A, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793901,gi|71042575,gi|71042585,gi|75765179,gi|75765190,gi|82407287	49,194.40	100.00%	4	4	4	0.04%	14.80%	EVESMGAHLNAYSTR	2.73	1,680.76
ATP	6011	Chain A, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793901,gi|71042575,gi|71042585,gi|75765179,gi|75765190,gi|82407287	49,194.40	100.00%	4	4	4	0.04%	14.80%	MVLAAAGGLEHR	3.52	1,240.65
ATP	6011	Chain A, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793901,gi|71042575,gi|71042585,gi|75765179,gi|75765190,gi|82407287	49,194.40	100.00%	4	4	4	0.04%	14.80%	TATYAQALQSVPETQVSQLDNGLR	3.49	2,590.31
ATP	6011	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	gi|111308529,gi|128825,gi|163414,gi|27807355	79,425.10	100.00%	3	3	3	0.03%	6.19%	ILQDIASGSHPFSQVLQEAK	3.77	2,168.13
ATP	6011	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	gi|111308529,gi|128825,gi|163414,gi|27807355	79,425.10	100.00%	3	3	3	0.03%	6.19%	NRLEEVSPNLVR	2.83	1,425.78

ATP	6011	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	gi|111308529,gi|128825,gi|163414,gi|27807355	79,425.10	100.00%	3	3	3	0.03%	6.19%	VALIGSPVDLTYR	3.22	1,403.79
ATP	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	9	12	15	0.16%	30.40%	AQQVAVQEQEIAR	3.84	1,469.77
ATP	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	9	12	15	0.16%	30.40%	DIHDDQDYLHSLGK	2.87	1,655.77
ATP	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	9	12	15	0.16%	30.40%	ISLNTLTLNVK	2.93	1,215.73
ATP	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	9	12	15	0.16%	30.40%	ITLVSSGSGAMGAAK	4.42	1,365.70
ATP	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	9	12	15	0.16%	30.40%	KAEAFQLYQEAAQLDMLLEK	4.44	2,355.19
ATP	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	9	12	15	0.16%	30.40%	SQLIMQAEAEAEAVR	4.55	1,661.82
ATP	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	9	12	15	0.16%	30.40%	TEAEIAHIALETLEGHQR	5.29	2,018.03
ATP	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	9	12	15	0.16%	30.40%	VSAQYLSEIEMAK	3.72	1,484.73
ATP	6011	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	9	12	15	0.16%	30.40%	VTGEVLDILSR	3.04	1,201.68

ATP	6011	PREDICTED: similar to ribosomal protein S24	gi|119914811,gi|194677142,gi|58760477,gi|70778760,gi|74268388,gi|91207637	15,283.40	99.80%	2	2	2	0.02%	20.50%	KQMVIDVLHPGK	3.41	1,380.77
ATP	6011	PREDICTED: similar to ribosomal protein S24	gi|119914811,gi|194677142,gi|58760477,gi|70778760,gi|74268388,gi|91207637	15,283.40	99.80%	2	2	2	0.02%	20.50%	TTGFGMIYDSLDYAK	3.66	1,697.77
ATP	6011	similar to 40S ribosomal protein S18	gi|28189422,gi|28189549,gi|28189799,gi|74268023,gi|75812924,gi|91207636	15,380.70	100.00%	3	3	4	0.04%	25.20%	IAFAITAIK	2.28	947.5925
ATP	6011	similar to 40S ribosomal protein S18	gi|28189422,gi|28189549,gi|28189799,gi|74268023,gi|75812924,gi|91207636	15,380.70	100.00%	3	3	4	0.04%	25.20%	RAGELTEDEVER	4.51	1,403.68
ATP	6011	similar to 40S ribosomal protein S18	gi|28189422,gi|28189549,gi|28189799,gi|74268023,gi|75812924,gi|91207636	15,380.70	100.00%	3	3	4	0.04%	25.20%	YSQVLANGLDNK	3.78	1,321.67
ATP	6011	glutathione peroxidase 8	gi|114052907,gi|122143886,gi|84708688	23,965.80	99.80%	2	3	3	0.03%	11.00%	ILGSEAEPAFR	3.62	1,189.62
ATP	6011	glutathione peroxidase 8	gi|114052907,gi|122143886,gi|84708688	23,965.80	99.80%	2	3	3	0.03%	11.00%	NNFGVTFPIFHK	2.73	1,420.74
ATP	6011	PREDICTED: similar to Neuroblast differentiation-associated protein AHNAK (Desmoyokin), partial	gi|194687805	140,614.00	99.80%	2	2	2	0.02%	2.31%	ISMPDVDLNLKGPK	2.99	1,542.82

ATP	6011	PREDICTED: similar to Neuroblast differentiation-associated protein AHNAK (Desmoyokin), partial	gi|194687805	140,614.00	99.80%	2	2	2	0.02%	2.31%	VDIEAPDVSLEGPEGK	3.17	1,654.82
ATP	6011	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	8	13	0.14%	25.50%	GVGMVADPDNPLVLDILTGSSTSYSFFPDKPITQYPHAVGK	4.57	4,350.16
ATP	6011	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	8	13	0.14%	25.50%	LPDVYGVFQFK	3.56	1,312.69
ATP	6011	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	8	13	0.14%	25.50%	SSLNPILFR	2.44	1,046.60
ATP	6011	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	8	13	0.14%	25.50%	TADDPSLSLIK	3.14	1,159.62
ATP	6011	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	8	13	0.14%	25.50%	TAVIDHHNYDVSDLGQHTLIVADTENLLK	6.12	3,231.63
ATP	6011	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|151555878,gi|155371877,gi|215275740	48,774.90	100.00%	6	8	13	0.14%	25.50%	TLVLLDNLNLR	3.45	1,283.77
ATP	6011	reticulon 4 isoform 2	gi|164259354,gi|92096636	40,940.20	99.80%	2	2	3	0.03%	7.12%	GPLPAAPLAAPER	2.78	1,259.71
ATP	6011	reticulon 4 isoform 2	gi|164259354,gi|92096636	40,940.20	99.80%	2	2	3	0.03%	7.12%	HQAQIDHYLGLANK	4.33	1,607.83
ATP	6011	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	4	6	6	0.07%	12.90%	ALASILLQDHIR	3.27	1,349.79
ATP	6011	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	4	6	6	0.07%	12.90%	IYQGEDLPHPK	3.13	1,296.66

ATP	6011	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	4	6	6	0.07%	12.90%	LKDIASEFKEQLQTLILHVLNPANLMEK	2.79	3,251.77
ATP	6011	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	4	6	6	0.07%	12.90%	SMLQATAEANNLAAAASAK	4.29	1,848.91
ATP	6011	RecName: Full=Glutathione S-transferase P; AltName: Full=GST class-pi	gi|121744,gi|29135329,gi|404,gi|74268086	23,595.90	99.80%	2	3	3	0.03%	15.70%	ALPQHLKPFETLLSQNK	2.37	1,964.10
ATP	6011	RecName: Full=Glutathione S-transferase P; AltName: Full=GST class-pi	gi|121744,gi|29135329,gi|404,gi|74268086	23,595.90	99.80%	2	3	3	0.03%	15.70%	FQDGDLTLYQSNAILR	5.07	1,853.94
ATP	6011	Poliovirus receptor-related 2 (herpesvirus entry mediator B)	gi|109658349,gi|115497936	43,243.10	100.00%	3	3	3	0.03%	13.60%	ETQGSGPLPGTVTVTSR	4.39	1,686.87
ATP	6011	Poliovirus receptor-related 2 (herpesvirus entry mediator B)	gi|109658349,gi|115497936	43,243.10	100.00%	3	3	3	0.03%	13.60%	VIAQPQNHAEKQEVTFNLDPVPAR	2.51	2,800.47
ATP	6011	Poliovirus receptor-related 2 (herpesvirus entry mediator B)	gi|109658349,gi|115497936	43,243.10	100.00%	3	3	3	0.03%	13.60%	YTVTPLSEADGVK	3.08	1,379.71
ATP	6011	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	10	10	0.11%	19.90%	IRIDSLSAQLSQLQK	3.31	1,699.97
ATP	6011	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	10	10	0.11%	19.90%	LADALQELR	2.96	1,028.57
ATP	6011	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	10	10	0.11%	19.90%	LKDLEALLNSK	3.49	1,243.73
ATP	6011	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	10	10	0.11%	19.90%	LQEKEDLQELNDR	4.57	1,629.81
ATP	6011	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	10	10	0.11%	19.90%	LQTLKEELDFQK	2.85	1,491.81

ATP	6011	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	10	10	0.11%	19.90%	LRDLEDSLAR	2.8	1,187.64
ATP	6011	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	10	10	0.11%	19.90%	MQQQLDEYQELLDIK	3.45	1,909.92
ATP	6011	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	10	10	0.11%	19.90%	QNGDDPLLTYRFPPK	2.56	1,760.90
ATP	6011	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	10	10	0.11%	19.90%	TALINSTGEEVAMR	2.8	1,507.74
ATP	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	15	26	0.28%	36.80%	AVAISLPK	2.39	798.5084
ATP	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	15	26	0.28%	36.80%	AVLSAEQLRDDEVHAGLGELLR	4.56	2,391.26
ATP	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	15	26	0.28%	36.80%	DQAVENILLSPVVVASSLGLVSLGGK	5.29	2,565.45

ATP	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	15	26	0.28%	36.80%	DTQSGSLLFIGR	2.83	1,293.68
ATP	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	15	26	0.28%	36.80%	GVVEVTHDLQK	4	1,224.66
ATP	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	15	26	0.28%	36.80%	HLAGLGLTEAIDK	3.15	1,337.74
ATP	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	15	26	0.28%	36.80%	HLAGLGLTEAIDKNK	5.84	1,579.88

ATP	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	15	26	0.28%	36.80%	KAVAISLPK	3.32	926.6034
ATP	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	15	26	0.28%	36.80%	LFYADHPFIFLVR	2.54	1,637.88
ATP	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	15	26	0.28%	36.80%	LSSLIIIMPHHVEPLER	2.45	2,000.10
ATP	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	15	26	0.28%	36.80%	LYGPSSVSFAEDFVR	3.98	1,673.82

ATP	6011	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	12	15	26	0.28%	36.80%	SAGLAFSLYQAMAK	4.45	1,473.74
ATP	6011	PREDICTED: hypothetical protein	gi|194667311	68,113.30	100.00%	3	4	4	0.04%	4.97%	ELESQISELQEDLESER	3.84	2,033.95
ATP	6011	PREDICTED: hypothetical protein	gi|194667311	68,113.30	100.00%	3	4	4	0.04%	4.97%	IRELESQISELQEDLESER	3.8	2,303.14
ATP	6011	PREDICTED: hypothetical protein	gi|194667311	68,113.30	100.00%	3	4	4	0.04%	4.97%	XXXXXXXXXXX	3.36	1,240.02
ATP	6011	PREDICTED: transmembrane emp24 protein transport domain containing 4	gi|194666384	37,465.50	99.70%	2	2	3	0.03%	5.97%	DKLTELQLR	2.69	1,115.64
ATP	6011	PREDICTED: transmembrane emp24 protein transport domain containing 4	gi|194666384	37,465.50	99.70%	2	2	3	0.03%	5.97%	QLLDQVEQIQK	3.91	1,341.74
ATP	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	12	17	0.19%	14.60%	DGQVIFPAPTPK	2.58	1,269.68
ATP	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	12	17	0.19%	14.60%	EVLASDLVVK	2.68	1,072.62
ATP	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	12	17	0.19%	14.60%	FFTGQITAAGK	3.22	1,140.60

ATP	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	12	17	0.19%	14.60%	GITHIGYTDLPSR	3.52	1,429.74
ATP	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	12	17	0.19%	14.60%	GTVVMKDGQVIFPAPTPK	3.4	1,901.02
ATP	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	12	17	0.19%	14.60%	MATQASTLYSNNITK	5.23	1,658.81
ATP	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	12	17	0.19%	14.60%	SLGAEPLEVDLK	2.91	1,270.69
ATP	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	12	17	0.19%	14.60%	SLGVGYAAVDNPIFYKPNTAMLLGDAK	3.93	2,841.45
ATP	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	12	17	0.19%	14.60%	TSGTLISFIYPAQNPDLLNK	3.11	2,192.16
ATP	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	12	17	0.19%	14.60%	VALSPAGVQALVK	3	1,252.76
ATP	6011	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	12	17	0.19%	14.60%	VTIAQGYDALSSMANIAGYK	4.29	2,089.03
ATP	6011	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	8	13	23	0.25%	32.40%	IPDQLVILDMK	4.21	1,300.72
ATP	6011	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	8	13	23	0.25%	32.40%	IPDQLVILDMKHGVEAK	2.7	1,922.04

ATP	6011	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	8	13	23	0.25%	32.40%	ITDSAGHILYSK	4.69	1,304.68
ATP	6011	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	8	13	23	0.25%	32.40%	ITDSAGHILYSKEDATK	5.62	1,848.93
ATP	6011	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	8	13	23	0.25%	32.40%	LKPLEVELR	3.68	1,096.67
ATP	6011	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	8	13	23	0.25%	32.40%	NYEEIAKVEK	3.32	1,222.63
ATP	6011	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	8	13	23	0.25%	32.40%	RLEDLSESIVNDFAYMK	3.62	2,045.99
ATP	6011	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	8	13	23	0.25%	32.40%	RLEDLSESIVNDFAYMKK	5.24	2,174.08
ATP	6011	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	100.00%	3	3	3	0.03%	5.63%	LIDGIVLTK	2.45	971.6138
ATP	6011	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	100.00%	3	3	3	0.03%	5.63%	NQGFDVVLVDTAGR	3.77	1,490.76
ATP	6011	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	100.00%	3	3	3	0.03%	5.63%	VMGTFSTVTSTVK	2.74	1,373.70
ATP	6011	CAPZA1 protein	gi|133777466,gi|134085807,gi|152941212,gi|218563517	32,913.90	99.80%	2	2	2	0.02%	9.79%	FITHAPPGEFNEVFNDVR	3.29	2,089.01

ATP	6011	CAPZA1 protein	gi|133777466,gi|134085807,gi|152941212,gi|218563517	32,913.90	99.80%	2	2	2	0.02%	9.79%	LLLNNDNLLR	2.92	1,197.70
ATP	6011	Stromal interaction molecule 1	gi|154426132,gi|61555683,gi|75057528,gi|78369570	77,134.40	99.80%	2	2	2	0.02%	5.42%	DLTHSDSESSLHMSDR	3.48	1,832.77
ATP	6011	Stromal interaction molecule 1	gi|154426132,gi|61555683,gi|75057528,gi|78369570	77,134.40	99.80%	2	2	2	0.02%	5.42%	KAAAEEDNGSIGEETDSSPGR	3.71	2,119.94
ATP	6011	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	5	6	0.07%	22.60%	FSDLDSASVDSDMYDLPK	3.58	2,020.87
ATP	6011	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	5	6	0.07%	22.60%	FSDLDSASVDSDMYDLPKKEDALLYQSK	3.27	3,196.49
ATP	6011	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	5	6	0.07%	22.60%	GFRQPSASLSDADPFHR	3.72	1,887.91
ATP	6011	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	5	6	0.07%	22.60%	LSPPSSSASSFSYR	1.75	1,472.70
ATP	6011	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	5	6	0.07%	22.60%	QPSASLSDADPFHR	2.11	1,527.72
ATP	6011	Lu-ECAM-1	gi|2623763,gi|2623765,gi|2623767,gi|30794326	100,991.10	100.00%	3	3	3	0.03%	4.75%	QESYDQADVIVANPYLK	3.74	1,952.96
ATP	6011	Lu-ECAM-1	gi|2623763,gi|2623765,gi|2623767,gi|30794326	100,991.10	100.00%	3	3	3	0.03%	4.75%	SGSITQQAIQLESK	4.78	1,489.79
ATP	6011	Lu-ECAM-1	gi|2623763,gi|2623765,gi|2623767,gi|30794326	100,991.10	100.00%	3	3	3	0.03%	4.75%	YGDDPYTLQYGR	3.54	1,447.65
ATP	6011	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	4	4	5	0.05%	25.60%	ATIGADFLTK	2.22	1,036.57
ATP	6011	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	4	4	5	0.05%	25.60%	DPENFPFVVLGNK	4.23	1,475.75
ATP	6011	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	4	4	5	0.05%	25.60%	FQSLGVAFYR	2.81	1,187.62

ATP	6011	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	4	4	5	0.05%	25.60%	NALKQETEVELYNEFPEPIK	3.52	2,391.21
ATP	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	16	0.17%	21.10%	ARFEELNADLFR	2.77	1,480.75
ATP	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	16	0.17%	21.10%	DAGTIAGLNVLR	3.58	1,199.67
ATP	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	16	0.17%	21.10%	FEELNADLFR	2.31	1,253.62
ATP	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	16	0.17%	21.10%	IINEPTAAAIAYGLDK	4.5	1,659.90
ATP	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	16	0.17%	21.10%	IINEPTAAAIAYGLDKK	2.55	1,787.99
ATP	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	16	0.17%	21.10%	LLQDFFNGK	2.5	1,081.57
ATP	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	16	0.17%	21.10%	NQVAMNPTNTVFDAK	4.14	1,665.79
ATP	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	16	0.17%	21.10%	NSLESYAFNMK	2.88	1,319.59
ATP	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	16	0.17%	21.10%	SFYPEEVSSMVLTK	3.24	1,632.78
ATP	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	16	0.17%	21.10%	STAGDTHLGGEDFDNR	3.08	1,691.73
ATP	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	16	0.17%	21.10%	TTPSYVAFTDTER	3.33	1,487.70
ATP	6011	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	11	14	16	0.17%	21.10%	TVTNAVVTVPAYFNDSQR	3.63	1,982.00
ATP	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	9	11	34	0.37%	27.90%	AAYFGIYDTAK	3.61	1,219.60
ATP	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	9	11	34	0.37%	27.90%	DFLAGGIAAAISK	4.91	1,233.68

ATP	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	9	11	34	0.37%	27.90%	EQGVLSFWR	2.4	1,121.57
ATP	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	9	11	34	0.37%	27.90%	GMGGAFVLVLYDELK	4.71	1,627.84
ATP	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	9	11	34	0.37%	27.90%	GMGGAFVLVLYDELKK	4.62	1,755.94
ATP	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	9	11	34	0.37%	27.90%	LLLQVQHASK	2.93	1,136.68
ATP	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	9	11	34	0.37%	27.90%	QIFLGGVDKR	2.24	1,132.65
ATP	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	9	11	34	0.37%	27.90%	YFPTQALNFAFK	3.82	1,446.74
ATP	6011	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	9	11	34	0.37%	27.90%	YFPTQALNFAFKDK	3.93	1,689.86
ATP	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	8	8	8	0.09%	5.53%	FADEHVPGSPFTVK	3.43	1,530.76
ATP	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	8	8	8	0.09%	5.53%	GAGIGGLGITVEGPSESK	3.24	1,628.85

ATP	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	8	8	8	0.09%	5.53%	GLVEPVNVVDNGDGTHTVTYTPSQEGPYMVSVK	6.06	3,505.68
ATP	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	8	8	8	0.09%	5.53%	GQHVTGSPFQFTVGPLGEGGAHK	3.09	2,308.15
ATP	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	8	8	8	0.09%	5.53%	IFAQDGDGQPIDIQMK	3	1,791.86
ATP	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	8	8	8	0.09%	5.53%	LIALLEVLSQK	2.56	1,226.77
ATP	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	8	8	8	0.09%	5.53%	SPFEVQVGPEAGMQK	4.24	1,619.77
ATP	6011	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	8	8	8	0.09%	5.53%	VLFASQEIPTSPFR	3.6	1,591.85
ATP	6011	septin 2	gi|114052905,gi|122069932,gi|84708845	41,554.10	99.80%	2	2	2	0.02%	9.14%	ASIPFSVVGSNQLIEAK	2.73	1,759.96
ATP	6011	septin 2	gi|114052905,gi|122069932,gi|84708845	41,554.10	99.80%	2	2	2	0.02%	9.14%	KVENEDMNKDQILLEK	4.21	1,961.99

ATP	6011	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	3	3	3	0.03%	6.48%	EANHDGDFGITLAELR	3.09	1,757.85
ATP	6011	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	3	3	3	0.03%	6.48%	GIIDSTVSEQR	2.82	1,204.62
ATP	6011	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	3	3	3	0.03%	6.48%	KADVGFAMGIAGTDVAK	3.28	1,666.85
ATP	6011	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	3	3	3	0.03%	6.48%	QVVAVTGDGTNDGPALK	4.91	1,641.84
ATP	6011	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	3	3	3	0.03%	6.48%	SATSSSPGSPLHSLETSL	3.19	1,757.86
ATP	6011	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	99.80%	2	2	2	0.02%	2.06%	IIGNLLYYR	2.52	1,124.65
ATP	6011	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	99.80%	2	2	2	0.02%	2.06%	VNLLAALTNIDLALEQGSAPALFK	4.56	2,482.39
ATP	6011	UNC84B protein	gi|151553917,gi|156121283	81,429.80	99.80%	2	3	3	0.03%	4.26%	IRPTAVTLEHVPK	3.01	1,460.86
ATP	6011	UNC84B protein	gi|151553917,gi|156121283	81,429.80	99.80%	2	3	3	0.03%	4.26%	LEGQLAGLRQELAALTLK	3.43	1,924.12
ATP	6011	heat shock protein beta-1	gi|71037405,gi|74354863,gi|85542053	22,375.10	100.00%	4	4	4	0.04%	31.80%	KYTLPPGVDPTLVSSSLSPEGTLTVEAPLPK	3.83	3,193.72
ATP	6011	heat shock protein beta-1	gi|71037405,gi|74354863,gi|85542053	22,375.10	100.00%	4	4	4	0.04%	31.80%	LFDQAFGLPR	3.58	1,163.62
ATP	6011	heat shock protein beta-1	gi|71037405,gi|74354863,gi|85542053	22,375.10	100.00%	4	4	4	0.04%	31.80%	QLSSGVSEIQQTADR	4.34	1,618.80

ATP	6011	heat shock protein beta-1	gi|71037405,gi|74354863,gi|85542053	22,375.10	100.00%	4	4	4	0.04%	31.80%	RVPFSLLR	2.3	987.6098
ATP	6011	ribosomal protein L4	gi|61553010,gi|62460480,gi|73917531,gi|74267758	47,395.70	99.80%	2	2	2	0.02%	8.53%	APIRPDIVNFVHTNLR	2.2	1,862.04
ATP	6011	ribosomal protein L4	gi|61553010,gi|62460480,gi|73917531,gi|74267758	47,395.70	99.80%	2	2	2	0.02%	8.53%	IEEVPELPLVVEDKVEGYKK	1.77	2,313.26
ATP	6011	PREDICTED: similar to carnitine palmitoyltransferase 1C	gi|194679924	80,680.30	99.80%	2	2	2	0.02%	3.81%	LPVPAVQDTVNR	2.83	1,308.73
ATP	6011	PREDICTED: similar to carnitine palmitoyltransferase 1C	gi|194679924	80,680.30	99.80%	2	2	2	0.02%	3.81%	MTALAQDFAVNLGPR	3.25	1,619.82
ATP	6011	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	5	5	5	0.05%	7.98%	LLGVEGSTLR	2.79	1,044.60
ATP	6011	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	5	5	5	0.05%	7.98%	LLQSNPVLEAFGNAKTLRNDNSSR	2.61	2,644.38
ATP	6011	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	5	5	5	0.05%	7.98%	MSLLELVEILK	3.4	1,303.75
ATP	6011	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	5	5	5	0.05%	7.98%	VLQALGSEPIQYAVPVVK	3.5	1,911.10
ATP	6011	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	5	5	5	0.05%	7.98%	VNNININQGSITFAGGPGR	3.52	1,928.99
ATP	6011	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	4	4	4	0.04%	5.07%	GQPLGPAGVQVSLR	3.53	1,378.78
ATP	6011	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	4	4	4	0.04%	5.07%	SSIDSEPALVLGPLK	3.65	1,525.85

ATP	6011	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	4	4	4	0.04%	5.07%	VLNGPEGEGVPDAVVTLNSQIK	4.28	2,236.18
ATP	6011	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	4	4	4	0.04%	5.07%	VQVMVPEAETR	2.92	1,274.64
ATP	6011	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	4	6	9	0.10%	39.40%	ADALQAGASQFETSAAK	3.6	1,665.81
ATP	6011	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	4	6	9	0.10%	39.40%	LQQTQNQVDEVVDIMR	5.38	1,931.95
ATP	6011	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	4	6	9	0.10%	39.40%	LSELDDRADALQAGASQFETSAAK	5.4	2,494.21
ATP	6011	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	4	6	9	0.10%	39.40%	RLQQTQNQVDEVVDIMR	4.87	2,088.05
ATP	6011	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	7	7	13	0.14%	27.70%	DKLSELQLR	2.86	1,101.63
ATP	6011	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	7	7	13	0.14%	27.70%	EEYQPATPGLGMFVEVKDPEDK	2.75	2,495.17
ATP	6011	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	7	7	13	0.14%	27.70%	EEYQPATPGLGMFVEVKDPEDKVILAR	2.96	3,047.54
ATP	6011	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	7	7	13	0.14%	27.70%	FSLFAGGMLR	3.46	1,114.57

ATP	6011	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	7	7	13	0.14%	27.70%	QLVEQVEQIQK	4.45	1,341.74
ATP	6011	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	7	7	13	0.14%	27.70%	QLVEQVEQIQKEQNYQR	3.31	2,160.10
ATP	6011	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	7	7	13	0.14%	27.70%	QREEYQPATPGLGMFVEVKDPEDK	3.53	2,779.32
ATP	6011	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	6	11	0.12%	36.10%	EFADSLGIPFLETSAK	3.98	1,724.87
ATP	6011	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	6	11	0.12%	36.10%	FADDTYTESYISTIGVDFK	2.44	2,172.00
ATP	6011	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	6	11	0.12%	36.10%	LLLIGDSGVGK	3.3	1,071.64
ATP	6011	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	6	11	0.12%	36.10%	LQIWDTAGQER	2.72	1,316.66
ATP	6011	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	4	6	11	0.12%	36.10%	NATNVEQSFMTMAAEIK	2.56	1,900.88
ATP	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	11	15	21	0.23%	26.80%	FKAEHDQLLLNYAK	3.01	1,689.90
ATP	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	11	15	21	0.23%	26.80%	IESLSSQLSNLQK	4.38	1,446.78
ATP	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	11	15	21	0.23%	26.80%	IQELEDLLAK	3.2	1,171.66
ATP	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	11	15	21	0.23%	26.80%	LALDMEISAYRK	2.67	1,425.74
ATP	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	11	15	21	0.23%	26.80%	LAQALHEMREQHDAQVK	2.38	2,020.00
ATP	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	11	15	21	0.23%	26.80%	LREYEAALNSK	3.2	1,293.68

ATP	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	11	15	21	0.23%	26.80%	LYKEELEQTYHAK	3.83	1,651.83
ATP	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	11	15	21	0.23%	26.80%	MRIESLSSQLSNLQK	3.44	1,749.92
ATP	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	11	15	21	0.23%	26.80%	NMYEEEINETR	3.39	1,443.61
ATP	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	11	15	21	0.23%	26.80%	SLESDLEDLKDQIAQLEASLAAAK	5.35	2,558.32
ATP	6011	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	11	15	21	0.23%	26.80%	TTIPEEEEEEEAAEVAVEEELFHQQGAPR	4.46	3,425.55
ATP	6011	RecName: Full=40S ribosomal protein S20	gi|108860955,gi|61822677,gi|73587131,gi|77735823	13,355.00	100.00%	3	4	4	0.04%	22.70%	DTGKTPVEPEVAIHR	3.71	1,648.87
ATP	6011	RecName: Full=40S ribosomal protein S20	gi|108860955,gi|61822677,gi|73587131,gi|77735823	13,355.00	100.00%	3	4	4	0.04%	22.70%	LIDLHSPSEIVK	1.93	1,350.76
ATP	6011	RecName: Full=40S ribosomal protein S20	gi|108860955,gi|61822677,gi|73587131,gi|77735823	13,355.00	100.00%	3	4	4	0.04%	22.70%	TPVEPEVAIHR	4.14	1,247.67
ATP	6011	peroxiredoxin 1	gi|12407845,gi|151556396,gi|27806081,gi|28189861,gi|59858511,gi|66773956	22,148.30	99.80%	2	2	2	0.02%	11.10%	GLFIIDDKGILR	2.74	1,359.80
ATP	6011	peroxiredoxin 1	gi|12407845,gi|151556396,gi|27806081,gi|28189861,gi|59858511,gi|66773956	22,148.30	99.80%	2	2	2	0.02%	11.10%	TIAQDYGVLK	2.68	1,107.60
ATP	6011	CALM3 protein	gi|111308539,gi|114053089,gi|115305083,gi|157831834,gi|157879669,gi|194671098,gi|28189857,gi|49037473,gi|86822265	19,973.60	100.00%	3	5	7	0.08%	26.40%	EAFSLFDKDGDGTITTK	2.85	1,844.89

ATP	6011	CALM3 protein	gi|111308539,gi|114053089,gi|115305083,gi|157831834,gi|157879669,gi|194671098,gi|28189857,gi|49037473,gi|86822265	19,973.60	100.00%	3	5	7	0.08%	26.40%	MKDTDSEEEIREAFR	2.55	1,871.84
ATP	6011	CALM3 protein	gi|111308539,gi|114053089,gi|115305083,gi|157831834,gi|157879669,gi|194671098,gi|28189857,gi|49037473,gi|86822265	19,973.60	100.00%	3	5	7	0.08%	26.40%	VFDKDGNGYISAAELR	4.87	1,754.87
ATP	6011	RecName: Full=Cytochrome c oxidase polypeptide 7A2, mitochondrial; AltName: Full=Cytochrome c oxidase polypeptide VIIa-liver/heart; Short=Cytochrome c oxidase subunit VIIa-L; Short=VIIC; Flags: Precursor	gi|117120,gi|28461241,gi|488158,gi|74354141	9,305.40	99.80%	2	3	5	0.05%	27.70%	GGIADALLYR	3.32	1,048.58

ATP	6011	RecName: Full=Cytochrome c oxidase polypeptide 7A2, mitochondrial; AltName: Full=Cytochrome c oxidase polypeptide VIIa-liver/heart; Short=Cytochrome c oxidase subunit VIIa-L; Short=VIIIC; Flags: Precursor	gi|117120,gi|28461241,gi|488158,gi|74354141	9,305.40	99.80%	2	3	5	0.05%	27.70%	LFQEDNGIPVHLK	2.73	1,509.81
ATP	6011	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	2	2	2	0.02%	6.76%	ATTPVIMVGPGTGVAPFIGFIQER	4.06	2,474.31
ATP	6011	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	2	2	2	0.02%	6.76%	GMAADPEEYDLADLSSLPEIEK	4.17	2,409.10
ATP	6011	MTCH1 protein	gi|154426180,gi|157074126	41,499.70	100.00%	2	2	2	0.02%	8.23%	LLIQVGHEPMPPTIGTNVLGR	2.87	2,258.23
ATP	6011	MTCH1 protein	gi|154426180,gi|157074126	41,499.70	100.00%	2	2	2	0.02%	8.23%	LMSNALSTVTR	3.15	1,208.63
ATP	6011	RecName: Full=Histone H2A.V; AltName: Full=H2A.F/Z	gi|109940032,gi|163150,gi|27807373,gi|410,gi|81674301,gi|81674755,gi|83288407,gi|84000371	13,535.20	100.00%	3	6	8	0.09%	41.40%	ATIAGGGVIPHIHK	3.76	1,370.79

ATP	6011	RecName: Full=Histone H2A.V; AltName: Full=H2A.F/Z	gi|109940032,gi|163150,gi|27807373,gi|410,gi|81674301,gi|81674755,gi|83288407,gi|84000371	13,535.20	100.00%	3	6	8	0.09%	41.40%	GDEELDSLIK	3.01	1,118.56
ATP	6011	RecName: Full=Histone H2A.V; AltName: Full=H2A.F/Z	gi|109940032,gi|163150,gi|27807373,gi|410,gi|81674301,gi|81674755,gi|83288407,gi|84000371	13,535.20	100.00%	3	6	8	0.09%	41.40%	VGATAAVYSAILEYLTAEVLELAGNASK	4.75	2,895.54
ATP	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	13	15	0.16%	22.40%	ALEEAMEQKAELER	3.83	1,662.80
ATP	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	13	15	0.16%	22.40%	ANLQIDQLNTDLNLER	4.81	1,869.97
ATP	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	13	15	0.16%	22.40%	ELEDATETADAMNR	3.54	1,581.67
ATP	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	13	15	0.16%	22.40%	IAQLEEELEEEQGNTELVNDR	4.03	2,458.16
ATP	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	13	15	0.16%	22.40%	IAQLEEQLDNETK	3.85	1,530.76
ATP	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	13	15	0.16%	22.40%	IAQLEEQLDNETKER	2.61	1,815.91
ATP	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	13	15	0.16%	22.40%	LKDVLLQVDDERR	3.62	1,598.89
ATP	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	13	15	0.16%	22.40%	NAEQYKDQADKASTR	3.23	1,724.82
ATP	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	13	15	0.16%	22.40%	QAQQERDELADEIANSSGK	4.38	2,088.98
ATP	6011	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	10	13	15	0.16%	22.40%	QISTLHAQVTDMR	2.57	1,515.76

ATP	6011	NADH dehydrogenase	gi|240,gi|28461207,gi|400384,gi|74267733	15,035.50	99.80%	2	2	2	0.02%	14.80%	FFHETEAPRPK	2.75	1,358.69
ATP	6011	NADH dehydrogenase	gi|240,gi|28461207,gi|400384,gi|74267733	15,035.50	99.80%	2	2	2	0.02%	14.80%	VVDLLVIK	2.05	898.5973
ATP	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	12	17	28	0.31%	30.40%	AASFLLALEPELEAR	4.75	1,629.88
ATP	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	12	17	28	0.31%	30.40%	IDHILDAL	2.49	909.5042
ATP	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	12	17	28	0.31%	30.40%	ISVIVEAVYTHVLQPYPTQITQSEK	3.22	2,843.52
ATP	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	12	17	28	0.31%	30.40%	LPVALDPGAK	1.78	980.5777
ATP	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	12	17	28	0.31%	30.40%	LVDHVFDEQVIDSLTVK	3.21	1,957.03
ATP	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	12	17	28	0.31%	30.40%	NIQVDSPYEISR	3.48	1,420.71
ATP	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	12	17	28	0.31%	30.40%	QFVVFEGNHYFYSPYPTK	4.18	2,223.05
ATP	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	12	17	28	0.31%	30.40%	SEDLLDYGPFR	4.18	1,311.62
ATP	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	12	17	28	0.31%	30.40%	THYIVGYNLPSYEYLYNLGDQYALK	4.2	2,997.47
ATP	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	12	17	28	0.31%	30.40%	TVDLSSHLAK	3.1	1,070.58
ATP	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	12	17	28	0.31%	30.40%	VHSENNSPFLTITSMTR	4.29	1,949.94
ATP	6011	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	12	17	28	0.31%	30.40%	VTAEVVLAHAGSGSSPR	5.37	1,637.86
ATP	6011	RecName: Full=60S ribosomal protein L8	gi|108860941,gi|154426156,gi|74267654,gi|77736197	28,006.80	99.80%	2	2	2	0.02%	6.61%	ASGNYATVISHNPETK	1.88	1,688.82
ATP	6011	RecName: Full=60S ribosomal protein L8	gi|108860941,gi|154426156,gi|74267654,gi|77736197	28,006.80	99.80%	2	2	2	0.02%	6.61%	ASGNYATVISHNPETKK	3.12	1,816.92
ATP	6011	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	3	3	3	0.03%	4.61%	ALTLGALTLPLAR	2.81	1,309.82

ATP	6011	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	3	3	3	0.03%	4.61%	GEGSGTLGSLSLPLSELLVADR	4.36	2,171.16
ATP	6011	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	3	3	3	0.03%	4.61%	LLVPLVPDLQDVAQLR	2.44	1,789.06
ATP	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	7	7	0.08%	13.10%	ALLDSLQLGPDALTVHLINEVTK	2.33	2,460.37
ATP	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	7	7	0.08%	13.10%	LKVTEGGEPYR	2.65	1,248.66
ATP	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	7	7	0.08%	13.10%	LSFQHDPETSVLILR	4.38	1,754.94
ATP	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	7	7	0.08%	13.10%	MLDYLQGSGETPQTDVR	4.95	1,925.89
ATP	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	7	7	0.08%	13.10%	QYASLTGTQALPPLFSLGYHQSR	3.61	2,535.30
ATP	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	7	7	0.08%	13.10%	VVIIGAGKPATVVLQTK	3.98	1,694.06
ATP	6011	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	7	7	0.08%	13.10%	YHGPQTLYLPVTLSSIPVFQR	4.3	2,416.30
ATP	6011	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	99.80%	2	2	2	0.02%	2.58%	DVIDKQHTEQEASYGR	4.36	1,875.88
ATP	6011	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	99.80%	2	2	2	0.02%	2.58%	LNQPQPDFTK	2.43	1,187.61
ATP	6011	RecName: Full=Pyruvate dehydrogenase E1 component subunit beta, mitochondrial; Short=PDHE1-B; Flags: Precursor	gi|116242689,gi|151556071,gi|164420789	39,108.20	99.90%	2	2	2	0.02%	8.91%	EAINQGMDEELERDEK	2.84	1,921.84

ATP	6011	RecName: Full=Pyruvate dehydrogenase E1 component subunit beta, mitochondrial; Short=PDHE1-B; Flags: Precursor	gi|116242689,gi|151556071,gi|164420789	39,108.20	99.90%	2	2	2	0.02%	8.91%	IMEGPAFNFLDAPAVR	4.19	1,763.88
ATP	6011	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	5	16	0.17%	20.10%	DYPLPDVAHVK	2.59	1,253.65
ATP	6011	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	5	16	0.17%	20.10%	FKESFAEMNR	3.98	1,274.58

ATP	6011	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	5	16	0.17%	20.10%	SEDYALPSYVDR	3.66	1,414.65
ATP	6011	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	5	16	0.17%	20.10%	SEDYALPSYVDRR	2.14	1,570.75
ATP	6011	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	6	10	18	0.20%	11.10%	APVPTGEVYFADSFDR	3.95	1,770.83
ATP	6011	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	6	10	18	0.20%	11.10%	KIPNPDFFEDLEPFK	5.69	1,835.92
ATP	6011	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	6	10	18	0.20%	11.10%	LPGDKGLVLMSR	2.09	1,301.72
ATP	6011	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	6	10	18	0.20%	11.10%	TPELNLDQFHDK	3.34	1,456.71
ATP	6011	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	6	10	18	0.20%	11.10%	TPELNLDQFHDKTPYTIMFGPDK	4.38	2,723.30

ATP	6011	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	6	10	18	0.20%	11.10%	TPYTIMFGPDK	3.58	1,285.61
ATP	6011	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	10	17	0.19%	29.10%	AKMDAQQEPNIQLDHLNLLK	2.44	2,335.21
ATP	6011	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	10	17	0.19%	29.10%	DLELLIQTATR	2.97	1,272.72
ATP	6011	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	10	17	0.19%	29.10%	ELQQAVLQMEQR	3.47	1,488.75
ATP	6011	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	10	17	0.19%	29.10%	KQQQQSHNNPAPGPEGQLK	3.3	2,086.04
ATP	6011	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	10	17	0.19%	29.10%	LVTLEEFLASTQR	2.79	1,506.82
ATP	6011	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	10	17	0.19%	29.10%	TFFILHDINSDGVLDEQELEALFTK	3.8	2,894.45
ATP	6011	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	10	17	0.19%	29.10%	VNVPGSQAQLK	2.62	1,140.64
ATP	6011	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	10	17	0.19%	29.10%	YLESLGEEQRK	3.28	1,351.69
ATP	6011	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	9	10	17	0.19%	29.10%	YLQEVINVLETDGHFR	3.62	1,932.98
ATP	6011	nicalin	gi|115494944,gi|94534903	63,091.10	99.80%	2	2	2	0.02%	6.23%	AAQLVDKDGTFLSTLEHYLSR	6	2,364.22
ATP	6011	nicalin	gi|115494944,gi|94534903	63,091.10	99.80%	2	2	2	0.02%	6.23%	MQQYDLQGQPYGTR	4.57	1,700.77
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	DDKESVPISDTIIPAVPPPTDLR	3.03	2,475.30
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	DLQFVEVTDVK	3.46	1,292.67
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	EINLAPDSSSVVVSGLMVATK	4.47	2,133.11
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	GATYNIIVEAVK	3.27	1,277.71

ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	GDSPASSKPVSINYR	4.1	1,577.79
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	GLAFTDVDVDSIK	3.06	1,379.71
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	GLRPGVVYEGQLISVQHYGQR	5.16	2,356.25
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	NLQPGSEYAVSLVAVK	4.54	1,674.91
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	NSITLTNLNPGTEYVVSIVALNSK	4.03	2,547.37
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	NTFAEVTGLSPGVTYHFK	4.83	1,967.99
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	QYNVGPAASQYPLR	3.86	1,563.79
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	RPGAEPGNEGSTAHSYNQYSQR	5.11	2,406.08
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	SSPVVIDASTAIDAPSNLR	3.71	1,913.00
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	STATISGLKPGVDYTITVYAVTGR	3.5	2,470.32
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	SYTITGLQPGTDYK	3.8	1,543.76

ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	TEIDKPSQMQVTDVQDNSISVR	6.16	2,506.21
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	TETITGFQVDAIPANGQTPIQR	3.53	2,357.21
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	TKTETITGFQVDAIPANGQTPIQR	3.51	2,586.35
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	TPFITNPGYDTGNGIQLPGTSGQQPSLGQQMIFEEHGFRR	3.16	4,392.11
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	VDVIPVNLPGEHGQR	2.52	1,629.87
ATP	6011	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	21	25	29	0.32%	16.00%	VPGTSASATLTGLTR	4.64	1,431.78
ATP	6011	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	4	6	10	0.11%	22.70%	KLPPLPLTLALGAFLNHR	3.45	1,971.19
ATP	6011	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	4	6	10	0.11%	22.70%	MQDTSVSFGYQLDLPK	3.94	1,844.87
ATP	6011	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	4	6	10	0.11%	22.70%	QLSPTEAFPVLVGDMDNSGSLNAQVIHQLGPGLR	4.32	3,576.81
ATP	6011	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	4	6	10	0.11%	22.70%	RPGEEGAVMSLAGK	3.06	1,417.71

ATP	6011	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	4	4	4	0.04%	5.30%	KADVGFAMGIAGTDVAK	3.28	1,666.85
ATP	6011	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	4	4	4	0.04%	5.30%	QVVAVTGDGTNDGPALK	4.91	1,641.84
ATP	6011	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	4	4	4	0.04%	5.30%	TNPVEGLSGNPADLEK	2.95	1,640.81
ATP	6011	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	4	4	4	0.04%	5.30%	TPLLDEQEEEIFEK	3.6	1,719.83
ATP	6011	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	6	8	29	0.32%	35.40%	AGLQFPVGR	3.25	944.5313
ATP	6011	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	6	8	29	0.32%	35.40%	HLQLAIR	2.59	850.5258
ATP	6011	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	6	8	29	0.32%	35.40%	HLQLAIRNDEELNK	2.61	1,692.90

ATP	6011	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	6	8	29	0.32%	35.40%	HLQLAIRNDEELNKLLGK	2.73	2,104.19
ATP	6011	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	6	8	29	0.32%	35.40%	NDEELNKLLGK	3.86	1,272.68
ATP	6011	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	6	8	29	0.32%	35.40%	VTIAQGGVLPNIQAVLLPK	5.09	1,931.17
ATP	6011	cpn10 protein	gi|1167,gi|27805927,gi|47606334,gi|74354139	10,913.70	99.80%	2	2	2	0.02%	25.50%	VLQATVVAVGSGSK	3.31	1,315.76
ATP	6011	cpn10 protein	gi|1167,gi|27805927,gi|47606334,gi|74354139	10,913.70	99.80%	2	2	2	0.02%	25.50%	VVLDDKDYFLFR	2.43	1,529.80
ATP	6011	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	100.00%	3	3	3	0.03%	8.29%	EIPVLVTQISSTNHPVK	4.83	1,862.04
ATP	6011	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	100.00%	3	3	3	0.03%	8.29%	VGLSDAFVVVHR	4.56	1,298.72
ATP	6011	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	100.00%	3	3	3	0.03%	8.29%	VNLSFDFPFYGHFLR	3.2	1,858.93

ATP	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	15	21	30	0.33%	39.10%	ASLDRPFTSLESAFYSIVGLSSLGAQVPDVK	4.71	3,254.69
ATP	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	15	21	30	0.33%	39.10%	EETVLATVQALQTASYLSQQADLR	3	2,635.36

ATP	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	15	21	30	0.33%	39.10%	FELDTSER	2.42	996.4633
ATP	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	15	21	30	0.33%	39.10%	FSSGYYDFSVK	3.53	1,299.59

ATP	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	15	21	30	0.33%	39.10%	ISTEVGITNVDLSTVDKDQSIAPK	5.37	2,530.33
ATP	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	15	21	30	0.33%	39.10%	KNFESLSEAFSVASAAALSENR	3.36	2,399.18

ATP	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	15	21	30	0.33%	39.10%	LDELGGVYLQFEEGLETTALFVAATYK	3.7	2,977.51
ATP	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	15	21	30	0.33%	39.10%	LMDHVGTEPSIKEDQVIQLMNAIFSK	3.18	2,959.49

ATP	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	15	21	30	0.33%	39.10%	LQVTNVLSQPLTQATVK	4.97	1,840.05
ATP	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	15	21	30	0.33%	39.10%	LSKEETVLATVQALQTASYLSQQADLR	5.76	2,963.57

ATP	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	15	21	30	0.33%	39.10%	NFESLSEAFSVASAAAALSENR	3.55	2,271.09
ATP	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	15	21	30	0.33%	39.10%	SIVEEIEDLVAR	4	1,372.73

ATP	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	15	21	30	0.33%	39.10%	TGQEVVFVAEPDSK	3.63	1,505.75
ATP	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	15	21	30	0.33%	39.10%	TSFTLIGDVFELNFMNVKFSSGYYDFSVK	2.35	3,355.62

ATP	6011	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	15	21	30	0.33%	39.10%	YIANTVELR	3.23	1,078.59
ATP	6011	RecName: Full=60S acidic ribosomal protein P2	gi|1173072,gi|27807523,gi|600177,gi|82571755	11,684.40	100.00%	6	7	7	0.08%	73.90%	ILDSVGIEADDDRLNK	5.1	1,772.90
ATP	6011	RecName: Full=60S acidic ribosomal protein P2	gi|1173072,gi|27807523,gi|600177,gi|82571755	11,684.40	100.00%	6	7	7	0.08%	73.90%	KILDSVGIEADDDRLNK	3.02	1,901.00
ATP	6011	RecName: Full=60S acidic ribosomal protein P2	gi|1173072,gi|27807523,gi|600177,gi|82571755	11,684.40	100.00%	6	7	7	0.08%	73.90%	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	3.49	2,774.43
ATP	6011	RecName: Full=60S acidic ribosomal protein P2	gi|1173072,gi|27807523,gi|600177,gi|82571755	11,684.40	100.00%	6	7	7	0.08%	73.90%	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKKEEK	3.69	3,288.71
ATP	6011	RecName: Full=60S acidic ribosomal protein P2	gi|1173072,gi|27807523,gi|600177,gi|82571755	11,684.40	100.00%	6	7	7	0.08%	73.90%	NIEDVIAQGIGK	3.66	1,256.68
ATP	6011	RecName: Full=60S acidic ribosomal protein P2	gi|1173072,gi|27807523,gi|600177,gi|82571755	11,684.40	100.00%	6	7	7	0.08%	73.90%	YVASYLLAALGGNSSPSAK	4.59	1,868.98

ATP	6011	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	99.80%	2	3	3	0.03%	7.70%	GLLPQLLGVAPEK	2.35	1,334.80
ATP	6011	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	99.80%	2	3	3	0.03%	7.70%	IAPLEEGTLPFNLAEAQR	3.8	1,969.04
ATP	6011	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	99.80%	2	3	3	0.03%	7.70%	LTVNDFVR	2.32	963.5258

ATP	6011	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	99.80%	2	3	3	0.03%	7.70%	YLNIFGESQPNPK	4	1,506.76
ATP	6011	RecName: Full=DnaJ homolog subfamily B member 11; AltName: Full=ER-associated dnaJ protein 3; AltName: Full=ERj3p; AltName: Full=ERdj3; AltName: Full=ER-associated Hsp40 co-chaperon	gi|122140749,gi|73587163,gi|77735491	40,486.60	100.00%	3	3	3	0.03%	18.40%	FQDLGAAYEVLSDSEK	2.83	1,771.84

ATP	6011	RecName: Full=DnaJ homolog subfamily B member 11; AltName: Full=ER-associated dnaJ protein 3; AltName: Full=ERj3p; AltName: Full=ERdj3; AltName: Full=ER-associated Hsp40 co-chaperon	gi|122140749,gi|73587163,gi|77735491	40,486.60	100.00%	3	3	3	0.03%	18.40%	FQMTQEVVCDECPNVK	3.21	1,885.81
ATP	6011	RecName: Full=DnaJ homolog subfamily B member 11; AltName: Full=ER-associated dnaJ protein 3; AltName: Full=ERj3p; AltName: Full=ERdj3; AltName: Full=ER-associated Hsp40 co-chaperon	gi|122140749,gi|73587163,gi|77735491	40,486.60	100.00%	3	3	3	0.03%	18.40%	TLEVEIEPGVRDGMEYPFIGEGEPHVDGEPGDLR	3.63	3,754.75
ATP	6011	FXYD domain containing ion transport regulator 6	gi|75775070,gi|77735753,gi|91206665	10,447.10	99.80%	2	2	2	0.02%	26.30%	APGDEEAQVENLVTANATEPQK	3.88	2,311.11
ATP	6011	FXYD domain containing ion transport regulator 6	gi|75775070,gi|77735753,gi|91206665	10,447.10	99.80%	2	2	2	0.02%	26.30%	APGDEEAQVENLVTANATEPQKAEN	4.53	2,625.23
ATP	6011	Synaptojanin 2 binding protein	gi|74354054,gi|78369420	15,792.00	99.80%	2	4	7	0.08%	19.30%	LQEGDKILSVNGQDLK	5.41	1,756.94

ATP	6011	Synaptojanin 2 binding protein	gi|74354054,gi|78369420	15,792.00	99.80%	2	4	7	0.08%	19.30%	NLLHQDAVDLFR	3.81	1,440.76
ATP	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	13	18	33	0.36%	19.70%	DYAKDDPLEFK	3.09	1,340.64
ATP	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	13	18	33	0.36%	19.70%	FDLQIQSSNLFDK	3.93	1,554.78
ATP	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	13	18	33	0.36%	19.70%	FDLQIQSSNLFDKVSPVVSYK	3.81	2,414.26
ATP	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	13	18	33	0.36%	19.70%	FGSAIAPLGDLDQDGFNDIAIAAPYGGEDKK	3.88	3,165.54
ATP	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	13	18	33	0.36%	19.70%	FSVHQQSEMDTSVK	4.09	1,638.74
ATP	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	13	18	33	0.36%	19.70%	GATDIDKNGYPDLIVGAFGVDR	4.02	2,293.15
ATP	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	13	18	33	0.36%	19.70%	GIVYIFNGRPTGLNAVPSQILEGK	4.29	2,543.40
ATP	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	13	18	33	0.36%	19.70%	IYIGDDNPLTLIVK	4.06	1,573.88
ATP	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	13	18	33	0.36%	19.70%	MFLLVGAPK	3.42	991.5647
ATP	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	13	18	33	0.36%	19.70%	PTGLNAVPSQILEGK	3.85	1,523.84
ATP	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	13	18	33	0.36%	19.70%	SSASFNVIEFPYK	3.95	1,488.74
ATP	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	13	18	33	0.36%	19.70%	VRPPQEEQEREQLQPHENGEGNSET	2.14	2,917.33
ATP	6011	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	13	18	33	0.36%	19.70%	YKENPETEEDVGPVVQHIYELR	6.24	2,644.29
ATP	6011	poly(A) binding protein, cytoplasmic 1	gi|41386798,gi|47117093,gi|74268035,gi|8979741	70,653.30	100.00%	3	3	3	0.03%	6.60%	ALDTMNFDVIK	2.65	1,282.64
ATP	6011	poly(A) binding protein, cytoplasmic 1	gi|41386798,gi|47117093,gi|74268035,gi|8979741	70,653.30	100.00%	3	3	3	0.03%	6.60%	IVATKPLYVALAQR	3.61	1,542.94
ATP	6011	poly(A) binding protein, cytoplasmic 1	gi|41386798,gi|47117093,gi|74268035,gi|8979741	70,653.30	100.00%	3	3	3	0.03%	6.60%	SLGYAYVNFQQPADAER	3.68	1,928.91

ATP	6011	RecName: Full=Monocarboxylate transporter 1; Short=MCT 1; AltName: Full=Solute carrier family 16 member 1	gi|122139973,gi|77567740,gi|82617542	54,281.70	100.00%	4	4	5	0.05%	6.99%	ESKDEETNVDVAEKPK	2.38	1,817.88
ATP	6011	RecName: Full=Monocarboxylate transporter 1; Short=MCT 1; AltName: Full=Solute carrier family 16 member 1	gi|122139973,gi|77567740,gi|82617542	54,281.70	100.00%	4	4	5	0.05%	6.99%	GASDANTDLIGGNPK	3.54	1,429.69
ATP	6011	RecName: Full=Monocarboxylate transporter 1; Short=MCT 1; AltName: Full=Solute carrier family 16 member 1	gi|122139973,gi|77567740,gi|82617542	54,281.70	100.00%	4	4	5	0.05%	6.99%	GASDANTDLIGGNPKEEK	3.14	1,815.87
ATP	6011	RecName: Full=Monocarboxylate transporter 1; Short=MCT 1; AltName: Full=Solute carrier family 16 member 1	gi|122139973,gi|77567740,gi|82617542	54,281.70	100.00%	4	4	5	0.05%	6.99%	GASDANTDLIGGNPKEEKK	2.74	1,943.97

ATP	6011	PREDICTED: similar to programmed cell death 6 interacting protein isoform 1	gi|119914274	96,862.00	99.80%	2	2	2	0.02%	4.69%	EPSAPSIPTPTYQSSPAGGHAPTPPTPAPR	2.17	2,966.46
ATP	6011	PREDICTED: similar to programmed cell death 6 interacting protein isoform 1	gi|119914274	96,862.00	99.80%	2	2	2	0.02%	4.69%	NIQVSHQEFSK	3.53	1,316.66
ATP	6011	Actin related protein 2/3 complex, subunit 4, 20kDa	gi|109939945,gi|115495705,gi|119361249,gi|149243014,gi|149243029,gi|149243036,gi|149243043,gi|149243050,gi|149243057,gi|149243064,gi|56966197	19,649.40	99.80%	2	2	2	0.02%	11.30%	AENFFILR	2.25	1,009.55
ATP	6011	Actin related protein 2/3 complex, subunit 4, 20kDa	gi|109939945,gi|115495705,gi|119361249,gi|149243014,gi|149243029,gi|149243036,gi|149243043,gi|149243050,gi|149243057,gi|149243064,gi|56966197	19,649.40	99.80%	2	2	2	0.02%	11.30%	ELLLQPVTISR	3.37	1,268.76
ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	AVDSLVPIGR	3.56	1,026.59
ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	EAYPGDVFYLHSR	2.82	1,553.74

ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	EVAAFAQFGSDLDAATQQLLSR	4.72	2,338.17
ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	FENAFLSHVISQHQALLSK	3.17	2,169.15
ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	GIRPAINVGLSVSR	3.62	1,438.85
ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	GMSLNLEPDNVGVVVFGNDK	4.07	2,120.03
ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	GYLDKLEPSK	1.89	1,149.62
ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	HALIIYDDLSK	3.71	1,287.69

ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	ILGADTSVDLEETGR	4.26	1,575.79
ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	ITKFENAFLSHVISQHQALLSK	3.32	2,511.37
ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	LELAQYR	2.6	892.4887
ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	LKEIVTNFLAGFEA	3.52	1,551.84
ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	TGAIVDVPVGEELLGR	4.28	1,624.89
ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	TGTAEVSSILEER	4.35	1,391.70

ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	TSIAIDTIINQK	3.11	1,316.74
ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	VGLKAPGIIPR	3.02	1,120.72
ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	VLSIGDGIAR	2.42	1,000.58
ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	VVDALGNAIDGK	3.49	1,171.63
ATP	6011	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	19	24	43	0.47%	46.70%	VVDALGNAIDGKGPIGSK	5.37	1,710.94
ATP	6011	PREDICTED: similar to 60S ribosomal protein L9	gi|119904384,gi|119905715,gi|164420694,gi|76607197,gi|91207745	21,858.70	99.80%	2	3	3	0.03%	15.10%	FLDGIYVSEK	3.06	1,170.60
ATP	6011	PREDICTED: similar to 60S ribosomal protein L9	gi|119904384,gi|119905715,gi|164420694,gi|76607197,gi|91207745	21,858.70	99.80%	2	3	3	0.03%	15.10%	TILSNQTVDIPENVDINLK	4.35	2,126.13

ATP	6011	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	10	13	0.14%	38.20%	IMVANIEEVLQR	4.44	1,430.77
ATP	6011	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	10	13	0.14%	38.20%	KLAFAYLEDLHSEFDEQHGK	5.11	2,377.15
ATP	6011	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	10	13	0.14%	38.20%	KVPTVSRPYSFIEFDTYIQK	2.98	2,418.27
ATP	6011	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	10	13	0.14%	38.20%	NLGSINTELQDVQR	5	1,586.81
ATP	6011	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	10	13	0.14%	38.20%	RNLGSINTELQDVQR	3.4	1,742.91
ATP	6011	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	10	13	0.14%	38.20%	VADGLPLAASMQEDEQSGR	4.21	1,989.92
ATP	6011	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	7	10	13	0.14%	38.20%	VADGLPLAASMQEDEQSGRDLQQYQSQAK	4.51	3,179.49
ATP	6011	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	3	3	5	0.05%	13.60%	INVNEIFYDLVR	4.77	1,494.80
ATP	6011	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	3	3	5	0.05%	13.60%	LVVLGSGGVGK	2.85	985.6042
ATP	6011	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	3	3	5	0.05%	13.60%	SKINVNEIFYDLVR	4.02	1,709.92
ATP	6011	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	3	4	4	0.04%	7.89%	KREEAAAAPAPAADDQGVLK	3.26	2,079.08
ATP	6011	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	3	4	4	0.04%	7.89%	TELGLDLGLEPK	3.18	1,284.70
ATP	6011	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	3	4	4	0.04%	7.89%	TISTSDPADALIK	2.98	1,331.71

ATP	6011	Reticulocalbin 2, EF-hand calcium binding domain	gi|111304972,gi|115497628	36,892.40	100.00%	3	3	3	0.03%	17.70%	ADYDREALLGGQEEVDEYVK	4.21	2,299.07
ATP	6011	Reticulocalbin 2, EF-hand calcium binding domain	gi|111304972,gi|115497628	36,892.40	100.00%	3	3	3	0.03%	17.70%	KLSEEEILENQDLFLTSEATDYGR	2.68	2,800.35
ATP	6011	Reticulocalbin 2, EF-hand calcium binding domain	gi|111304972,gi|115497628	36,892.40	100.00%	3	3	3	0.03%	17.70%	QLHDEYFYHDEL	3.05	1,608.70
ATP	6011	RecName: Full=ATP synthase subunit g, mitochondrial; Short=ATPase subunit g	gi|2493093,gi|74354012,gi|75799222,gi|94400870	11,604.00	100.00%	3	5	10	0.11%	37.50%	APALVNAAVTYSKPR	3.69	1,557.87
ATP	6011	RecName: Full=ATP synthase subunit g, mitochondrial; Short=ATPase subunit g	gi|2493093,gi|74354012,gi|75799222,gi|94400870	11,604.00	100.00%	3	5	10	0.11%	37.50%	NLAEKAPALVNAAVTYSKPR	4.31	2,113.18
ATP	6011	RecName: Full=ATP synthase subunit g, mitochondrial; Short=ATPase subunit g	gi|2493093,gi|74354012,gi|75799222,gi|94400870	11,604.00	100.00%	3	5	10	0.11%	37.50%	VELVPPTPAEIPTAIQSLK	3	2,003.14
ATP	6011	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	100.00%	3	3	3	0.03%	16.20%	DTILQLNLK	2.6	1,057.63
ATP	6011	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	100.00%	3	3	3	0.03%	16.20%	VADPAYLPTQQDVLR	3.61	1,685.89

ATP	6011	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	100.00%	3	3	3	0.03%	16.20%	VRVPTTGIIEYPFDLQSVIFR	5.7	2,450.34
ATP	6011	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	100.00%	3	3	3	0.03%	16.20%	VSAFENPYVDAIK	3.69	1,452.74
ATP	6011	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	99.90%	2	2	2	0.02%	3.66%	LPVPASAPIPFFHR	3.46	1,548.87
ATP	6011	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	99.90%	2	2	2	0.02%	3.66%	VLMEFVENSR	2.69	1,239.60
ATP	6011	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	4	4	4	0.04%	14.00%	GFKDQIYDIFQK	3.93	1,501.77
ATP	6011	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	4	4	4	0.04%	14.00%	GIYAYGFEKPSAIQQR	2.74	1,827.94

ATP	6011	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	4	4	4	0.04%	14.00%	GYDVIAQAQSGTGK	3.41	1,394.69
ATP	6011	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	4	4	4	0.04%	14.00%	LQMEAPHIIVGTPGR	3.26	1,634.87
ATP	6011	RecName: Full=Mitochondrial Rho GTPase 1; Short=MIRO-1; AltName: Full=Ras homolog gene family member T1	gi|108860795,gi|114051724,gi|88682961	72,061.70	100.00%	2	3	3	0.03%	4.91%	ISDQDNDGTLNDAELNFFQR	3.97	2,312.04

ATP	6011	RecName: Full=Mitochondrial Rho GTPase 1; Short=MIRO-1; AltName: Full=Ras homolog gene family member T1	gi|108860795,gi|114051724,gi|88682961	72,061.70	100.00%	2	3	3	0.03%	4.91%	NISELFYYAQK	2.69	1,375.69
ATP	6011	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	11	15	0.16%	27.00%	GAAGRPLELSDFR	2.15	1,388.73
ATP	6011	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	11	15	0.16%	27.00%	GPPDFSSDEEREPTPVLGSGAAVAGR	4.62	2,598.24
ATP	6011	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	11	15	0.16%	27.00%	HAAPILPITEFSDIPR	3.17	1,776.96
ATP	6011	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	11	15	0.16%	27.00%	LKSELVANNVTLPAGEQR	5.41	1,939.06
ATP	6011	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	11	15	0.16%	27.00%	LKSELVANNVTLPAGEQRK	3.71	2,067.16
ATP	6011	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	11	15	0.16%	27.00%	SELVANNVTLPAGEQR	4.3	1,697.88
ATP	6011	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	11	15	0.16%	27.00%	SSTPLPTISSSVENTR	2.99	1,675.85
ATP	6011	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	11	15	0.16%	27.00%	YGVNPGPIVGTTR	3.1	1,330.71
ATP	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	10	10	0.11%	19.70%	FGLYLPK	2.67	837.487
ATP	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	10	10	0.11%	19.70%	FKPPSVAVVQPK	3.44	1,296.77
ATP	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	10	10	0.11%	19.70%	FTLGSVAGAVGATAVYPIDLVK	3.98	2,149.19
ATP	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	10	10	0.11%	19.70%	GLIPQLIGVAPEK	2.35	1,334.80
ATP	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	10	10	0.11%	19.70%	HLNYTEFTQFLQELQLEHAR	4.98	2,517.25
ATP	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	10	10	0.11%	19.70%	IAPLAEGALPYNLAELQR	3.77	1,939.06
ATP	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	10	10	0.11%	19.70%	LATATFAGIENK	3.28	1,235.66

ATP	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	10	10	0.11%	19.70%	LTLADIER	2.17	930.5256
ATP	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	10	10	0.11%	19.70%	LTVNDFVR	2.32	963.5258
ATP	6011	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	10	10	0.11%	19.70%	YLGLYNDPNSNPK	4.07	1,494.72
ATP	6011	RecName: Full=Cytochrome b5	gi|117806,gi|1372997,gi|157830773,gi|27806667,gi|298,gi|79160196	15,311.60	100.00%	3	3	3	0.03%	34.30%	EQAGGDATENFEDVGHSTDAR	2.79	2,205.93
ATP	6011	RecName: Full=Cytochrome b5	gi|117806,gi|1372997,gi|157830773,gi|27806667,gi|298,gi|79160196	15,311.60	100.00%	3	3	3	0.03%	34.30%	FLEEHPGGEEVLR	2.32	1,511.75
ATP	6011	RecName: Full=Cytochrome b5	gi|117806,gi|1372997,gi|157830773,gi|27806667,gi|298,gi|79160196	15,311.60	100.00%	3	3	3	0.03%	34.30%	TFIIGELHPDDR	3.39	1,412.72
ATP	6011	ALDH3A2 protein	gi|151557095,gi|156120617	54,059.30	99.80%	2	2	2	0.02%	4.95%	IAFGGEMDEATR	3.04	1,312.58
ATP	6011	ALDH3A2 protein	gi|151557095,gi|156120617	54,059.30	99.80%	2	2	2	0.02%	4.95%	NADEAIQFINER	3.02	1,419.69
ATP	6011	IKK interacting protein	gi|126010633,gi|126165284,gi|193806036	39,199.60	100.00%	3	3	3	0.03%	13.50%	LEPLVNDLTLR	2.45	1,282.74
ATP	6011	IKK interacting protein	gi|126010633,gi|126165284,gi|193806036	39,199.60	100.00%	3	3	3	0.03%	13.50%	METSEFQGLQSK	3.89	1,400.64
ATP	6011	IKK interacting protein	gi|126010633,gi|126165284,gi|193806036	39,199.60	100.00%	3	3	3	0.03%	13.50%	MSGLVTDVTSLTDSVQELENKIEK	3.51	2,652.33
ATP	6011	defender against cell death 1	gi|59858361,gi|73918963,gi|74354770,gi|77736467,gi|83286811	12,477.50	99.80%	2	2	4	0.04%	19.50%	ADFQGISPER	3	1,119.54
ATP	6011	defender against cell death 1	gi|59858361,gi|73918963,gi|74354770,gi|77736467,gi|83286811	12,477.50	99.80%	2	2	4	0.04%	19.50%	FLEEYLSATPQR	3.28	1,453.73
ATP	6011	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	2	2	2	0.02%	3.31%	GNSSESIEAIRDYEEEFFQNSK	3.89	2,579.15

ATP	6011	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	2	2	2	0.02%	3.31%	TSVLEMIAQAR	2.75	1,234.65
ATP	6011	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	5	8	10	0.11%	12.60%	ELQALTDAMYTNLR	3.7	1,654.81
ATP	6011	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	5	8	10	0.11%	12.60%	LLLFPFLSPQK	2.47	1,302.78
ATP	6011	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	5	8	10	0.11%	12.60%	LLLFPFLSPQKDPEIYTDPEVFK	2.48	2,736.45
ATP	6011	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	5	8	10	0.11%	12.60%	LTAAPFITR	2.7	989.5779
ATP	6011	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	5	8	10	0.11%	12.60%	VLDSMPVLDSVLSESLR	4.16	1,875.97
ATP	6011	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	3	3	3	0.03%	6.03%	AFITNIPFDVK	2.35	1,264.69
ATP	6011	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	3	3	3	0.03%	6.03%	GNFGGSFAGSFGGAGGHAPGVAR	3.72	2,034.95
ATP	6011	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	3	3	3	0.03%	6.03%	INEILSNALK	2.69	1,114.65
ATP	6011	PREDICTED: similar to signal peptidase complex subunit 2 homolog	gi|194673376	24,871.10	99.80%	2	2	3	0.03%	13.30%	FFDHSGTLVMDAYEPEISR	5.07	2,230.01

ATP	6011	PREDICTED: similar to signal peptidase complex subunit 2 homolog	gi|194673376	24,871.10	99.80%	2	2	3	0.03%	13.30%	YVENFGLIDGR	2.87	1,282.64
ATP	6011	KRT6A protein	gi|133778363,gi|134085706	60,803.10	99.80%	2	2	3	0.03%	11.60%	AQYEEIAQR	2.63	1,107.54
ATP	6011	KRT6A protein	gi|133778363,gi|134085706	60,803.10	99.80%	2	2	3	0.03%	11.60%	NKYEDEINKR	3.37	1,308.65
ATP	6011	KRT6A protein	gi|133778363,gi|134085706	60,803.10	99.80%	2	2	3	0.03%	11.60%	NLDLDSIIAEVK	4.82	1,329.73
ATP	6011	KRT6A protein	gi|133778363,gi|134085706	60,803.10	99.80%	2	2	3	0.03%	11.60%	QNLEPLFEQYINNLR	3.73	1,890.97
ATP	6011	KRT6A protein	gi|133778363,gi|134085706	60,803.10	99.80%	2	2	3	0.03%	11.60%	WTLLQEQGTK	3.48	1,203.64
ATP	6011	KRT6A protein	gi|133778363,gi|134085706	60,803.10	99.80%	2	2	3	0.03%	11.60%	YEELQVTAGR	2.67	1,165.58
ATP	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	6	0.07%	46.60%	AILVDLEPGTMDSVR	4	1,631.83
ATP	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	6	0.07%	46.60%	ALTVPELTQQVFDAK	3.57	1,659.90
ATP	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	6	0.07%	46.60%	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	3.88	3,213.49
ATP	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	6	0.07%	46.60%	EVDEQMLNVQNK	2.82	1,462.68
ATP	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	6	0.07%	46.60%	GHYTEGAELVDSVLDVVR	3.5	1,958.98
ATP	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	6	0.07%	46.60%	GHYTEGAELVDSVLDVVRK	3.56	2,087.08
ATP	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	6	0.07%	46.60%	IMNTFSVVPSPK	3.78	1,335.70
ATP	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	6	0.07%	46.60%	IREEYPDRIMNTFSVVPSPK	3.08	2,394.21
ATP	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	6	0.07%	46.60%	ISEQFTAMFR	3	1,245.59
ATP	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	6	0.07%	46.60%	ISVYYNEATGGK	3.93	1,301.64

ATP	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	6	0.07%	46.60%	LAVNMVPFPR	3.53	1,159.63
ATP	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	6	0.07%	46.60%	LHFFMPGFAPLTSR	3.38	1,636.83
ATP	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	6	0.07%	46.60%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	4.25	4,479.06
ATP	6011	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	3	6	0.07%	46.60%	YLTVAAVFR	2.56	1,039.59
ATP	6011	melanoma cell adhesion molecule	gi|2323281	9,468.30	99.80%	2	3	6	0.07%	22.10%	SDKLPEEMGLLQGSSGDK	4.99	1,906.91
ATP	6011	melanoma cell adhesion molecule	gi|2323281	9,468.30	99.80%	2	3	6	0.07%	22.10%	SDKLPEEMGLLQGSSGDKR	4.4	2,063.01
ATP	6011	RecName: Full=Ornithine aminotransferase, mitochondrial; AltName: Full=Ornithine--oxo-acid aminotransferase; Flags: Precursor	gi|122140925,gi|73586966,gi|77735431	48,058.30	99.80%	2	2	2	0.02%	5.24%	GLLNAIVIR	2.78	968.6252
ATP	6011	RecName: Full=Ornithine aminotransferase, mitochondrial; AltName: Full=Ornithine--oxo-acid aminotransferase; Flags: Precursor	gi|122140925,gi|73586966,gi|77735431	48,058.30	99.80%	2	2	2	0.02%	5.24%	TVQGPPSSDYIFER	3.64	1,595.77
ATP	6011	RAP2B protein	gi|134025188,gi|154425870,gi|156523174	20,470.40	99.80%	2	2	2	0.02%	22.40%	EIEVDSSPSVLEILDTAGTEQFASMR	2.8	2,840.35

ATP	6011	RAP2B protein	gi|134025188,gi|154425870,gi|156523174	20,470.40	99.80%	2	2	2	0.02%	22.40%	VDLEGEREVSFGEGK	2.59	1,650.80
ATP	6011	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	3	5	106	1.16%	25.50%	LLGNVLVVVLAR	5.08	1,265.83
ATP	6011	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	3	5	106	1.16%	25.50%	VKVDEVGGEALGR	3.74	1,328.72
ATP	6011	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	3	5	106	1.16%	25.50%	VVTGVANALAHR	2.96	1,207.69
ATP	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	10	10	0.11%	6.99%	AFGPGLQGGSAGSPAR	4.44	1,429.72
ATP	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	10	10	0.11%	6.99%	ANLPQSFQVDTSK	3.37	1,434.72
ATP	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	10	10	0.11%	6.99%	AYGPGIEPTGNMVK	3.34	1,449.70
ATP	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	10	10	0.11%	6.99%	FNEEHIPDSPFVVPVASPSGDAR	3.65	2,467.19
ATP	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	10	10	0.11%	6.99%	GAGTGGLGLAVEGPSEAK	4.4	1,570.81
ATP	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	10	10	0.11%	6.99%	GLVEPVDVVDNADGTQTVNYVPSR	2.8	2,544.26

ATP	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	10	10	0.11%	6.99%	IANLQTDLSDGLR	3.76	1,415.75
ATP	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	10	10	0.11%	6.99%	LIALLEVLSQK	2.56	1,226.77
ATP	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	10	10	0.11%	6.99%	LPQLPITNFSR	2.24	1,285.73
ATP	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	10	10	0.11%	6.99%	VTAQGPGLEPSGNIANK	4.28	1,652.86
ATP	6011	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	10	10	10	0.11%	6.99%	YTPVQQGPVGINVTYGGDAIPK	3.98	2,274.18
ATP	6011	NRAS protein	gi|146186548,gi|148226664	21,211.30	99.90%	2	2	2	0.02%	11.10%	QGVEDAFYTLVR	3.25	1,397.71
ATP	6011	NRAS protein	gi|146186548,gi|148226664	21,211.30	99.90%	2	2	2	0.02%	11.10%	SFADINLYR	2.63	1,098.56
ATP	6011	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	6	9	16	0.17%	29.40%	ANQVTDESLESTR	3.51	1,449.68
ATP	6011	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	6	9	16	0.17%	29.40%	ANQVTDESLESTRR	1.85	1,605.78
ATP	6011	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	6	9	16	0.17%	29.40%	ILGLAIESQDAGIK	4.37	1,427.81
ATP	6011	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	6	9	16	0.17%	29.40%	TITMLDEQGEQLK	4.27	1,521.75

ATP	6011	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	6	9	16	0.17%	29.40%	TITMLDEQGEQLKR	2.89	1,677.85
ATP	6011	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	6	9	16	0.17%	29.40%	VTNGQPQQATAGAASGGYIK	5.2	1,918.96
ATP	6011	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	4	5	16	0.17%	8.12%	AKIQDKEGIPPDQQR	2.68	1,722.91
ATP	6011	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	4	5	16	0.17%	8.12%	ESTLHLVLR	3.03	1,067.62
ATP	6011	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	4	5	16	0.17%	8.12%	IQDKEGIPPDQQR	3.33	1,523.78
ATP	6011	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	4	5	16	0.17%	8.12%	TITLEVEPSDTIENVK	2.88	1,787.93
ATP	6011	TPA: predicted NADPH oxidase-5	gi|151427572,gi|155372001	86,454.40	99.80%	2	2	3	0.03%	3.71%	AIGLQMALDLLAK	3.78	1,372.79
ATP	6011	TPA: predicted NADPH oxidase-5	gi|151427572,gi|155372001	86,454.40	99.80%	2	2	3	0.03%	3.71%	MAALHIVEVNLLPSK	4.46	1,650.92
ATP	6011	RecName: Full=Small nuclear ribonucleoprotein Sm D1; Short=Sm-D1; AltName: Full=snRNP core protein D1	gi|109894869,gi|73586929,gi|78050059	13,263.90	99.80%	2	4	5	0.05%	27.70%	NREPVQLETLSIR	4.27	1,554.86

ATP	6011	RecName: Full=Small nuclear ribonucleoprotein Sm D1; Short=Sm-D1; AltName: Full=snRNP core protein D1	gi|109894869,gi|73586929,gi|78050059	13,263.90	99.80%	2	4	5	0.05%	27.70%	YFILPDSLPLDTLLVDVEPK	4.43	2,287.25
ATP	6011	RecName: Full=Syntaxin-4	gi|122140085,gi|74356383,gi|78050061	34,382.50	99.80%	2	2	3	0.03%	10.10%	AIEPQKEEADENYNSVNTR	4.26	2,207.02
ATP	6011	RecName: Full=Syntaxin-4	gi|122140085,gi|74356383,gi|78050061	34,382.50	99.80%	2	2	3	0.03%	10.10%	VALVVHPGTAR	3.21	1,119.66
ATP	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	11	12	14	0.15%	15.50%	AKDIVPGDIVEIAVGDKVPADIR	3.51	2,390.33
ATP	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	11	12	14	0.15%	15.50%	AMGVVVATGVNTEIGK	3.68	1,561.83
ATP	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	11	12	14	0.15%	15.50%	EFTLEFSR	2.04	1,028.50
ATP	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	11	12	14	0.15%	15.50%	ISLPVILMDETLK	2.96	1,487.84

ATP	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	11	12	14	0.15%	15.50%	KSEIGIAMGSGTAVAK	4.52	1,535.81
ATP	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	11	12	14	0.15%	15.50%	LDEFGEQLSK	3.11	1,165.57
ATP	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	11	12	14	0.15%	15.50%	NAENAIEALKEYEPEMGK	3.03	2,051.96
ATP	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	11	12	14	0.15%	15.50%	NMLFSGTNIAAGK	3.1	1,339.67
ATP	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	11	12	14	0.15%	15.50%	SEIGIAMGSGTAVAK	4.59	1,407.72
ATP	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	11	12	14	0.15%	15.50%	TASEMVLADDNFSTIVAAVEEGR	3.82	2,441.15

ATP	6011	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	11	12	14	0.15%	15.50%	VDQSILTGESVSVIK	3.61	1,574.86
ATP	6011	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	100.00%	3	4	4	0.04%	6.08%	DEEDDDEDMYSDNINAATEEK	6.23	2,463.91
ATP	6011	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	100.00%	3	4	4	0.04%	6.08%	HSLEGNPRDEEDDDEDMYSDNINAATEEK	6.75	3,354.35
ATP	6011	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	100.00%	3	4	4	0.04%	6.08%	NLSLPFIFHEK	2.23	1,344.73
ATP	6011	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	100.00%	4	4	4	0.04%	9.80%	FATLYSTQHR	2.88	1,223.62
ATP	6011	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	100.00%	4	4	4	0.04%	9.80%	FFYAGTPPAGPAAAHVR	2.51	1,800.92
ATP	6011	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	100.00%	4	4	4	0.04%	9.80%	ILEVVNQVQDEER	4.23	1,570.81
ATP	6011	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	100.00%	4	4	4	0.04%	9.80%	IPVYSAFR	1.89	952.525

ATP	6011	PREDICTED: similar to hCG1980844	gi|194674945	298,419.90	99.80%	2	2	2	0.02%	0.87%	QLQPNEEADYLGVR	2.91	1,631.80
ATP	6011	PREDICTED: similar to hCG1980844	gi|194674945	298,419.90	99.80%	2	2	2	0.02%	0.87%	YLLTQELLR	2.85	1,148.67
ATP	6011	PREDICTED: similar to karyopherin beta 1 isoform 2	gi|76644624	97,210.30	100.00%	3	3	3	0.03%	5.25%	AAVENLPTFLVELSR	3.71	1,658.91
ATP	6011	PREDICTED: similar to karyopherin beta 1 isoform 2	gi|76644624	97,210.30	100.00%	3	3	3	0.03%	5.25%	LAATNALLNSLEFTK	4.56	1,605.88
ATP	6011	PREDICTED: similar to karyopherin beta 1 isoform 2	gi|76644624	97,210.30	100.00%	3	3	3	0.03%	5.25%	LLETTDRPDGHQNNLR	1.54	1,878.94
ATP	6011	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	100.00%	4	4	4	0.04%	14.20%	DLLSHENAATLNDVK	5.01	1,639.83
ATP	6011	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	100.00%	4	4	4	0.04%	14.20%	DRQYLLFFHK	3.66	1,366.73
ATP	6011	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	100.00%	4	4	4	0.04%	14.20%	LEDLKEQLAPLEK	4.47	1,525.85
ATP	6011	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	100.00%	4	4	4	0.04%	14.20%	LRDPLQVHLPLR	3.54	1,456.87
ATP	6011	sorting and assembly machinery component 50 homolog	gi|114051051,gi|87578317,gi|95769210	52,025.30	99.80%	2	3	3	0.03%	5.33%	ETSYGLSFFKPQPGNFDR	3.23	2,090.00

ATP	6011	sorting and assembly machinery component 50 homolog	gi|114051051,gi|87578317,gi|95769210	52,025.30	99.80%	2	3	3	0.03%	5.33%	LPNLLGR	1.99	782.4884
ATP	6011	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	5	5	5	0.05%	6.05%	FADIVSILDK	3.04	1,120.63
ATP	6011	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	5	5	5	0.05%	6.05%	IAYSLLGLK	2.61	977.6031
ATP	6011	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	5	5	5	0.05%	6.05%	IDTIAPDEITGSSDFEAR	3.69	1,936.91
ATP	6011	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	5	5	5	0.05%	6.05%	VIGAGEFGEVYK	3.3	1,268.65
ATP	6011	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	5	5	5	0.05%	6.05%	YSEPPLGLTR	2.35	1,132.60
ATP	6011	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	3	3	4	0.04%	17.50%	FYGPEGPYGVFAGR	3.52	1,516.72
ATP	6011	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	3	3	4	0.04%	17.50%	GDQPAASDSDDDEPPPLPR	3.72	1,978.86
ATP	6011	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	3	3	4	0.04%	17.50%	KFYGPEGPYGVFAGR	4.33	1,644.82
ATP	6011	similar to ribosomal protein L27	gi|28189717,gi|47117099,gi|74268027,gi|77404275	15,780.40	99.80%	2	2	2	0.02%	22.10%	NIDDGTSDRPYSHALVAGIDR	3.72	2,272.10
ATP	6011	similar to ribosomal protein L27	gi|28189717,gi|47117099,gi|74268027,gi|77404275	15,780.40	99.80%	2	2	2	0.02%	22.10%	YSVDIPLDK	2.43	1,049.55

ATP	6011	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.08%	12.80%	GVMLAVDAVIAELKK	1.88	1,572.90
ATP	6011	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.08%	12.80%	ISSVQSIVPALEIANAHR	3.63	1,905.06
ATP	6011	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.08%	12.80%	KISSVQSIVPALEIANAHR	2.93	2,033.15
ATP	6011	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.08%	12.80%	LVQDVANNTNEEAGDGTTTATVLAR	5.89	2,560.25
ATP	6011	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.08%	12.80%	TLNDELEIIEGMKFDR	2.52	1,938.95
ATP	6011	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	6	7	7	0.08%	12.80%	VGEVIVTKDDAMLLK	2.4	1,646.90
ATP	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	7	8	13	0.14%	35.00%	DILLRPELEELRNEHSAR	1.77	2,190.16
ATP	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	7	8	13	0.14%	35.00%	GPNGLLVYQGK	3.73	1,145.63
ATP	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	7	8	13	0.14%	35.00%	IDGNLVIRPYTPVSSDDDKGFVDLVIK	2.87	2,975.57
ATP	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	7	8	13	0.14%	35.00%	LIDKEVISHDTR	3.27	1,425.77

ATP	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	7	8	13	0.14%	35.00%	LIDKEVISHDTRR	2.63	1,581.87
ATP	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	7	8	13	0.14%	35.00%	STPAITLENPDIKYPLR	4.64	1,928.05
ATP	6011	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	7	8	13	0.14%	35.00%	SVGMIAGGTGITPMLQVIR	5.47	1,917.03
ATP	6011	endothelial cell adhesion molecule	gi|118151218,gi|119919027,gi|86823868	41,779.80	99.80%	2	3	4	0.04%	10.10%	ALEEPANDIKEDAIAPR	4.6	1,851.94
ATP	6011	endothelial cell adhesion molecule	gi|118151218,gi|119919027,gi|86823868	41,779.80	99.80%	2	3	4	0.04%	10.10%	SPPSSQVFFAPVLDAIHGSLSLK	3.6	2,397.28
ATP	6011	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	6	6	6	0.07%	2.46%	HPTPLALGQFHTVTLLR	3.3	1,901.08
ATP	6011	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	6	6	6	0.07%	2.46%	IPGDQVVSVVFIK	3.94	1,400.81
ATP	6011	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	6	6	6	0.07%	2.46%	IQVVVLPGATTPPVR	4.07	1,546.93
ATP	6011	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	6	6	6	0.07%	2.46%	LDVEFKPLAPDGVLLFSGGK	3.78	2,102.15
ATP	6011	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	6	6	6	0.07%	2.46%	LRSPVISIDPPSSTVQQGQDASFK	6.09	2,557.33
ATP	6011	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	6	6	6	0.07%	2.46%	VVPYFTQTPYSFLPLPTIK	2.93	2,211.21
ATP	6011	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	12	13	22	0.24%	29.60%	ALEEANADLEVK	3.16	1,301.66
ATP	6011	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	12	13	22	0.24%	29.60%	ASLENSLEETK	2.39	1,220.60

ATP	6011	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	12	13	22	0.24%	29.60%	ASLENSLEETKGR	3.77	1,433.72
ATP	6011	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	12	13	22	0.24%	29.60%	GQVGGDVNVEMDAAPGVDLSR	3.51	2,101.98
ATP	6011	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	12	13	22	0.24%	29.60%	ILNEMRDQYEK	3.5	1,438.70
ATP	6011	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	12	13	22	0.24%	29.60%	LASYLDKVR	3.26	1,064.61
ATP	6011	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	12	13	22	0.24%	29.60%	LEQEIATYR	3.71	1,122.58
ATP	6011	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	12	13	22	0.24%	29.60%	LLEGEDAHLSSSQFSSGSQSSR	5.46	2,309.06
ATP	6011	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	12	13	22	0.24%	29.60%	QRPAEIKDYSPYFK	3.12	1,741.89
ATP	6011	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	12	13	22	0.24%	29.60%	TEELNREVATNSELVQSGK	6.01	2,104.05
ATP	6011	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	12	13	22	0.24%	29.60%	TRLEQEIATYR	3.46	1,379.73
ATP	6011	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	100.00%	12	13	22	0.24%	29.60%	VLDELTLAR	4.3	1,029.59
ATP	6011	PTBP1 protein	gi|158454983	47,010.90	99.80%	2	2	2	0.02%	8.97%	KLPGDVTEGEVISLGLPFGK	3.35	2,056.13
ATP	6011	PTBP1 protein	gi|158454983	47,010.90	99.80%	2	2	2	0.02%	8.97%	NNQFQALLQYADPVSAQHAK	3.47	2,243.12
ATP	6011	Transmembrane protein 49	gi|111307060,gi|115496266,gi|122133514	46,165.40	99.80%	2	2	3	0.03%	11.30%	EQYNGNFTDPSSVNEK	4.07	1,828.80
ATP	6011	Transmembrane protein 49	gi|111307060,gi|115496266,gi|122133514	46,165.40	99.80%	2	2	3	0.03%	11.30%	LSGAEPDDEEYQEFEEMLEHAETAQDFASR	5.55	3,489.46
ATP	6011	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	8	12	55	0.60%	13.00%	FASFIDK	2.21	827.4298

ATP	6011	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	8	12	55	0.60%	13.00%	FASFIDKVR	1.68	1,082.60
ATP	6011	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	8	12	55	0.60%	13.00%	LALDVEIATYR	3.01	1,263.69
ATP	6011	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	8	12	55	0.60%	13.00%	LRSEIDNVKK	3.61	1,201.69
ATP	6011	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	8	12	55	0.60%	13.00%	NKYEDEINKR	3.37	1,308.65
ATP	6011	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	8	12	55	0.60%	13.00%	SFSTASAITPSVSR	3.46	1,410.72
ATP	6011	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	8	12	55	0.60%	13.00%	SLDLDSIIAEVK	3.79	1,302.72
ATP	6011	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	8	12	55	0.60%	13.00%	VDALMDEINFMK	3.52	1,441.67
ATP	6011	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	2	2	2	0.02%	2.80%	FNVEDGEIVQQVR	2.81	1,532.77
ATP	6011	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	2	2	2	0.02%	2.80%	NFPQAALVSFATTGEK	3.8	1,680.86
ATP	6011	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	100.00%	3	3	3	0.03%	14.00%	AQIQEQNPSIEVVYYNK	4	2,023.01
ATP	6011	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	100.00%	3	3	3	0.03%	14.00%	ELQVGIPVTNEQGQR	2.83	1,667.87
ATP	6011	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	100.00%	3	3	3	0.03%	14.00%	NLLLSGAQLEASR	3.19	1,371.76
ATP	6011	RAB21, member RAS oncogene family	gi|109658186,gi|115496760,gi|122144675	24,128.60	99.80%	2	2	2	0.02%	12.20%	FHALGPIYYR	2.47	1,236.65
ATP	6011	RAB21, member RAS oncogene family	gi|109658186,gi|115496760,gi|122144675	24,128.60	99.80%	2	2	2	0.02%	12.20%	HVSIQEAESYAESVGAK	2.95	1,804.87
ATP	6011	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	99.90%	2	2	2	0.02%	9.51%	LNQAVEFDVLPAFDALGQLTK	5.15	2,289.21
ATP	6011	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	99.90%	2	2	2	0.02%	9.51%	PVILDPADPTGNVAGK	3.64	1,563.84

ATP	6011	ARP3 actin-related protein 3 homolog (yeast)	gi|115304856,gi|148744289,gi|149243031,gi|149243038,gi|149243045,gi|149243052,gi|149243059,gi|217422,gi|27806335,gi|47117646	47,353.80	99.80%	2	2	2	0.02%	7.66%	AEPEDHYFLLTEPPLNTPENR	3.18	2,482.19
ATP	6011	ARP3 actin-related protein 3 homolog (yeast)	gi|115304856,gi|148744289,gi|149243031,gi|149243038,gi|149243045,gi|149243052,gi|149243059,gi|217422,gi|27806335,gi|47117646	47,353.80	99.80%	2	2	2	0.02%	7.66%	DITYFIQQLLR	3.36	1,409.78
ATP	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	21	49	0.53%	49.30%	AVFPSIVGRPR	3.04	1,198.71
ATP	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	21	49	0.53%	49.30%	DLTDYLMK	2.34	1,014.48
ATP	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	21	49	0.53%	49.30%	DLYANTVLSGGTTMYPGIADR	5.59	2,231.07
ATP	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	21	49	0.53%	49.30%	EITALAPSTMK	3.13	1,177.61
ATP	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	21	49	0.53%	49.30%	FRCPEALFQPSFLGMESCGIHETTFNSIMK	4.42	3,436.58
ATP	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	21	49	0.53%	49.30%	GYSFTTTAER	3.61	1,132.53
ATP	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	21	49	0.53%	49.30%	IKIIAPPER	2.45	1,036.65
ATP	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	21	49	0.53%	49.30%	KDLYANTVLSGGTTMYPGIADR	6.65	2,359.16
ATP	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	21	49	0.53%	49.30%	LDLAGRDLTDYLMK	3	1,639.84
ATP	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	21	49	0.53%	49.30%	QEYDESGPSIVHR	3.01	1,516.70

ATP	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	21	49	0.53%	49.30%	QEYDESGPSIVHRK	2.69	1,644.80
ATP	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	21	49	0.53%	49.30%	SYELPDGQVITIGNER	4.26	1,790.89
ATP	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	21	49	0.53%	49.30%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	5.42	3,183.61
ATP	6011	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	21	49	0.53%	49.30%	VAPEEHPVLLTEAPLNPK	4.61	1,954.06
ATP	6011	RecName: Full=Peptidyl-tRNA hydrolase 2, mitochondrial; Short=PTH 2; AltName: Full=Bcl-2 inhibitor of transcription; Flags: Precursor	gi|109892883,gi|116292141,gi|60650282,gi|73587109,gi|77735985	19,272.70	99.90%	2	2	2	0.02%	16.20%	APDEETLVELLTHAK	3.3	1,665.87
ATP	6011	RecName: Full=Peptidyl-tRNA hydrolase 2, mitochondrial; Short=PTH 2; AltName: Full=Bcl-2 inhibitor of transcription; Flags: Precursor	gi|109892883,gi|116292141,gi|60650282,gi|73587109,gi|77735985	19,272.70	99.90%	2	2	2	0.02%	16.20%	VLGLTVSLIQDAGR	3.7	1,441.84
ATP	6011	RCN1 protein	gi|134024617,gi|157073966	38,734.90	99.80%	2	2	2	0.02%	9.67%	IVDRIDSDGDGFVTTEELK	3.99	2,109.04
ATP	6011	RCN1 protein	gi|134024617,gi|157073966	38,734.90	99.80%	2	2	2	0.02%	9.67%	TFDQLTSEESKER	3.93	1,569.74

ATP	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	17	20	25	0.27%	36.00%	DLFSEAHSEFLK	3.7	1,422.69
ATP	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	17	20	25	0.27%	36.00%	EATNPPVIQEEKPK	2.95	1,579.83
ATP	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	17	20	25	0.27%	36.00%	ELSDFISYLK	2.84	1,214.63
ATP	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	17	20	25	0.27%	36.00%	FLEDYFDGNLK	3.12	1,360.64
ATP	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	17	20	25	0.27%	36.00%	FLEDYFDGNLKR	2.11	1,516.74
ATP	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	17	20	25	0.27%	36.00%	FVMQEEFSR	3.17	1,188.54
ATP	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	17	20	25	0.27%	36.00%	GFPTIYFSPANKK	3.51	1,469.78
ATP	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	17	20	25	0.27%	36.00%	IFRDGEESGAYDGPR	5.09	1,668.76
ATP	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	17	20	25	0.27%	36.00%	KLAPEYEAAATR	3.47	1,319.70
ATP	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	17	20	25	0.27%	36.00%	KTFSHELSDFGLESTTGEIPVVAVR	3.95	2,719.39
ATP	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	17	20	25	0.27%	36.00%	LAPEYEAAATR	2.95	1,191.60
ATP	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	17	20	25	0.27%	36.00%	LRKDPNIVIAK	3.22	1,266.79
ATP	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	17	20	25	0.27%	36.00%	MDATANDVPSPYEVR	4.84	1,680.75
ATP	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	17	20	25	0.27%	36.00%	SEPIPESNDGPVK	2.82	1,368.66
ATP	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	17	20	25	0.27%	36.00%	TADGIVSHLKK	1.82	1,168.67
ATP	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	17	20	25	0.27%	36.00%	TFSHELSDFGLESTTGEIPVVAVR	3.82	2,591.30
ATP	6011	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	17	20	25	0.27%	36.00%	YGVSGYPTLK	2.73	1,084.57
ATP	6011	PECAM1 protein	gi|111308531	82,597.50	100.00%	6	8	25	0.27%	8.94%	APVHFTIEK	2.51	1,041.57
ATP	6011	PECAM1 protein	gi|111308531	82,597.50	100.00%	6	8	25	0.27%	8.94%	CTVQVTHQAQSFPEIIIQK	2.95	2,170.13
ATP	6011	PECAM1 protein	gi|111308531	82,597.50	100.00%	6	8	25	0.27%	8.94%	FHIIPEGK	2.87	940.5252
ATP	6011	PECAM1 protein	gi|111308531	82,597.50	100.00%	6	8	25	0.27%	8.94%	GTETVYSEIR	2.87	1,154.57
ATP	6011	PECAM1 protein	gi|111308531	82,597.50	100.00%	6	8	25	0.27%	8.94%	PAVPLLNSNNEK	2.25	1,295.70
ATP	6011	PECAM1 protein	gi|111308531	82,597.50	100.00%	6	8	25	0.27%	8.94%	QMPVEMSRPAVPLLNSNNEK	2.14	2,270.13

ATP	6011	PREDICTED: DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 isoform 1	gi|119912544,gi|74354729	69,131.70	99.80%	2	2	2	0.02%	3.58%	APILIATDVASR	3.56	1,226.71
ATP	6011	PREDICTED: DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 isoform 1	gi|119912544,gi|74354729	69,131.70	99.80%	2	2	2	0.02%	3.58%	QVSDLISVLR	2.38	1,129.66
ATP	6011	RecName: Full=40S ribosomal protein S16	gi|108860953,gi|74354274,gi|75812950	16,427.90	99.90%	2	2	2	0.02%	14.40%	GPLQSVQVFGR	3.26	1,187.65
ATP	6011	RecName: Full=40S ribosomal protein S16	gi|108860953,gi|74354274,gi|75812950	16,427.90	99.90%	2	2	2	0.02%	14.40%	LLEPVLLLGK	2.26	1,094.72
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	DGQVINETSQHHDDLE	3.38	1,836.80
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	DNLAEDIMR	2.58	1,092.50
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	EEAESTLQSFRQDVDNASLAR	4.39	2,366.12
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	EMEENFSVEAANYQDTIGR	4.2	2,218.96
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	ETNLDSLPLVDTHSK	3.62	1,668.84
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	ETNLDSLPLVDTHSKR	4.41	1,824.95
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	EYQDLLNVK	2.56	1,121.58
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	FADLSEAANR	4.22	1,093.53
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	FANYIDKVR	2.2	1,125.61
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	ILLAELEQLK	4.09	1,169.71
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	ILLAELEQLKGQGK	4.44	1,539.91
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	ISLPLPNFSSLNLR	4.55	1,570.90
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	KLHDEEIQELQAQIQEQHVQIDMDVSKPDLTAALR	5.48	4,085.06

ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	KVESLQEEIAFLK	5.67	1,533.85
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	KVESLQEEIAFLKK	5.42	1,661.95
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	LHDEEIQELQAQIQEQHVQIDMDVSKPDLTAALR	5.55	3,956.97
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	LLQDSVDFSLADAINTEFK	4.13	2,126.07
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	LQDEIQNMKEEMAR	3.24	1,750.81
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	LQEEMLQREEAESTLQSFR	4.61	2,340.11
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	LQEEMLQREEAESTLQSFRQDVDNASLAR	3.66	3,409.63
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	MALDIEIATYR	4.45	1,311.66
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	MALDIEIATYRK	2.37	1,439.76
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	MFGGPGTASRPSSTR	1.69	1,524.72
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	SRLGDLYEEEMR	2.8	1,513.70
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	TLYTSSPGGVYATR	3.93	1,472.74
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	TNEKVELQELNDR	4.65	1,587.80
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	TNEKVELQELNDRFANYIDK	3.5	2,439.22
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	VELQELNDR	3.09	1,115.57
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	VELQELNDRFANYIDK	2.47	1,966.99
ATP	6011	vimentin	gi|110347570	53,710.80	100.00%	30	46	123	1.34%	63.70%	VEVERDNLAEDIMR	4.03	1,688.83
ATP	6011	PREDICTED: dedicator of cytokinesis 11	gi|194680728	237,960.50	99.80%	2	2	2	0.02%	3.09%	TQIYSDPLRDLLMFPMEDISISVISRQR	2.75	3,339.71
ATP	6011	PREDICTED: dedicator of cytokinesis 11	gi|194680728	237,960.50	99.80%	2	2	2	0.02%	3.09%	TWLDSMAKIHIKNGDFSEAAMCYVHVAALVAEFLHR	3.7	4,090.01

ATP	6011	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	4	6	11	0.12%	17.30%	DKLDGNELDLSLSDLNEVPVK	6.28	2,313.18
ATP	6011	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	4	6	11	0.12%	17.30%	DKLDGNELDLSLSDLNEVPVKELAALPK	5.22	3,035.62
ATP	6011	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	4	6	11	0.12%	17.30%	LVNLQHLDLLNNR	3.35	1,561.88
ATP	6011	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	4	6	11	0.12%	17.30%	LVTLPVSFAQLK	3.27	1,315.80
ATP	6011	RecName: Full=CDGSH iron sulfur domain-containing protein 1; AltName: Full=MitoNEET	gi|110825757,gi|73587067,gi|77404223	11,964.80	99.80%	2	3	4	0.04%	26.40%	HNEETGDNVGPLIIK	4.73	1,635.83
ATP	6011	RecName: Full=CDGSH iron sulfur domain-containing protein 1; AltName: Full=MitoNEET	gi|110825757,gi|73587067,gi|77404223	11,964.80	99.80%	2	3	4	0.04%	26.40%	VVHAFDMEDLGDK	3.11	1,491.68
ATP	6011	17,000 dalton myosin light chain	gi|578,gi|74268209	16,942.80	100.00%	4	4	4	0.04%	35.10%	ALGQNPTNAEVLK	3.17	1,354.73
ATP	6011	17,000 dalton myosin light chain	gi|578,gi|74268209	16,942.80	100.00%	4	4	4	0.04%	35.10%	HVLVTLGEK	2.64	995.5885
ATP	6011	17,000 dalton myosin light chain	gi|578,gi|74268209	16,942.80	100.00%	4	4	4	0.04%	35.10%	NKDQGTYEDYVEGLR	3.55	1,786.82
ATP	6011	17,000 dalton myosin light chain	gi|578,gi|74268209	16,942.80	100.00%	4	4	4	0.04%	35.10%	VLDFEHFLPMLQTVAK	3.09	1,904.00

ATP	6011	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	8	8	9	0.10%	18.00%	DAGQISGLNVLR	4.12	1,242.68
ATP	6011	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	8	8	9	0.10%	18.00%	EQQIVIQSSGGLSKDDIENMVK	2.75	2,434.21

ATP	6011	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	8	8	9	0.10%	18.00%	MKETAENYLGHTAK	3.52	1,608.77
ATP	6011	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	8	8	9	0.10%	18.00%	QAVTNPNNTFYATK	3.21	1,568.77

ATP	6011	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	8	8	9	0.10%	18.00%	STNGDTFLGGEDFDQALLR	4.08	2,055.96
ATP	6011	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	8	8	9	0.10%	18.00%	TTPSVVAFTADGER	3.96	1,450.72

ATP	6011	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	8	8	9	0.10%	18.00%	VINEPTAAALAYGLDK	3.53	1,645.88
ATP	6011	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	8	8	9	0.10%	18.00%	VQQTVQDLFGR	2.65	1,290.68
ATP	6011	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	99.80%	2	2	2	0.02%	23.90%	AVFPSIVGRPR	3.04	1,198.71
ATP	6011	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	99.80%	2	2	2	0.02%	23.90%	DLTDYLMK	2.34	1,014.48
ATP	6011	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	99.80%	2	2	2	0.02%	23.90%	EITALAPSTMK	3.13	1,177.61
ATP	6011	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	99.80%	2	2	2	0.02%	23.90%	IKIIAPPER	2.45	1,036.65

ATP	6011	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	99.80%	2	2	2	0.02%	23.90%	LDLAGRDLTDYLMK	3	1,639.84
ATP	6011	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	99.80%	2	2	2	0.02%	23.90%	QEYDEAGPSIVHR	2.27	1,500.71
ATP	6011	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	99.80%	2	2	2	0.02%	23.90%	SYELPDGQVITIGNER	4.26	1,790.89
ATP	6011	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	99.80%	2	2	2	0.02%	23.90%	YPIEHGIITNWDDMEK	3.6	1,976.91
ATP	6011	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	5	6	8	0.09%	38.60%	GAAGALMVYDITR	3.6	1,353.68
ATP	6011	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	5	6	8	0.09%	38.60%	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	4.29	3,150.56
ATP	6011	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	5	6	8	0.09%	38.60%	LQIWDTAGQER	2.72	1,316.66
ATP	6011	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	5	6	8	0.09%	38.60%	NLTNPNTVIILIGNK	4.5	1,623.94
ATP	6011	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	5	6	8	0.09%	38.60%	TGENVEDAFLEAAK	3.28	1,493.71
ATP	6011	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	3	4	6	0.07%	19.00%	EHGLIFMETSAK	2.57	1,378.67
ATP	6011	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	3	4	6	0.07%	19.00%	GAAGALLVYDITR	3.75	1,319.73
ATP	6011	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	3	4	6	0.07%	19.00%	YIIIGDTGVGK	2.52	1,135.64
ATP	6011	RecName: Full=Phosphoglycerate kinase 1	gi|108860885,gi|74353972,gi|77735551	44,520.20	100.00%	3	3	3	0.03%	12.50%	ALESPERPFLAILGGAK	3.77	1,769.00
ATP	6011	RecName: Full=Phosphoglycerate kinase 1	gi|108860885,gi|74353972,gi|77735551	44,520.20	100.00%	3	3	3	0.03%	12.50%	VDFNVPMKNNQITNNQR	4.21	2,048.00
ATP	6011	RecName: Full=Phosphoglycerate kinase 1	gi|108860885,gi|74353972,gi|77735551	44,520.20	100.00%	3	3	3	0.03%	12.50%	VLNNMEIGTSLFDEEGSK	3.38	1,998.93

ATP	6011	RAB5A, member RAS oncogene family	gi|113911876,gi|115495947,gi|122144200	23,670.90	99.90%	2	3	4	0.04%	17.20%	GVDLTEPTQPTR	3.11	1,313.67
ATP	6011	RAB5A, member RAS oncogene family	gi|113911876,gi|115495947,gi|122144200	23,670.90	99.90%	2	3	4	0.04%	17.20%	LVLLGESAVGK	3.36	1,085.66
ATP	6011	RAB5A, member RAS oncogene family	gi|113911876,gi|115495947,gi|122144200	23,670.90	99.90%	2	3	4	0.04%	17.20%	TSMNVNEIFMAIAK	4.13	1,584.78
ATP	6011	Chain R, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Reduced State	gi|149241523,gi|149241540,gi|149241553,gi|149241570,gi|149241583,gi|149241600,gi|149241613,gi|42564216,gi|50872151,gi|60391934,gi|81674705	16,717.40	100.00%	5	6	18	0.20%	36.80%	EIYPYVIQELRPTLNELGISTPEELGLDKV	4.98	3,428.82
ATP	6011	Chain R, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Reduced State	gi|149241523,gi|149241540,gi|149241553,gi|149241570,gi|149241583,gi|149241600,gi|149241613,gi|42564216,gi|50872151,gi|60391934,gi|81674705	16,717.40	100.00%	5	6	18	0.20%	36.80%	GMNTLVGYDLVPEPK	4.35	1,648.83
ATP	6011	Chain R, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Reduced State	gi|149241523,gi|149241540,gi|149241553,gi|149241570,gi|149241583,gi|149241600,gi|149241613,gi|42564216,gi|50872151,gi|60391934,gi|81674705	16,717.40	100.00%	5	6	18	0.20%	36.80%	KGMNTLVGYDLVPEPK	3.79	1,776.92

ATP	6011	Chain R, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Reduced State	gi|149241523,gi|149241540,gi|149241553,gi|149241570,gi|149241583,gi|149241600,gi|149241613,gi|42564216,gi|50872151,gi|60391934,gi|81674705	16,717.40	100.00%	5	6	18	0.20%	36.80%	LNDFASAVR	3.19	992.5159
ATP	6011	Chain R, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Reduced State	gi|149241523,gi|149241540,gi|149241553,gi|149241570,gi|149241583,gi|149241600,gi|149241613,gi|42564216,gi|50872151,gi|60391934,gi|81674705	16,717.40	100.00%	5	6	18	0.20%	36.80%	RLNDFASAVR	3.65	1,148.62
ATP	6011	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	3	3	3	0.03%	5.72%	IKFDQSVDPEIIAR	3.12	1,630.88
ATP	6011	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	3	3	3	0.03%	5.72%	LAETQHTAPSFVK	2.75	1,428.75
ATP	6011	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	3	3	3	0.03%	5.72%	LSPETQSAIEQEIR	3.41	1,600.82
ATP	6011	RecName: Full=Vesicle-associated membrane protein 8; Short=VAMP-8	gi|122140420,gi|74353894,gi|77735533	11,339.40	99.80%	2	3	4	0.04%	24.00%	NKTEDLEATSEHFK	4.8	1,648.78
ATP	6011	RecName: Full=Vesicle-associated membrane protein 8; Short=VAMP-8	gi|122140420,gi|74353894,gi|77735533	11,339.40	99.80%	2	3	4	0.04%	24.00%	NLRDEVEGVK	3.3	1,158.61

ATP	6011	RecName: Full=Annexin A1; AltName: Full=Annexin-1; AltName: Full=Annexin I; AltName: Full=Lipocortin I; AltName: Full=Calpactin II; AltName: Full=Chromobindin-9; AltName: Full=p35; AltName: Full=Phospholipase A2	gi|118597373,gi|264182,gi|61553085,gi|73587269,gi|73853762,gi|74	38,881.20	99.90%	2	2	2	0.02%	10.10%	GDRSEELAVNDDLADSDAR	5.5	2,047.92
ATP	6011	RecName: Full=Annexin A1; AltName: Full=Annexin-1; AltName: Full=Annexin I; AltName: Full=Lipocortin I; AltName: Full=Calpactin II; AltName: Full=Chromobindin-9; AltName: Full=p35; AltName: Full=Phospholipase A2	gi|118597373,gi|264182,gi|61553085,gi|73587269,gi|73853762,gi|74	38,881.20	99.90%	2	2	2	0.02%	10.10%	GLGTDEDTLNEILASR	3.55	1,703.84
ATP	6011	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	5	5	5	0.05%	10.80%	IPQAVVDVSSHLQK	1.62	1,520.84
ATP	6011	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	5	5	5	0.05%	10.80%	LELPLIMLSGLPDTVFEITELQSLK	3.24	2,815.54
ATP	6011	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	5	5	5	0.05%	10.80%	NLEELYLVGSLSHDISR	4.03	1,945.00
ATP	6011	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	5	5	5	0.05%	10.80%	SIEEIVSFQHLR	2.88	1,457.77
ATP	6011	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	5	5	5	0.05%	10.80%	SNTTQSGPEGSLVNSQSLK	4.27	1,933.95

ATP	6011	MGAT1 protein	gi|154426138,gi|59858237,gi|62751783	51,684.70	99.80%	2	2	2	0.02%	6.04%	LPSDSALDDDPASLTR	4.32	1,672.80
ATP	6011	MGAT1 protein	gi|154426138,gi|59858237,gi|62751783	51,684.70	99.80%	2	2	2	0.02%	6.04%	VYGAPLLQVEK	2.24	1,216.69
ATP	6011	PREDICTED: similar to Thioredoxin domain-containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein ERp46) isoform 1	gi|119915902	45,792.10	99.80%	2	2	4	0.04%	4.55%	FFKPGQEAVK	2.51	1,150.63
ATP	6011	PREDICTED: similar to Thioredoxin domain-containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein ERp46) isoform 1	gi|119915902	45,792.10	99.80%	2	2	4	0.04%	4.55%	GYPTLLLFR	2.4	1,079.62

ATP	6011	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	4	6	18	0.20%	25.60%	FFDEESYSLLR	3.51	1,405.66
ATP	6011	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	4	6	18	0.20%	25.60%	FFDEESYSLLRK	2.45	1,533.76

ATP	6011	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	4	6	18	0.20%	25.60%	NNEDVSVIPPLFTVSVDHR	5.49	2,138.09
ATP	6011	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	4	6	18	0.20%	25.60%	VQNMALYADVSGK	4.73	1,411.69
ATP	6011	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	6	7	7	0.08%	18.60%	ASPAPGSGHPDGPGTHLEMNSLDR	2.58	2,416.10

ATP	6011	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	6	7	7	0.08%	18.60%	LDNKKECLEDVTAVCILEGFQNQQSMLLADK	3.58	3,511.71
ATP	6011	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	6	7	7	0.08%	18.60%	LRPESALAQAQK	3.39	1,311.74
ATP	6011	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	6	7	7	0.08%	18.60%	NVDLSTFYQNR	4.02	1,356.65
ATP	6011	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	6	7	7	0.08%	18.60%	SDEDKDKEGEALEVK	2.8	1,691.80
ATP	6011	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	6	7	7	0.08%	18.60%	SYFSSFTDDIISQPMLKGEK	2.65	2,309.10
ATP	6011	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	3	3	6	0.07%	5.16%	IPLNDIFR	3.21	987.5623

ATP	6011	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	3	3	6	0.07%	5.16%	VALKIPLNDIFR	3.6	1,398.85
ATP	6011	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	3	3	6	0.07%	5.16%	YLDFVFAVK	2.39	1,101.60
ATP	6011	Nicastrin	gi|74267600,gi|77735901	79,055.00	99.80%	2	2	2	0.02%	2.65%	ALAGVATVLAR	3.25	1,041.64
ATP	6011	Nicastrin	gi|74267600,gi|77735901	79,055.00	99.80%	2	2	2	0.02%	2.65%	LLYGFLVR	2.6	980.5928
ATP	6011	RecName: Full=ATP synthase subunit O, mitochondrial; AltName: Full=Oligomycin sensitivity conferral protein; Short=OSCP; Flags: Precursor	gi|143811365,gi|157881386,gi|159164706,gi|163451,gi|27806307,gi|28189911,gi|74268299	23,332.20	100.00%	3	4	5	0.05%	19.70%	FSPLTSNLINLLAENGR	2.77	1,859.00
ATP	6011	RecName: Full=ATP synthase subunit O, mitochondrial; AltName: Full=Oligomycin sensitivity conferral protein; Short=OSCP; Flags: Precursor	gi|143811365,gi|157881386,gi|159164706,gi|163451,gi|27806307,gi|28189911,gi|74268299	23,332.20	100.00%	3	4	5	0.05%	19.70%	LVRPPVQIYGIEGR	3.26	1,596.92

ATP	6011	RecName: Full=ATP synthase subunit O, mitochondrial; AltName: Full=Oligomycin sensitivity conferral protein; Short=OSCP; Flags: Precursor	gi|143811365,gi|157881386,gi|159164706,gi|163451,gi|27806307,gi|28189911,gi|74268299	23,332.20	100.00%	3	4	5	0.05%	19.70%	YATALYSAASK	2.5	1,145.58
ATP	6011	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	5	6	0.07%	18.80%	DFSLEQLR	2.94	1,007.52
ATP	6011	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	5	6	0.07%	18.80%	FYGPAGPYGIFAGR	3.57	1,472.73
ATP	6011	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	5	6	0.07%	18.80%	GLGAGAGAGEESPAASLPR	5.57	1,667.83
ATP	6011	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	5	6	0.07%	18.80%	RGLGAGAGAGEESPAASLPR	3.75	1,823.94
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	AEDIPQMDDAFSQTVK	2.31	1,810.82
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	ALSQIHEAAVR	4.18	1,194.66
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	EELYMPPLVIK	3.08	1,347.72
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	FGKPDPIVSVIFKDEK	4.06	1,819.00
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	GNNPFFDELFFYNVHLTPSELMDEIISIR	3.41	3,473.67

ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	IDVGFVYDEPGHAVMR	2.64	1,820.86
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	ILVELSTLLEK	3.7	1,257.77
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	IYRAEDIPQMDDAFSQTVK	4.18	2,243.07
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	LQSNIEALK	3.02	1,015.58
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	NLMALDKDSFSDPYAHVSFLHR	3.57	2,579.23
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	NLVDPFVEVSFAGK	3.3	1,521.79
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	SLLTEADAGHTEFTDEVYQNESR	4.79	2,612.17
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	TLHSSFQPNISQGR	3.76	1,571.79
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	TQGLVPEHVETR	2.65	1,365.71
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	VEMTLEVLNEKEADERPAGK	3.66	2,274.13
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	VGETIIDLENR	3.04	1,258.66

ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	VIEDRDNYIPNTLNPVFGR	3.98	2,232.14
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	VIIELFDNDQVGKDEFLGR	3.12	2,207.13
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	VIVESASNIPK	3.55	1,156.66
ATP	6011	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	20	24	30	0.33%	15.80%	VSMFVLGTGDEPPPEKQDRDNDSDDVESNLLLPAGIALR	2.62	4,226.06
ATP	6011	TXNDC13 protein	gi|148878448,gi|149642897	38,865.40	99.80%	2	2	2	0.02%	7.18%	FFVTTLPAFFHAK	3.03	1,525.82
ATP	6011	TXNDC13 protein	gi|148878448,gi|149642897	38,865.40	99.80%	2	2	2	0.02%	7.18%	VDVIQEPGLSGR	2.75	1,269.68
ATP	6011	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	2	2	2	0.02%	18.60%	ADFREPNAEVPRPIPHIGADYIPTEEER	4	3,218.59
ATP	6011	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	2	2	2	0.02%	18.60%	SVPLAATSMLITQGLISK	3.83	1,846.04
ATP	6011	Na-K-Cl cotransporter	gi|2264408,gi|27807511	130,380.80	100.00%	2	2	2	0.02%	4.58%	KPDVNWGSSTQALTYLNALQHSIRLSGVEDHVK	2.63	3,663.89
ATP	6011	Na-K-Cl cotransporter	gi|2264408,gi|27807511	130,380.80	100.00%	2	2	2	0.02%	4.58%	LQEGLDISHLQGQEELLSSQEK	4.21	2,481.25
ATP	6011	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	4	4	5	0.05%	14.00%	IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK	3.77	3,829.95

ATP	6011	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	4	4	5	0.05%	14.00%	IITITGTQDQIQNAQYLLQNSVK	6.48	2,589.39
ATP	6011	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	4	4	5	0.05%	14.00%	RPAEDMEEEQAFKR	3.7	1,751.80
ATP	6011	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	4	4	5	0.05%	14.00%	TDYNASVSVPDSSGPER	3.67	1,780.80
ATP	6011	myristoylated alanine-rich protein kinase C substrate	gi|115495497,gi|148872484,gi|163340,gi|94534743	31,960.80	99.80%	2	3	4	0.04%	6.87%	GEATAERPGEAAVASSPSK	4.93	1,814.89
ATP	6011	myristoylated alanine-rich protein kinase C substrate	gi|115495497,gi|148872484,gi|163340,gi|94534743	31,960.80	99.80%	2	3	4	0.04%	6.87%	TAAKGEATAERPGEAAVASSPSK	2.53	2,186.10
ATP	6011	RecName: Full=DnaJ homolog subfamily C member 11	gi|110808198,gi|114050887,gi|84708894	63,220.40	99.80%	2	2	2	0.02%	9.48%	GTISVGIDATDLFDRYEEEYEDVSGSGFPQIEINK	3.35	3,893.82
ATP	6011	RecName: Full=DnaJ homolog subfamily C member 11	gi|110808198,gi|114050887,gi|84708894	63,220.40	99.80%	2	2	2	0.02%	9.48%	LFNLVHQAYEVLSDPQTR	3.38	2,130.10

ATP	6011	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	8	10	12	0.13%	14.20%	FKMLAELYGSDPQEELVY	3.04	2,148.02
ATP	6011	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	8	10	12	0.13%	14.20%	KPLIGSVLAKDPDAAQR	2.86	1,779.01
ATP	6011	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	8	10	12	0.13%	14.20%	NLESPSSFTIK	2.41	1,222.63
ATP	6011	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	8	10	12	0.13%	14.20%	PSLYAQVQKPPR	2.17	1,383.77
ATP	6011	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	8	10	12	0.13%	14.20%	TSDKGQFFGITK	3.47	1,328.68
ATP	6011	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	8	10	12	0.13%	14.20%	VDKNTGDVYALER	4.25	1,479.74
ATP	6011	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	8	10	12	0.13%	14.20%	VGSPLGSLFVEDPDEPQNR	4.69	2,056.00
ATP	6011	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	8	10	12	0.13%	14.20%	YSFVQGEYR	2.94	1,148.54

ATP	6011	RecName: Full=Alpha-enolase; AltName: Full=2-phospho-D-glycerate hydro-lyase; AltName: Full=Non-neural enolase; Short=NNE; AltName: Full=Enolase 1; AltName: Full=Phosphopyruvate hydratase	gi|109940077,gi|74354056,gi|87196501	47,309.10	100.00%	3	3	3	0.03%	10.80%	AAVPSGASTGIYEALELR	2.54	1,804.94
ATP	6011	RecName: Full=Alpha-enolase; AltName: Full=2-phospho-D-glycerate hydro-lyase; AltName: Full=Non-neural enolase; Short=NNE; AltName: Full=Enolase 1; AltName: Full=Phosphopyruvate hydratase	gi|109940077,gi|74354056,gi|87196501	47,309.10	100.00%	3	3	3	0.03%	10.80%	DATNVGDEGGFAPNILENK	4.4	1,960.92

ATP	6011	RecName: Full=Alpha-enolase; AltName: Full=2-phospho-D-glycerate hydro-lyase; AltName: Full=Non-neural enolase; Short=NNE; AltName: Full=Enolase 1; AltName: Full=Phosphopyruvate hydratase	gi|109940077,gi|74354056,gi|87196501	47,309.10	100.00%	3	3	3	0.03%	10.80%	IGAEVYHNLK	2.71	1,143.62
ATP	6011	LOC515309 protein	gi|148878460,gi|149773584	31,548.40	99.80%	2	3	3	0.03%	11.00%	KEEEEEEEEYDEGSNLKR	4.58	2,241.96
ATP	6011	LOC515309 protein	gi|148878460,gi|149773584	31,548.40	99.80%	2	3	3	0.03%	11.00%	SNPEDQILYQTER	4.05	1,592.76
ATP	6011	PREDICTED: lamin B2	gi|194668843	70,532.10	100.00%	4	4	5	0.05%	12.10%	ETENGEEGEDEAAEFGEEDLFHQQGDPR	3.23	3,164.28
ATP	6011	PREDICTED: lamin B2	gi|194668843	70,532.10	100.00%	4	4	5	0.05%	12.10%	LALDMEISAYRK	2.67	1,425.74
ATP	6011	PREDICTED: lamin B2	gi|194668843	70,532.10	100.00%	4	4	5	0.05%	12.10%	QVLEGEEISYK	2.22	1,294.65
ATP	6011	PREDICTED: lamin B2	gi|194668843	70,532.10	100.00%	4	4	5	0.05%	12.10%	TLYEAELADAR	3.43	1,251.62
ATP	6011	PREDICTED: lamin B2	gi|194668843	70,532.10	100.00%	4	4	5	0.05%	12.10%	TTLVNADGEEVAMR	4.05	1,521.72
ATP	6011	SCO cytochrome oxidase deficient homolog 1 (yeast)	gi|119223914,gi|122692513,gi|134035032	33,641.50	99.80%	2	3	4	0.04%	12.10%	LIGLTGTKEEIDQVAR	4.51	1,742.97
ATP	6011	SCO cytochrome oxidase deficient homolog 1 (yeast)	gi|119223914,gi|122692513,gi|134035032	33,641.50	99.80%	2	3	4	0.04%	12.10%	SIGKPLLGGPFSLTTHTGEPK	3.55	2,137.17
ATP	6011	PREDICTED: thrombomodulin	gi|119905421	60,710.90	99.80%	2	2	3	0.03%	4.84%	GPATFLAASR	2.55	990.5367

ATP	6011	PREDICTED: thrombomodulin	gi|119905421	60,710.90	99.80%	2	2	3	0.03%	4.84%	SSVAEDVISLLLSGDGPR	3.71	1,814.95
ATP	6011	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	100.00%	4	5	5	0.05%	12.70%	KPDLPPPGTLAPPTLQGR	2.72	1,855.04
ATP	6011	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	100.00%	4	5	5	0.05%	12.70%	LQTVQSADQVLVLR	3.47	1,569.90
ATP	6011	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	100.00%	4	5	5	0.05%	12.70%	QVVLVGQEPVLFSGSVR	4.7	1,814.02
ATP	6011	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	100.00%	4	5	5	0.05%	12.70%	VNFQNVSFAYPSRPDQPALQGLTFTLSPGQMTALVGPNGSGK	2.57	4,408.20
ATP	6011	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	9	10	0.11%	27.80%	AGAGSATLSMAYAGAR	4.3	1,470.70
ATP	6011	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	9	10	0.11%	27.80%	ANAFVAELK	2.56	962.5305
ATP	6011	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	9	10	0.11%	27.80%	ANAFVAELKDLDPAR	3.54	1,629.86

ATP	6011	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	9	10	0.11%	27.80%	LTLYDIAHTPGVAADLSHIETR	6.25	2,393.25
ATP	6011	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	9	10	0.11%	27.80%	MIAEAIPELK	2.97	1,130.61
ATP	6011	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	9	10	0.11%	27.80%	VAVLGASGGIGQPLSLLLK	4.23	1,793.09
ATP	6011	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	9	10	0.11%	27.80%	VNVPVIGGHAGK	3.6	1,147.66
ATP	6011	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	6	18	0.20%	26.20%	FGLIPEEFFQFLYPK	2.9	1,874.97
ATP	6011	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	6	18	0.20%	26.20%	HYLFDVQR	2.72	1,077.55

ATP	6011	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	6	18	0.20%	26.20%	NNIAMALEVTYR	3.88	1,410.70
ATP	6011	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	6	18	0.20%	26.20%	PVPPLPEHGGK	2.06	1,127.62
ATP	6011	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	5	6	18	0.20%	26.20%	QIQDAIDMEK	2.65	1,206.57
ATP	6011	Ribosomal protein S8	gi|119224110,gi|58760384,gi|59858489,gi|70778956,gi|74268417,gi|75070020	24,188.40	99.80%	2	2	2	0.02%	13.50%	IIDVVYNASNNELVR	5.24	1,718.91
ATP	6011	Ribosomal protein S8	gi|119224110,gi|58760384,gi|59858489,gi|70778956,gi|74268417,gi|75070020	24,188.40	99.80%	2	2	2	0.02%	13.50%	ISSLLEEQFQQGK	3.83	1,506.78
ATP	6011	PREDICTED: similar to oxysterol 7alpha-hydroxylase	gi|194672764	90,479.20	100.00%	3	3	3	0.03%	6.82%	AMAVLRDEIDHLLQSTGQK	3.86	2,141.10
ATP	6011	PREDICTED: similar to oxysterol 7alpha-hydroxylase	gi|194672764	90,479.20	100.00%	3	3	3	0.03%	6.82%	FLFGIPYPDSDVLFR	2.74	1,785.92
ATP	6011	PREDICTED: similar to oxysterol 7alpha-hydroxylase	gi|194672764	90,479.20	100.00%	3	3	3	0.03%	6.82%	MLTDSDLIDEIHSTYQFLQGK	3.18	2,470.18
ATP	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	8	10	14	0.15%	26.40%	AVFVDLEPTVIDEVR	4.59	1,701.91

ATP	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	8	10	14	0.15%	26.40%	DVNAAIATIK	2.92	1,015.58
ATP	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	8	10	14	0.15%	26.40%	EIIDLVLDR	2.5	1,085.62
ATP	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	8	10	14	0.15%	26.40%	IHFPLATYAPVISAEK	2.52	1,756.96
ATP	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	8	10	14	0.15%	26.40%	LISQIVSSITASLR	3.34	1,487.88
ATP	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	8	10	14	0.15%	26.40%	NLDIERPTYTNLNR	3.34	1,718.88
ATP	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	8	10	14	0.15%	26.40%	QLFHPEQLITGKEDAANNYAR	3.35	2,415.21
ATP	6011	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	8	10	14	0.15%	26.40%	TIGGGDDSFNTFFSETGAGK	3.87	2,007.89
ATP	6011	PREDICTED: similar to transmembrane protein 165	gi|76619924	34,667.10	99.80%	2	2	2	0.02%	13.30%	MSPDEGQEELEEVQAELK	4.12	2,076.93
ATP	6011	PREDICTED: similar to transmembrane protein 165	gi|76619924	34,667.10	99.80%	2	2	2	0.02%	13.30%	NKEPPAPAQQLQPQPAAVQGPEPAR	5.09	2,619.36
ATP	6011	RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8; AltName: Full=NADH-ubiquinone oxidoreductase 19 kDa subunit; AltName: Full=Complex I-19kD;	gi|1171870,gi|28461275,gi|599681,gi|86827664	20,073.10	99.80%	2	2	2	0.02%	18.60%	ARPEPNPEVEGDLKPAR	5.98	1,874.97

ATP	6011	RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8; AltName: Full=NADH-ubiquinone oxidoreductase 19 kDa subunit; AltName: Full=Complex I-19kD;	gi|1171870, gi|28461275,gi|599681,gi|86827664	20,073.10	99.80%	2	2	2	0.02%	18.60%	VKTDRPLPENPYHSR	2.25	1,808.94
ATP	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	13	17	20	0.22%	14.80%	AAAQDIFSPK	2.89	1,047.55

ATP	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	13	17	20	0.22%	14.80%	ATILYASETGR	3.15	1,181.62
ATP	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	13	17	20	0.22%	14.80%	AVDTRLEELGGER	2.91	1,444.74

ATP	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	13	17	20	0.22%	14.80%	DFINQYYSSIKR	3.29	1,533.77
ATP	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	13	17	20	0.22%	14.80%	ESSNTDSAGALGTLR	4.43	1,478.71

ATP	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	13	17	20	0.22%	14.80%	LLSTLAEEPSEQQELETLSQDPR	4.22	2,613.29
ATP	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	13	17	20	0.22%	14.80%	LSTQAEGLQLLPGLIHVHR	3.04	2,082.18

ATP	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	13	17	20	0.22%	14.80%	MFQATVLSVENLQSSK	3.44	1,797.91
ATP	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	13	17	20	0.22%	14.80%	SAITVFPQR	2.75	1,018.57

ATP	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	13	17	20	0.22%	14.80%	TYVQDILR	2.77	1,007.55
ATP	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	13	17	20	0.22%	14.80%	VEDPPPPTESVAVEQLEK	3.91	1,963.99

ATP	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	13	17	20	0.22%	14.80%	VLTAFSREPDSPK	3.59	1,446.76
ATP	6011	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	13	17	20	0.22%	14.80%	YHEDIFGLTLR	2.41	1,363.70
ATP	6011	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	4	5	7	0.08%	11.00%	IGGIGTVPVGR	2.67	1,025.61

ATP	6011	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	4	5	7	0.08%	11.00%	VETGVLKPGMVVTFAPVNVTTEVK	4.58	2,531.38
ATP	6011	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	4	5	7	0.08%	11.00%	YYVTIIDAPGHR	3.54	1,404.73
ATP	6011	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	4	5	7	0.08%	11.00%	YYVTIIDAPGHRDFIK	2.57	1,908.00
ATP	6011	cell division cycle 42 (GTP binding protein, 25kDa)	gi|114052486,gi|122063301,gi|86821687	21,240.70	99.80%	2	2	4	0.04%	19.90%	NVFDEAILAALEPPEPK	3.47	1,852.97
ATP	6011	cell division cycle 42 (GTP binding protein, 25kDa)	gi|114052486,gi|122063301,gi|86821687	21,240.70	99.80%	2	2	4	0.04%	19.90%	TPFLLVGTQIDLRDDPSTIEK	2.91	2,358.26
ATP	6011	RecName: Full=Golgi SNAP receptor complex member 1	gi|108935998,gi|83638559,gi|84370083	28,524.90	99.80%	2	2	3	0.03%	13.20%	ENMTSQRGMLKSIQSK	3.24	1,837.93
ATP	6011	RecName: Full=Golgi SNAP receptor complex member 1	gi|108935998,gi|83638559,gi|84370083	28,524.90	99.80%	2	2	3	0.03%	13.20%	MNTLANRFPAVNSLIQR	4.01	1,961.04
ATP	6011	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	5	7	8	0.09%	31.50%	EDGNEEDKENQGDETQGQQPPQR	3.67	2,628.10

ATP	6011	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	5	7	8	0.09%	31.50%	EDGNEEDKENQGDETQGQQPPQRR	2	2,784.21
ATP	6011	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	5	7	8	0.09%	31.50%	GAEAANVTGPGGVPVQGSK	4.35	1,695.87
ATP	6011	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	5	7	8	0.09%	31.50%	NYQQNYQNSESGEKNEGSESAPEGQAQQR	5.52	3,257.40
ATP	6011	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	5	7	8	0.09%	31.50%	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	3.52	3,239.53
ATP	6011	H3 histone, family 3A	gi|59858289,gi|62177168,gi|95769331	15,310.70	99.80%	2	3	7	0.08%	14.70%	EIAQDFKTDLR	3.24	1,335.69
ATP	6011	H3 histone, family 3A	gi|59858289,gi|62177168,gi|95769331	15,310.70	99.80%	2	3	7	0.08%	14.70%	YRPGTVALR	2.24	1,032.59
ATP	6011	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	100.00%	4	4	5	0.05%	13.70%	FTSLGLLPR	2.82	1,003.59
ATP	6011	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	100.00%	4	4	5	0.05%	13.70%	LTEDGLPLGINLGK	4.56	1,439.81
ATP	6011	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	100.00%	4	4	5	0.05%	13.70%	VFRLPEDQAIINR	4.16	1,570.87
ATP	6011	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	100.00%	4	4	5	0.05%	13.70%	VPIVGVGGVSSGQDALEK	5.18	1,711.92
ATP	6011	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	4	4	4	0.04%	10.30%	AENLGEVLRGDR	2.5	1,328.69
ATP	6011	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	4	4	4	0.04%	10.30%	ISEDYYVHLIADNLPVATR	4.36	2,189.12
ATP	6011	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	4	4	4	0.04%	10.30%	IVNTPFQVLMNSEK	3.84	1,635.84

ATP	6011	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	4	4	4	0.04%	10.30%	KCEVLCGQSNKPVTLTVEQSR	3.14	2,319.18
ATP	6011	PREDICTED: similar to plexin B2 isoform 1	gi|194681262	204,931.90	99.90%	2	2	2	0.02%	2.22%	NLDTVQGSPLLVGSDLLK	3.98	1,869.03
ATP	6011	PREDICTED: similar to plexin B2 isoform 1	gi|194681262	204,931.90	99.90%	2	2	2	0.02%	2.22%	TPKLTHDANETLPLHLYVKSAGK	3.53	2,533.38
ATP	6011	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	100.00%	4	4	6	0.07%	21.00%	AITIFQERDPANIK	2.91	1,615.88
ATP	6011	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	100.00%	4	4	6	0.07%	21.00%	GAAQNIIPASTGAAK	4.45	1,369.74
ATP	6011	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	100.00%	4	4	6	0.07%	21.00%	IVSNASCTTNCLAPLAK	2.57	1,705.86
ATP	6011	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	100.00%	4	4	6	0.07%	21.00%	VIHDHFGIVEGLMTTVHAITATQK	3.22	2,634.37
ATP	6011	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	99.80%	2	3	3	0.03%	6.25%	FFLSAGLIDKVDNFK	2.46	1,713.92
ATP	6011	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	99.80%	2	3	3	0.03%	6.25%	LEDPHVDIIR	2.87	1,206.65
ATP	6011	intergral membrane protein 1	gi|114051696,gi|122136222,gi|152941168,gi|86823970	80,641.10	99.80%	2	2	2	0.02%	3.69%	FESVIHEFDPYFNYR	4.07	1,962.90

ATP	6011	intergral membrane protein 1	gi|114051696,gi|122136222,gi|152941168,gi|86823970	80,641.10	99.80%	2	2	2	0.02%	3.69%	FYSLLDPSYAK	2.97	1,303.66
ATP	6011	Myeloid-associated differentiation marker	gi|111308557,gi|115497460	35,291.10	99.80%	2	4	5	0.05%	12.70%	ARPGEITGYMATVPGLLK	3.67	1,890.02
ATP	6011	Myeloid-associated differentiation marker	gi|111308557,gi|115497460	35,291.10	99.80%	2	4	5	0.05%	12.70%	TTVTTTMSSSSGLGSPTIVGSPR	4.35	2,240.11
ATP	6011	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	8	10	36	0.39%	14.10%	DAEAWFNEK	3.05	1,109.49
ATP	6011	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	8	10	36	0.39%	14.10%	IRLENEIQTYR	4.44	1,434.77
ATP	6011	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	8	10	36	0.39%	14.10%	LASYLDKVR	3.26	1,064.61

ATP	6011	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	8	10	36	0.39%	14.10%	LENEIQTYR	3.91	1,165.58
ATP	6011	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	8	10	36	0.39%	14.10%	QSLEASLAETEGR	4.43	1,390.68
ATP	6011	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	8	10	36	0.39%	14.10%	QSVEADINGLR	3.08	1,201.62
ATP	6011	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	8	10	36	0.39%	14.10%	RVLDELTLTK	2.91	1,187.70
ATP	6011	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	8	10	36	0.39%	14.10%	SQYEQLAEKNR	4.45	1,365.68

ATP	6011	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	8	10	36	0.39%	14.10%	VLDELTLTK	3.79	1,031.60
ATP	6011	MATR3 protein	gi|134024643,gi|156523084	93,810.30	99.80%	2	2	2	0.02%	5.57%	DLDELSRYPEDKITPENLPQILLQLK	3.34	3,080.65
ATP	6011	MATR3 protein	gi|134024643,gi|156523084	93,810.30	99.80%	2	2	2	0.02%	5.57%	YQLLQLVEPFGVISNHLILNK	3.51	2,438.38
ATP	6011	Transferrin	gi|113911795,gi|114326282	77,721.80	100.00%	2	2	2	0.02%	3.41%	DKPDNFQLFQSPHGK	3.99	1,757.86
ATP	6011	Transferrin	gi|113911795,gi|114326282	77,721.80	100.00%	2	2	2	0.02%	3.41%	YYGYTGAFR	2.44	1,097.51
ATP	6011	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	4	7	10	0.11%	23.30%	GKESEKELALLK	3.93	1,344.77
ATP	6011	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	4	7	10	0.11%	23.30%	GVGDDQLGEESEERDDHLLPM	2.55	2,357.02
ATP	6011	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	4	7	10	0.11%	23.30%	HTLADNFNPVSEER	4.59	1,628.77
ATP	6011	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	4	7	10	0.11%	23.30%	SFESTVGQSPDMYSYVFR	3.56	2,115.93
ATP	6011	ADP-ribosylation-like factor 6 interacting protein 5	gi|59858163,gi|62460474,gi|74354855,gi|75057806	21,648.60	99.80%	2	3	3	0.03%	13.80%	FARPDFR	1.84	908.4737

ATP	6011	ADP-ribosylation-like factor 6 interacting protein 5	gi|59858163,gi|62460474,gi|74354855,gi|75057806	21,648.60	99.80%	2	3	3	0.03%	13.80%	TPMGIVLDALEQQEETITK	6.07	2,132.08
ATP	6011	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	3	3	5	0.05%	8.36%	EKPYFPIPEDYTFIQNVPLEDR	5.13	2,710.34
ATP	6011	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	3	3	5	0.05%	8.36%	LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR	5.88	3,142.43
ATP	6011	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	3	3	5	0.05%	8.36%	NFILDQTNVSAAAQR	3.29	1,647.84
ATP	6011	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	gi|124829038,gi|125630707,gi|171769867	51,147.90	100.00%	3	3	3	0.03%	9.27%	ADYLQNYEFPHLQNFIK	2.64	2,140.05
ATP	6011	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	gi|124829038,gi|125630707,gi|171769867	51,147.90	100.00%	3	3	3	0.03%	9.27%	LLLVSFDGFR	2.95	1,166.66
ATP	6011	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	gi|124829038,gi|125630707,gi|171769867	51,147.90	100.00%	3	3	3	0.03%	9.27%	VLEEIDEHIGELVHR	2.74	1,787.93
ATP	6011	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	5	5	5	0.05%	10.50%	EESREPAPASPAPAGVEIR	3.8	1,962.99

ATP	6011	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	5	5	5	0.05%	10.50%	GMTTVDDFFQGTK	2.84	1,462.65
ATP	6011	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	5	5	5	0.05%	10.50%	NHQSAAEYNIFEGMELR	3.97	2,024.91
ATP	6011	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	5	5	5	0.05%	10.50%	QIGDNLIVPGGVK	2.52	1,309.75
ATP	6011	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	5	5	5	0.05%	10.50%	SAADLISQAR	3.12	1,031.55
ATP	6011	TOMM22 protein	gi|151556851,gi|154152189	15,275.00	100.00%	3	5	7	0.08%	44.30%	GDAEKPEEELEEEDDEELDETLSER	3.52	2,935.23
ATP	6011	TOMM22 protein	gi|151556851,gi|154152189	15,275.00	100.00%	3	5	7	0.08%	44.30%	LQMEQQQQLQQR	4.36	1,573.78
ATP	6011	TOMM22 protein	gi|151556851,gi|154152189	15,275.00	100.00%	3	5	7	0.08%	44.30%	QILLGPNTGLSGGMPGALPSLPGKI	3.9	2,404.33
ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	AIAELGIYPAVDPLDSTSR	4.53	1,988.03
ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	DQEGQDVLLFIDNIFR	5.12	1,921.97
ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	FLSQPFQVAEVFTGHLGK	4.02	2,005.05

ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	FTQAGSEVSALLGR	4.15	1,435.75
ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	2.62	3,350.64
ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	2.67	3,714.89
ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	IMDPNIVGSEHYDVAR	3.78	1,831.86
ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	IMNVIGEPIDER	3.56	1,401.70

ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	IMNVIGEPIDERGPIK	3.69		1,796.96
ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	IPSAVGYQPTLATDMGTMQER	4.58		2,282.08
ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	IPVGPETLGR	3.01		1,038.59
ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	IVAVIGAVVDVQFDEGLPPILNALEVQGR	4.21		3,031.68
ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	LVLEVAQHLGESTVR	4.94		1,650.92

ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	QFAAIHAEAPEFVEMSVEQEILVTGIK	5.39	3,002.52
ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	TREGNDLYHEMIESGVINLK	2.79	2,334.14
ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	TVLIMELINNVAK	4.07	1,473.83
ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	VALTGLTVAEYFR	4.17	1,439.79
ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	VALVYGQMNEPPGAR	3.6	1,617.81

ATP	6011	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	19	25	44	0.48%	69.90%	VLDSGAPIRIPVGPETLGR	4.47	1,947.10
ATP	6011	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	4	6	7	0.08%	18.80%	AEQINQAAGEASAVLAK	4.48	1,670.87
ATP	6011	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	4	6	7	0.08%	18.80%	ASYGVEDPEYAVTQLAQTTMR	4.59	2,346.09
ATP	6011	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	4	6	7	0.08%	18.80%	ILEPGLNILIPVLDR	4.31	1,675.02
ATP	6011	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	4	6	7	0.08%	18.80%	STDASLDEELDRVK	3.7	1,577.77
ATP	6011	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	2	3	3	0.03%	2.59%	SYSQSILLDLTDSTLQTTLK	3.91	2,227.17
ATP	6011	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	2	3	3	0.03%	2.59%	VGSPFELVVIGNK	3.38	1,358.77
ATP	6011	S100 calcium binding protein A16	gi|111307529,gi|115497862,gi|122142422	11,758.80	100.00%	3	3	4	0.04%	26.20%	AADKLIQNLDANHDGR	2.58	1,750.88
ATP	6011	S100 calcium binding protein A16	gi|111307529,gi|115497862,gi|122142422	11,758.80	100.00%	3	3	4	0.04%	26.20%	AVVVLVENFYK	3.09	1,280.72

ATP	6011	S100 calcium binding protein A16	gi|111307529,gi|115497862,gi|122142422	11,758.80	100.00%	3	3	4	0.04%	26.20%	LIQNLDANHDGR	2.59	1,365.69
ATP	6011	CHMP4B protein	gi|116874509,gi|190360743	24,919.20	99.80%	2	2	3	0.03%	13.40%	EALENANTNTEVLK	3.84	1,545.78
ATP	6011	CHMP4B protein	gi|116874509,gi|190360743	24,919.20	99.80%	2	2	3	0.03%	13.40%	QLAQIDGTLSTIEFQR	3.3	1,819.96
ATP	6011	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	5	5	5	0.05%	13.60%	GYDFPAVLR	2.48	1,037.54
ATP	6011	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	5	5	5	0.05%	13.60%	LFELEEQDLFRDIQGLPR	4.42	2,218.15
ATP	6011	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	5	5	5	0.05%	13.60%	LLEALDEMLTHDIAK	4.19	1,727.89
ATP	6011	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	5	5	5	0.05%	13.60%	SKYDEIFYNLAPADGK	3.75	1,830.89
ATP	6011	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	5	5	5	0.05%	13.60%	TSFIQYLLEQEVPGSR	3.36	1,866.96
ATP	6011	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	100.00%	4	5	13	0.14%	21.70%	FLVGFTNK	2.54	925.5142
ATP	6011	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	100.00%	4	5	13	0.14%	21.70%	GEDFPANNIVK	3.86	1,203.60
ATP	6011	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	100.00%	4	5	13	0.14%	21.70%	GTEDFIVESLDASFR	4.22	1,685.80
ATP	6011	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	100.00%	4	5	13	0.14%	21.70%	QATFEYSFIPAEPMGGRPFGLVINLNYK	2.15	3,175.59
ATP	6011	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	5	6	7	0.08%	9.58%	ALGVEQDLALPAIAVIGDQSSGK	4.68	2,252.21
ATP	6011	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	5	6	7	0.08%	9.58%	LTQAQQALYEFPHFK	3.8	1,820.93
ATP	6011	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	5	6	7	0.08%	9.58%	LTQAQQALYEFPHFKG	4.43	1,877.95
ATP	6011	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	5	6	7	0.08%	9.58%	SSVLEALSGVALPR	4.6	1,398.80
ATP	6011	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	5	6	7	0.08%	9.58%	VAVENQPQDIGLQIK	4.51	1,651.90

ATP	6011	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	5	5	10	0.11%	26.00%	KQDAFYKEQLAR	4.78	1,496.79
ATP	6011	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	5	5	10	0.11%	26.00%	QNTQQTLSCSALASQYMR	3.82	2,045.94
ATP	6011	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	5	5	10	0.11%	26.00%	RVAEELALEQAKK	5.44	1,484.84
ATP	6011	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	5	5	10	0.11%	26.00%	RVTFEADENENITVVK	2.83	1,863.94
ATP	6011	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	5	5	10	0.11%	26.00%	VAEELALEQAK	4.56	1,200.65
ATP	6011	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	8	11	21	0.23%	14.70%	IGFGSFVEK	2.47	983.5197
ATP	6011	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	8	11	21	0.23%	14.70%	LLVFSTDAGFHFAGDGK	2.91	1,781.89
ATP	6011	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	8	11	21	0.23%	14.70%	LQPEDITQIQPQQLVLQLR	5.25	2,260.27
ATP	6011	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	8	11	21	0.23%	14.70%	LSENNIQTIFAVTEEFQPVYK	4.25	2,470.25
ATP	6011	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	8	11	21	0.23%	14.70%	NVLSLTDKGEVFNELVGK	5.2	1,962.05
ATP	6011	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	8	11	21	0.23%	14.70%	SGEPQTFTLK	2.48	1,107.57
ATP	6011	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	8	11	21	0.23%	14.70%	SLGTDLMNEMR	2.68	1,282.58
ATP	6011	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	8	11	21	0.23%	14.70%	TVMPYISTTPAK	2.77	1,324.68
ATP	6011	TPM3 protein	gi|79153472	29,015.30	100.00%	6	7	7	0.08%	25.40%	ALKDEEKMELQEIQLK	3.71	1,961.03
ATP	6011	TPM3 protein	gi|79153472	29,015.30	100.00%	6	7	7	0.08%	25.40%	AREQAEAEVASLNRR	3.65	1,699.88
ATP	6011	TPM3 protein	gi|79153472	29,015.30	100.00%	6	7	7	0.08%	25.40%	IQLVEEELDR	3.28	1,243.65

ATP	6011	TPM3 protein	gi|79153472	29,015.30	100.00%	6	7	7	0.08%	25.40%	IQLVEEELDRAQER	3.36	1,727.89
ATP	6011	TPM3 protein	gi|79153472	29,015.30	100.00%	6	7	7	0.08%	25.40%	KIQVLQQQADDAEERAER	3.58	2,127.08
ATP	6011	TPM3 protein	gi|79153472	29,015.30	100.00%	6	7	7	0.08%	25.40%	RIQLVEEELDRAQER	3.36	1,883.99
ATP	6011	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	4	5	6	0.07%	19.40%	LSQNNFALGYK	3.6	1,254.65
ATP	6011	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	4	5	6	0.07%	19.40%	LTLDTIFVPNTGK	2.98	1,418.79

ATP	6011	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	4	5	6	0.07%	19.40%	LTLDTIFVPNTGKK	3.62	1,546.88
ATP	6011	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	4	5	6	0.07%	19.40%	LTLSALIDGK	3.27	1,030.61
ATP	6011	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	4	5	6	0.07%	19.40%	VNNASLIGLGYTQTLRPGVK	4.28	2,101.18
ATP	6011	SLC25A3 protein	gi|151556064	39,986.50	100.00%	4	7	9	0.10%	9.70%	FGFYEVFK	2.08	1,036.51
ATP	6011	SLC25A3 protein	gi|151556064	39,986.50	100.00%	4	7	9	0.10%	9.70%	IQTQPGYANTLR	3.81	1,361.72
ATP	6011	SLC25A3 protein	gi|151556064	39,986.50	100.00%	4	7	9	0.10%	9.70%	LPRPPPPEMPESLK	4.07	1,603.85

ATP	6011	SLC25A3 protein	gi|151556064	39,986.50	100.00%	4	7	9	0.10%	9.70%	LPRPPPPEMPESLKK	4.34	1,731.95
ATP	6011	PREDICTED: similar to Desmoplakin (DP) (250/210 kDa paraneoplastic pemphigus antigen) isoform 1	gi|119915951	332,372.60	99.80%	2	2	2	0.02%	1.04%	AQQIHSQTSQQYPLYDLDLGK	3.31	2,433.20
ATP	6011	PREDICTED: similar to Desmoplakin (DP) (250/210 kDa paraneoplastic pemphigus antigen) isoform 1	gi|119915951	332,372.60	99.80%	2	2	2	0.02%	1.04%	IEVLEEELR	2.5	1,129.61
ATP	6011	ALCAM/CD166	gi|13111304,gi|41386784,gi|47605539	64,749.10	100.00%	2	2	2	0.02%	4.63%	KSVQYDDVPEYKDR	2.26	1,741.84
ATP	6011	ALCAM/CD166	gi|13111304,gi|41386784,gi|47605539	64,749.10	100.00%	2	2	2	0.02%	4.63%	VFKQPSKPEIVSK	2.84	1,486.86
ATP	6011	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor 1; AltName: Full=p40; AltName: Full=Protein C10	gi|122066007,gi|28189773,gi|73587277	18,591.70	99.90%	2	2	2	0.02%	17.50%	AIVAIENPADVSVISSR	3.86	1,740.95

ATP	6011	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor 1; AltName: Full=p40; AltName: Full=Protein C10	gi|122066007,gi|28189773,gi|73587277	18,591.70	99.90%	2	2	2	0.02%	17.50%	FAAATGATPIAGR	4.67	1,203.65
ATP	6011	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	3	4	5	0.05%	24.10%	LAEQAERYDDMAACMK	3.89	1,860.79
ATP	6011	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	3	4	5	0.05%	24.10%	SVTEQGAELSNEER	5.27	1,548.71
ATP	6011	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	3	4	5	0.05%	24.10%	TAFDEAIAELDTLSEESYKDSTLIMQLLR	4.67	3,318.63
ATP	6011	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,053.70	100.00%	3	3	3	0.03%	16.10%	IALTDNALIAR	3.29	1,170.68

ATP	6011	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,053.70	100.00%	3	3	3	0.03%	16.10%	KVPAVPETLK	2.36	1,081.66
ATP	6011	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,053.70	100.00%	3	3	3	0.03%	16.10%	TTHFVEGGDAGNREDQINR	2.48	2,115.98
ATP	6011	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	4	4	4	0.04%	13.60%	ADLINNLGTIAK	2.9	1,242.71
ATP	6011	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	4	4	4	0.04%	13.60%	GVVDSEDLPLNISR	4.86	1,513.79
ATP	6011	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	4	4	4	0.04%	13.60%	HLEINPDHSIIETLR	2.66	1,786.94
ATP	6011	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	4	4	4	0.04%	13.60%	HSQFIGYPITLFVEKER	3.03	2,064.09
ATP	6011	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	4	4	4	0.04%	13.60%	NPDDITNEEYGEFYK	3.93	1,833.78
ATP	6011	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	4	4	4	0.04%	13.60%	TLTIVDTGIGMTK	4.55	1,365.73
ATP	6011	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	4	4	4	0.04%	13.60%	YESLTDPSKLDSGK	2.97	1,539.75
ATP	6011	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	3	3	10	0.11%	19.80%	AMGIMNSFVNDIFER	4.34	1,759.81
ATP	6011	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	3	3	10	0.11%	19.80%	ESYSVYVYK	2.11	1,137.55
ATP	6011	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	3	3	10	0.11%	19.80%	KESYSVYVYK	3.32	1,265.64

ATP	6011	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	5	5	5	0.05%	13.30%	EATESFASDPILYRPVAVALDTK	2.33	2,493.29
ATP	6011	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	5	5	5	0.05%	13.30%	GDLGIEIPAEK	3.03	1,141.61
ATP	6011	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	5	5	5	0.05%	13.30%	GVNLPGAAVDLPAVSEK	3.34	1,636.89
ATP	6011	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	5	5	5	0.05%	13.30%	IYVDDGLISLLVK	3.58	1,447.84
ATP	6011	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	5	5	5	0.05%	13.30%	LDIDSPPITAR	3.1	1,197.65
ATP	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	10	18	0.20%	25.60%	AMGNLQIDFADPSR	4.24	1,550.73
ATP	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	10	18	0.20%	25.60%	AMGNLQIDFADPSRADDAR	3.43	2,078.96
ATP	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	10	18	0.20%	25.60%	AVVYSNTIQSIMAIVK	3.95	1,752.96
ATP	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	10	18	0.20%	25.60%	EYQLNDSAAYYLNDLER	3.3	2,076.95

ATP	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	10	18	0.20%	25.60%	IAQSDYIPTQQDVLR	4.46	1,746.90
ATP	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	10	18	0.20%	25.60%	LLLLGAGESGK	3.54	1,057.63
ATP	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	10	18	0.20%	25.60%	SREYQLNDSAAYYLNDLER	5.04	2,320.08
ATP	6011	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	8	10	18	0.20%	25.60%	YDEAASYIQSK	2.76	1,274.59
ATP	6011	Paraoxonase 2	gi|109939919,gi|61553203,gi|61888862,gi|71648804	39,404.60	100.00%	2	3	4	0.04%	7.91%	LLIGTLYHR	1.72	1,085.65
ATP	6011	Paraoxonase 2	gi|109939919,gi|61553203,gi|61888862,gi|71648804	39,404.60	100.00%	2	3	4	0.04%	7.91%	VVAEGFDSANGINISPDKK	4.41	1,961.00
ATP	6011	ILVBL protein	gi|151557079,gi|154426224,gi|166233819,gi|59857973,gi|62751470	68,205.30	99.80%	2	2	2	0.02%	5.85%	AAQGLGAQGLLLSR	3.42	1,354.78
ATP	6011	ILVBL protein	gi|151557079,gi|154426224,gi|166233819,gi|59857973,gi|62751470	68,205.30	99.80%	2	2	2	0.02%	5.85%	NAQIAQSPVLLLGGAASTLLQNR	3.81	2,335.31

ATP	6011	RecName: Full=Complement component 1 Q subcomponent-binding protein, mitochondrial; Flags: Precursor	gi|115311784,gi|74354078,gi|77736001	30,588.80	99.90%	2	3	4	0.04%	18.00%	AEEQEPELTSTPNFVVEVTK	4.56	2,247.10
ATP	6011	RecName: Full=Complement component 1 Q subcomponent-binding protein, mitochondrial; Flags: Precursor	gi|115311784,gi|74354078,gi|77736001	30,588.80	99.90%	2	3	4	0.04%	18.00%	GVDNTFADELVELSTALEHQEYISFLEDLK	5.45	3,425.66
ATP	6011	Na/K-ATPase beta 1 subunit [synthetic construct]	gi|22094876	35,156.20	99.80%	2	2	2	0.02%	8.88%	AYGENIGYSEKDR	3.85	1,501.69
ATP	6011	Na/K-ATPase beta 1 subunit [synthetic construct]	gi|22094876	35,156.20	99.80%	2	2	2	0.02%	8.88%	VAPPGLTQIPQIQK	3.21	1,489.87
ATP	6011	vascular cell adhesion molecule-1 7D variant	gi|11907511,gi|11990448,gi|41386707	81,381.40	99.80%	2	2	2	0.02%	3.25%	LPIDEMEFELK	2.55	1,363.68
ATP	6011	vascular cell adhesion molecule-1 7D variant	gi|11907511,gi|11990448,gi|41386707	81,381.40	99.80%	2	2	2	0.02%	3.25%	QSTQTLYVNVAPR	3.42	1,476.78
ATP	6011	ARF1 protein	gi|146327384,gi|28603778,gi|59858233,gi|62751462	20,583.70	99.90%	2	2	2	0.02%	16.00%	ILMVGLDAAGK	3.41	1,103.61
ATP	6011	ARF1 protein	gi|146327384,gi|28603778,gi|59858233,gi|62751462	20,583.70	99.90%	2	2	2	0.02%	16.00%	MLAEDELRDAVLLVFANK	4.16	2,063.08

ATP	6011	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	5	6	9	0.10%	11.40%	GLNTIPLFVQLLYSPIENIQR	3.57	2,428.36
ATP	6011	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	5	6	9	0.10%	11.40%	HAVVNLINYQDDAELATR	3.15	2,042.03
ATP	6011	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	5	6	9	0.10%	11.40%	LHYGLPVVVK	2.88	1,124.68
ATP	6011	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	5	6	9	0.10%	11.40%	LLNDEDQVVVNK	3.84	1,385.73
ATP	6011	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	5	6	9	0.10%	11.40%	MLGSPVDSVLFYAITTLHNLLLHQEGAK	3.62	3,083.62
ATP	6011	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	3	3	3	0.03%	1.58%	GPGDLEAPSNLVLSER	3.63	1,653.84
ATP	6011	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	3	3	3	0.03%	1.58%	ITYQPSTGEGNEQTTTIGGR	4.43	2,110.01
ATP	6011	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	3	3	3	0.03%	1.58%	NNVILQPLQPDTPYK	3.37	1,739.93
ATP	6011	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	2	4	5	0.05%	13.10%	ANVDKVFFDLMR	4.53	1,470.74

ATP	6011	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	2	4	5	0.05%	13.10%	VKEDENVPFLLVGNK	3.47	1,700.92
ATP	6011	hemoglobin alpha chain	gi|116812902,gi|126717493,gi|13634094,gi|194678485,gi|197724899,gi|197724901,gi|197724903,gi|6006421,gi|74268120	15,035.40	99.80%	2	2	2	0.02%	22.00%	AVEHLDDLPGALSELSDLHAHK	3.12	2,367.19
ATP	6011	hemoglobin alpha chain	gi|116812902,gi|126717493,gi|13634094,gi|194678485,gi|197724899,gi|197724901,gi|197724903,gi|6006421,gi|74268120	15,035.40	99.80%	2	2	2	0.02%	22.00%	MFLSFPTTK	2.4	1,087.55
ATP	6011	RecName: Full=Transmembrane emp24 domain-containing protein 1; Flags: Precursor	gi|114152289,gi|83638714,gi|84370158	25,119.90	99.80%	2	2	3	0.03%	11.50%	KADGVHTVEPTEAGDYK	4.42	1,816.87
ATP	6011	RecName: Full=Transmembrane emp24 domain-containing protein 1; Flags: Precursor	gi|114152289,gi|83638714,gi|84370158	25,119.90	99.80%	2	2	3	0.03%	11.50%	SIQVLTLLR	3.07	1,042.66
ATP	6011	growth and transformation-dependent protein	gi|114051522,gi|126258169,gi|84201630	17,719.20	100.00%	3	3	3	0.03%	20.50%	FKKEDEIPETVSFEMLDAAK	5.31	2,343.14
ATP	6011	growth and transformation-dependent protein	gi|114051522,gi|126258169,gi|84201630	17,719.20	100.00%	3	3	3	0.03%	20.50%	NETLTSLNLEK	2.82	1,261.66

ATP	6011	growth and transformation-dependent protein	gi|114051522,gi|126258169,gi|84201630	17,719.20	100.00%	3	3	3	0.03%	20.50%	RNETLTSLNLEK	3.9	1,417.76
ATP	6011	NADH:ubiquinone oxidoreductase ASHI subunit [Homo sapiens]	gi|33150722	21,747.60	100.00%	3	3	3	0.03%	24.70%	QYPYNNLYLER	2.28	1,472.72
ATP	6011	NADH:ubiquinone oxidoreductase ASHI subunit [Homo sapiens]	gi|33150722	21,747.60	100.00%	3	3	3	0.03%	24.70%	TASHMTKDMFPGPYPR	2.82	1,835.86
ATP	6011	NADH:ubiquinone oxidoreductase ASHI subunit [Homo sapiens]	gi|33150722	21,747.60	100.00%	3	3	3	0.03%	24.70%	VEDYEPYPDDGMGYGDYPK	3.2	2,225.89
ATP	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	13	17	33	0.36%	27.20%	IIGAVDQIQLTQAQLEER	4.65	2,025.10
ATP	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	13	17	33	0.36%	27.20%	IREGQVEVLK	3.66	1,170.68
ATP	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	13	17	33	0.36%	27.20%	KLEVNEAELLR	4.41	1,313.74
ATP	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	13	17	33	0.36%	27.20%	KLEVNEAELLRR	2.21	1,469.84
ATP	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	13	17	33	0.36%	27.20%	KSFTPDHVVYAR	2.83	1,419.74
ATP	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	13	17	33	0.36%	27.20%	LEVNEAELLR	3.79	1,185.65

ATP	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	13	17	33	0.36%	27.20%	QAEMEGAVQSIQGELSK	4.3	1,820.87
ATP	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	13	17	33	0.36%	27.20%	SDQVNGVLVLSLLDK	3.17	1,599.90
ATP	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	13	17	33	0.36%	27.20%	SDQVNGVLVLSLLDKIIGAVDQIQLTQAQLEER	4.14	3,605.98
ATP	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	13	17	33	0.36%	27.20%	SFTPDHVVYAR	2.49	1,291.64
ATP	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	13	17	33	0.36%	27.20%	VMIYQDEVK	2.77	1,140.56
ATP	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	13	17	33	0.36%	27.20%	VMIYQDEVKLPAK	3.22	1,549.83
ATP	6011	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	13	17	33	0.36%	27.20%	VPPFTFHVK	2.1	1,071.60
ATP	6011	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	6	7	10	0.11%	11.40%	FKDLGEEHFK	4.41	1,249.62
ATP	6011	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	6	7	10	0.11%	11.40%	HLVDEPQNLIK	2.68	1,305.72

ATP	6011	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	6	7	10	0.11%	11.40%	KQTALVELLK	3.01	1,142.71
ATP	6011	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	6	7	10	0.11%	11.40%	KVPQVSTPTLVEVSR	4.56	1,639.94
ATP	6011	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	6	7	10	0.11%	11.40%	LGEYGFQNALIVR	3.5	1,479.80
ATP	6011	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	6	7	10	0.11%	11.40%	LVNELTEFAK	3.52	1,163.63
ATP	6011	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	100.00%	4	7	11	0.12%	16.70%	KYMEENDLLKK	4.5	1,426.72
ATP	6011	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	100.00%	4	7	11	0.12%	16.70%	LQAAVDGPSDKKEE	2.26	1,486.74
ATP	6011	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	100.00%	4	7	11	0.12%	16.70%	VNLQNNPGAVEHFHMK	3.67	1,850.90
ATP	6011	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	100.00%	4	7	11	0.12%	16.70%	YMEENDLLKK	2.55	1,298.63
ATP	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	11	14	38	0.41%	46.80%	AQVSLLIR	2.45	899.5673
ATP	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	11	14	38	0.41%	46.80%	DLQMVNISLR	3.42	1,204.64

ATP	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	11	14	38	0.41%	46.80%	ESVFTVEGGHR	3.21	1,217.59
ATP	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	11	14	38	0.41%	46.80%	FNASQLITQR	3.97	1,177.63
ATP	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	11	14	38	0.41%	46.80%	IGGVQQDTILAEGLHFR	4.83	1,853.99
ATP	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	11	14	38	0.41%	46.80%	IPWFQYPIIYDIR	3.26	1,723.92
ATP	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	11	14	38	0.41%	46.80%	IVQAEGEAEAAR	4.05	1,243.63
ATP	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	11	14	38	0.41%	46.80%	IYLTADNLVLNLQDESFTR	6.12	2,225.15
ATP	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	11	14	38	0.41%	46.80%	LLLGAGAVAYGIR	3.45	1,273.76
ATP	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	11	14	38	0.41%	46.80%	VLPSIVNEVLK	2.99	1,210.74
ATP	6011	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	11	14	38	0.41%	46.80%	VLSRPNAMELPSMYQR	3.47	1,907.95
ATP	6011	TAP1 protein	gi|151557007	81,933.30	100.00%	4	5	6	0.07%	8.00%	GVVGAALGFR	3.1	946.5469
ATP	6011	TAP1 protein	gi|151557007	81,933.30	100.00%	4	5	6	0.07%	8.00%	IFEYLDR	2.26	955.4884
ATP	6011	TAP1 protein	gi|151557007	81,933.30	100.00%	4	5	6	0.07%	8.00%	SSQVAIEVLSAMPTVR	3.56	1,703.90
ATP	6011	TAP1 protein	gi|151557007	81,933.30	100.00%	4	5	6	0.07%	8.00%	STVAALLQNLYQPTEGQVLLDGEPLPK	4.58	2,894.55
ATP	6011	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	100.00%	3	4	5	0.05%	11.60%	AQYEEIAQR	2.63	1,107.54
ATP	6011	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	100.00%	3	4	5	0.05%	11.60%	FASFIDK	2.21	827.4298
ATP	6011	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	100.00%	3	4	5	0.05%	11.60%	FASFIDKVR	1.68	1,082.60

ATP	6011	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	100.00%	3	4	5	0.05%	11.60%	LALDVEIATYR	3.01	1,263.69
ATP	6011	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	100.00%	3	4	5	0.05%	11.60%	NKYEDEINKR	3.37	1,308.65
ATP	6011	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	100.00%	3	4	5	0.05%	11.60%	NLDLDSIIAEVK	4.82	1,329.73
ATP	6011	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	100.00%	3	4	5	0.05%	11.60%	QNLEPLFEQYINNLR	3.73	1,890.97
ATP	6011	MOSPD2 protein	gi|151556011,gi|155369632,gi|156120441	56,360.50	99.80%	2	2	2	0.02%	7.52%	EMAVNDLTEASIPR	2.74	1,561.75
ATP	6011	MOSPD2 protein	gi|151556011,gi|155369632,gi|156120441	56,360.50	99.80%	2	2	2	0.02%	7.52%	GPLLHISPAEELYFGSTDSGEKK	3.42	2,475.24
ATP	6011	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	10	12	14	0.15%	34.20%	AEDGSVIDYELIDQDAR	3.96	1,908.88

ATP	6011	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	10	12	14	0.15%	34.20%	GVDEVTIVNILTNR	3.77	1,542.85
ATP	6011	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	10	12	14	0.15%	34.20%	LSLEGDHSTPPSAYGSVK	5.6	1,844.90

ATP	6011	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	10	12	14	0.15%	34.20%	QDIAFAYQR	2.68	1,111.55
ATP	6011	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	10	12	14	0.15%	34.20%	RAEDGSVIDYELIDQDAR	4.94	2,064.98

ATP	6011	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	10	12	14	0.15%	34.20%	SALSGHLETVILGLLK	4.05	1,650.98
ATP	6011	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	10	12	14	0.15%	34.20%	SLYYYIQQDTK	3.32	1,421.69

<table>
<tr><td>ATP</td><td>6011</td><td>RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:</td><td>gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982</td><td>38,523.90</td><td>100.00%</td><td>10</td><td>12</td><td>14</td><td>0.15%</td><td>34.20%</td><td>SYSPYDMLESIKK</td><td>2.59</td><td>1,576.76</td></tr>
<tr><td>ATP</td><td>6011</td><td>RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:</td><td>gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982</td><td>38,523.90</td><td>100.00%</td><td>10</td><td>12</td><td>14</td><td>0.15%</td><td>34.20%</td><td>TDLEKDIVSDTSGDFR</td><td>2.64</td><td>1,797.85</td></tr>
</table>

ATP	6011	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	10	12	14	0.15%	34.20%	TDLEKDIVSDTSGDFRK	5.94	1,925.95
ATP	6011	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	4	5	6	0.07%	13.50%	ELIEVLQPLIAEHQAR	2.54	1,859.04
ATP	6011	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	4	5	6	0.07%	13.50%	GIDYDKLIVR	2.66	1,191.67

ATP	6011	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	4	5	6	0.07%	13.50%	ISFPAIQAAPSFSNSFPQIFR	4.17	2,325.20
ATP	6011	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	4	5	6	0.07%	13.50%	MSASDPNSSIFLTDTAK	4.2	1,800.83
ATP	6011	PREDICTED: similar to Transmembrane protein 16F	gi|119892265	106,290.10	99.80%	2	2	2	0.02%	4.28%	MNDFYIQDRDTFFNPATR	3.47	2,267.02
ATP	6011	PREDICTED: similar to Transmembrane protein 16F	gi|119892265	106,290.10	99.80%	2	2	2	0.02%	4.28%	TPEFEEFNGKPDSLYFNDGQR	4.13	2,490.12
ATP	6011	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	4	6	7	0.08%	16.90%	ALSSSLDDTEVKK	3.93	1,392.72
ATP	6011	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	4	6	7	0.08%	16.90%	FRGPFTDVVTTNLK	4.41	1,594.86
ATP	6011	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	4	6	7	0.08%	16.90%	GPFTDVVTTNLK	4.06	1,291.69
ATP	6011	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	4	6	7	0.08%	16.90%	VEQVLSLEPQHELK	5.24	1,648.89
ATP	6011	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	5	6	8	0.09%	16.30%	AQMVQEDLEKTR	2.99	1,463.72

ATP	6011	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	5	6	8	0.09%	16.30%	FYPEDVSEELIQDITQR	3.06	2,082.00
ATP	6011	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	5	6	8	0.09%	16.30%	TAMSTPHVAEPAENEQDEQDENGAEASAELR	6.91	3,342.43
ATP	6011	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	5	6	8	0.09%	16.30%	TQEQLALEMAELTAR	3.32	1,719.86
ATP	6011	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	5	6	8	0.09%	16.30%	VTTMDAELEFAIQPNTTGK	3.69	2,082.01
ATP	6011	unnamed protein product [Mus musculus]	gi|26331822	79,759.60	99.80%	2	2	2	0.02%	7.43%	KPMVVLGSSALQR	3.13	1,401.79
ATP	6011	unnamed protein product [Mus musculus]	gi|26331822	79,759.60	99.80%	2	2	2	0.02%	7.43%	NRLEEVSPNLVR	2.83	1,425.78
ATP	6011	unnamed protein product [Mus musculus]	gi|26331822	79,759.60	99.80%	2	2	2	0.02%	7.43%	PMVVLGSSALQRDDGAAILVAVSNMVQK	2.67	2,885.52
ATP	6011	unnamed protein product [Mus musculus]	gi|26331822	79,759.60	99.80%	2	2	2	0.02%	7.43%	VALIGSPVDLTYR	3.22	1,403.79
ATP	6011	PREDICTED: similar to Keratin, type I cytoskeletal 24 (Cytokeratin-24) (Keratin-24) (Type I keratin-24)	gi|194676109	55,111.70	100.00%	3	5	11	0.12%	5.52%	KVLDDLTMTR	2.6	1,191.64
ATP	6011	PREDICTED: similar to Keratin, type I cytoskeletal 24 (Cytokeratin-24) (Keratin-24) (Type I keratin-24)	gi|194676109	55,111.70	100.00%	3	5	11	0.12%	5.52%	SDLEMQIESLTEELAYLK	4.51	2,112.04

ATP	6011	PREDICTED: similar to Keratin, type I cytoskeletal 24 (Cytokeratin-24) (Keratin-24) (Type I keratin-24)	gi|194676109	55,111.70	100.00%	3	5	11	0.12%	5.52%	SDLEMQIESLTEELAYLKK	3.84	2,240.14
ATP	6011	H2A histone family, member Y	gi|114052404,gi|87578157	39,516.80	99.80%	2	3	5	0.05%	13.70%	AASADSTTEGTPADGFTVLSTK	4.67	2,127.01
ATP	6011	H2A histone family, member Y	gi|114052404,gi|87578157	39,516.80	99.80%	2	3	5	0.05%	13.70%	IGVGAPVYMAAVLEYLTAEILELAGNAAR	4.21	2,991.59
ATP	6011	PREDICTED: transmembrane protein 33 isoform 2	gi|119893815,gi|119922774	27,968.00	99.80%	2	2	2	0.02%	8.10%	ALLANALTSALR	4.03	1,213.73
ATP	6011	PREDICTED: transmembrane protein 33 isoform 2	gi|119893815,gi|119922774	27,968.00	99.80%	2	2	2	0.02%	8.10%	LPHFQLSR	2.24	997.5578
ATP	6011	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	7	14	0.15%	49.30%	DSLLQDGEFTMDLR	3.95	1,655.76
ATP	6011	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	7	14	0.15%	49.30%	SSFFVNGLTLGGQK	4.88	1,454.76

ATP	6011	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	7	14	0.15%	49.30%	STGGAPTFNITVTMTAK	4.46	1,712.85
ATP	6011	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	7	14	0.15%	49.30%	TFVNITPAEVGILVGK	4.9	1,657.95
ATP	6011	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	5	7	14	0.15%	49.30%	TLVLLMGK	2.38	890.5382
ATP	6011	Brain abundant, membrane attached signal protein 1	gi|115304757,gi|1930063,gi|27807507,gi|6686271	22,992.60	99.80%	2	2	4	0.04%	12.80%	AQAPAAPADEVKPAETPAANSDQTVAVK	3.49	2,747.38
ATP	6011	Brain abundant, membrane attached signal protein 1	gi|115304757,gi|1930063,gi|27807507,gi|6686271	22,992.60	99.80%	2	2	4	0.04%	12.80%	AQAPAAPADEVKPAETPAANSDQTVAVKE	3.1	2,876.43
ATP	6011	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	5	7	9	0.10%	25.60%	ALNLPSSGEGLAFFTFPNIASATK	4.29	2,453.27
ATP	6011	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	5	7	9	0.10%	25.60%	LVMASLYHIYVALEEEIER	4.47	2,294.17

ATP	6011	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	5	7	9	0.10%	25.60%	NKENPVYTPLYFPEELHR	6.44	2,246.12
ATP	6011	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	5	7	9	0.10%	25.60%	YLGDLSGGQVLK	3.41	1,249.68
ATP	6011	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	5	7	9	0.10%	25.60%	YLGDLSGGQVLKK	3.29	1,377.77
ATP	6011	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	100.00%	5	6	8	0.09%	25.90%	ALADYIR	1.85	821.4516
ATP	6011	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	100.00%	5	6	8	0.09%	25.90%	FSQMLHPIFEEASNVIKEEYPNANQVVFAR	4.12	3,523.73
ATP	6011	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	100.00%	5	6	8	0.09%	25.90%	HMYVFGDFRDVLIPGK	2.43	1,909.96
ATP	6011	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	100.00%	5	6	8	0.09%	25.90%	LHREFHHGPDPTDTAPGEEVQDVASSPPESSFQK	2.21	3,728.72
ATP	6011	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	100.00%	5	6	8	0.09%	25.90%	SDPIQELHDLAEITPDR	5.17	2,050.01

ATP	6011	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32, gi|59857977	33,881.70	99.80%	2	2	2	0.02%	7.72%	AVVVNAAQLASYSQSK	3.57	1,635.87
ATP	6011	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32, gi|59857977	33,881.70	99.80%	2	2	2	0.02%	7.72%	NVFNALFR	2.39	980.5311
ATP	6011	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	3	3	4	0.04%	10.70%	ISEIEDAAFLAR	3.98	1,334.70
ATP	6011	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	3	3	4	0.04%	10.70%	SVQTTLQTDEVK	3.12	1,348.70
ATP	6011	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	3	3	4	0.04%	10.70%	VAQVAEITFGQK	2.87	1,290.71
ATP	6011	GLI pathogenesis-related 2	gi|111307081,gi|115497826	17,191.20	100.00%	3	3	3	0.03%	31.20%	ASASDGSSFVVAR	4.43	1,253.61
ATP	6011	GLI pathogenesis-related 2	gi|111307081,gi|115497826	17,191.20	100.00%	3	3	3	0.03%	31.20%	EAQQYSEALASTR	2.85	1,453.69
ATP	6011	GLI pathogenesis-related 2	gi|111307081,gi|115497826	17,191.20	100.00%	3	3	3	0.03%	31.20%	YFPAGNVVNQGFFEENVLPKK	1.69	2,494.28
ATP	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	9	10	0.11%	16.40%	ITVLEALR	2.8	914.567
ATP	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	9	10	0.11%	16.40%	LKEYEAAVEQLKGDQIR	4.67	1,990.06

ATP	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	9	10	0.11%	16.40%	LLSKPQDALEGVVLSPSLEAR	4.52	2,222.24
ATP	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	9	10	0.11%	16.40%	MYFDKYVLKPATEGK	2.82	1,805.91
ATP	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	9	10	0.11%	16.40%	NVLMYGPPGTGK	3.33	1,249.62
ATP	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	9	10	0.11%	16.40%	QQQLLNEENLR	2.3	1,384.72
ATP	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	9	10	0.11%	16.40%	RLLSKPQDALEGVVLSPSLEAR	2.73	2,378.34
ATP	6011	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	9	10	0.11%	16.40%	TAGTLFGEGFR	3.3	1,155.58
ATP	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	8	10	13	0.14%	11.90%	DISTNYYASQK	2.64	1,289.60
ATP	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	8	10	13	0.14%	11.90%	ELISNASDALDKIR	3.6	1,544.83
ATP	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	8	10	13	0.14%	11.90%	FQSSHHPSDMTSLDQYVER	5.17	2,280.00
ATP	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	8	10	13	0.14%	11.90%	GVVDSDDLPLNVSR	4.99	1,485.75
ATP	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	8	10	13	0.14%	11.90%	LIINSLYK	2.73	963.5874
ATP	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	8	10	13	0.14%	11.90%	NLLHVTDTGVGMTR	4.18	1,529.77
ATP	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	8	10	13	0.14%	11.90%	NLLHVTDTGVGMTREELVK	3.35	2,128.11

ATP	6011	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	8	10	13	0.14%	11.90%	SILFVPTSAPR	3.07	1,187.68
ATP	6011	PREDICTED: similar to FXYD domain-containing ion transport regulator 5 isoform 1	gi|76641186	18,921.80	99.80%	2	2	2	0.02%	10.40%	EDDPFFYDEDTLR	3.54	1,661.70
ATP	6011	PREDICTED: similar to FXYD domain-containing ion transport regulator 5 isoform 1	gi|76641186	18,921.80	99.80%	2	2	2	0.02%	10.40%	QPGSKEDDPFFYDEDTLR	3.22	2,158.96
ATP	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	8	9	11	0.12%	9.90%	ALSAIADLLTNEHER	3.45	1,652.86
ATP	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	8	9	11	0.12%	9.90%	APSRQDVYGPQPQVR	4.39	1,697.87
ATP	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	8	9	11	0.12%	9.90%	FVGDADLER	2.65	1,021.50
ATP	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	8	9	11	0.12%	9.90%	KPTEDPTNDTVDFPKR	4.75	1,859.91
ATP	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	8	9	11	0.12%	9.90%	NFHYPPDGYSR	2.26	1,352.60
ATP	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	8	9	11	0.12%	9.90%	QDVYGPQPQVR	2.68	1,286.65
ATP	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	8	9	11	0.12%	9.90%	SLDNNYSTLNER	2.86	1,425.66
ATP	6011	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	8	9	11	0.12%	9.90%	VSPQDASPLLANGTLTR	3.73	1,739.93

ATP	6011	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	5	6	11	0.12%	15.30%	DPLVIELGQK	3.37	1,111.64
ATP	6011	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	5	6	11	0.12%	15.30%	IFDTSLTRDPLVIELGQK	5.09	2,045.13
ATP	6011	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	5	6	11	0.12%	15.30%	RVIIPSHLAYGK	4.87	1,353.80
ATP	6011	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	5	6	11	0.12%	15.30%	VIIPSHLAYGK	3.02	1,197.70
ATP	6011	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	5	6	11	0.12%	15.30%	VIIPSHLAYGKR	2.15	1,353.80
ATP	6011	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	3	3	3	0.03%	10.90%	EEQKDFVSLYQDFENFYTR	4.09	2,458.12
ATP	6011	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	3	3	3	0.03%	10.90%	NIGVVVVGFPATPIIESR	4.47	1,868.06
ATP	6011	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	3	3	3	0.03%	10.90%	SSAAAAAAAAGQIHHVTENGGLYK	3.75	2,295.15
ATP	6011	ribosomal protein S15-like	gi|58760350,gi|66792868,gi|74353853,gi|75060401	17,008.80	99.80%	2	2	2	0.02%	33.80%	GVDLDQLLDMSYEQLMQLYSAR	3.1	2,604.23
ATP	6011	ribosomal protein S15-like	gi|58760350,gi|66792868,gi|74353853,gi|75060401	17,008.80	99.80%	2	2	2	0.02%	33.80%	TFNQVEIKPEMIGHYLGEFSITYKPVK	2.44	3,184.64
ATP	6011	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	4	4	4	0.04%	8.99%	DKLNPQSTYSEA	3.44	1,352.63
ATP	6011	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	4	4	4	0.04%	8.99%	IESPGYLTSPGYPHSYHPSEKCEWLIQAPDPYQR	1.74	3,945.85
ATP	6011	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	4	4	4	0.04%	8.99%	SFEGNNNYDTPELR	3.39	1,655.73

ATP	6011	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	4	4	4	0.04%	8.99%	TGPIQDHTGDGNFIYSQADENQK	5.15	2,535.14
ATP	6011	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	99.80%	2	2	3	0.03%	4.26%	LFEAEAQDLFR	3.4	1,338.67
ATP	6011	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	99.80%	2	2	3	0.03%	4.26%	LIEAVDNMLTNK	3.76	1,376.71
ATP	6011	RPS7 protein	gi|148877374,gi|149642623,gi|205806695	22,109.50	100.00%	3	3	4	0.04%	23.70%	DVNFEFPEFQL	3.27	1,384.64
ATP	6011	RPS7 protein	gi|148877374,gi|149642623,gi|205806695	22,109.50	100.00%	3	3	4	0.04%	23.70%	KAIIIFVPVPQLK	3.97	1,465.95
ATP	6011	RPS7 protein	gi|148877374,gi|149642623,gi|205806695	22,109.50	100.00%	3	3	4	0.04%	23.70%	TLTAVHDAILEDLVFPSEIVGK	3.24	2,367.28
ATP	6011	RRAS2 protein	gi|148743916,gi|149944707	23,381.60	99.80%	2	3	3	0.03%	13.70%	LDILDTAGQEEFGAMR	4.17	1,781.84
ATP	6011	RRAS2 protein	gi|148743916,gi|149944707	23,381.60	99.80%	2	3	3	0.03%	13.70%	MNVDQAFHELVR	2.97	1,474.71
ATP	6011	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	gi|59858119,gi|60650208,gi|60650268,gi|61889066,gi|75070049,gi|88954151	42,933.90	99.80%	2	2	2	0.02%	10.70%	FTRPIIAGMEFSR	5.08	1,540.79
ATP	6011	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	gi|59858119,gi|60650208,gi|60650268,gi|61889066,gi|75070049,gi|88954151	42,933.90	99.80%	2	2	2	0.02%	10.70%	SDNSSHPQKDDGDNPETIMSSGNVNSSS	4.32	2,922.19
ATP	6011	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	3	3	5	0.05%	8.01%	SISHYHETLGEALQGVELEFSGLDIK	4.46	2,872.44
ATP	6011	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	3	3	5	0.05%	8.01%	VNAVPRPIPEK	2.04	1,219.72

ATP	6011	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	3	3	5	0.05%	8.01%	YLDPSFFQHR	1.63	1,309.63
ATP	6011	PREDICTED: similar to Transmembrane emp24 domain-containing protein 2 precursor (Membrane protein p24A)	gi|194674620	22,715.40	99.80%	2	3	8	0.09%	12.40%	IVMFTIDIGEAPK	4.02	1,449.77
ATP	6011	PREDICTED: similar to Transmembrane emp24 domain-containing protein 2 precursor (Membrane protein p24A)	gi|194674620	22,715.40	99.80%	2	3	8	0.09%	12.40%	YTFAAHMDGTYK	3.42	1,420.62
ATP	6011	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	6	8	11	0.12%	7.91%	EATSTFTNITYR	3.63	1,403.68
ATP	6011	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	6	8	11	0.12%	7.91%	GTGDSSQITQVSPQR	3.71	1,560.76
ATP	6011	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	6	8	11	0.12%	7.91%	HVLTLTDQVTR	3.71	1,282.71

ATP	6011	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	6	8	11	0.12%	7.91%	ILEARPLSDKGTGDSSQITQVSPQR	6.42	2,683.40
ATP	6011	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	6	8	11	0.12%	7.91%	NDASHLLVFTTDAK	4.54	1,531.78
ATP	6011	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	6	8	11	0.12%	7.91%	PLSDKGTGDSSQITQVSPQR	5.38	2,101.05
ATP	6011	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	7	7	10	0.11%	15.50%	ADLVNNLGTIAK	3.54	1,228.69
ATP	6011	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	7	7	10	0.11%	15.50%	ELISNASDALDKIR	3.6	1,544.83
ATP	6011	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	7	7	10	0.11%	15.50%	GVVDSEDLPLNISR	4.86	1,513.79
ATP	6011	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	7	7	10	0.11%	15.50%	HLEINPDHPIVETLR	4.35	1,782.95
ATP	6011	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	7	7	10	0.11%	15.50%	HSQFIGYPITLYLEK	3.37	1,808.96
ATP	6011	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	7	7	10	0.11%	15.50%	NPDDITQEEYGEFYK	3.55	1,847.80
ATP	6011	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	7	7	10	0.11%	15.50%	TLTLVDTGIGMTK	4.55	1,365.73
ATP	6011	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	7	7	10	0.11%	15.50%	YESLTDPSKLDSGK	2.97	1,539.75

ATP	6011	Solute carrier family 1 (neutral amino acid transporter), member 5	gi|115305216,gi|15145909,gi|21541958,gi|27807087	56,431.20	99.80%	2	2	2	0.02%	4.45%	EVLDSFLDLVR	3.2	1,305.71
ATP	6011	Solute carrier family 1 (neutral amino acid transporter), member 5	gi|115305216,gi|15145909,gi|21541958,gi|27807087	56,431.20	99.80%	2	2	2	0.02%	4.45%	NIFPSNLVSAAFR	1.96	1,435.77
ATP	6011	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	3	3	4	0.04%	9.15%	ALDLFSDNAPPPELLEIINEDVAK	3.53	2,623.35
ATP	6011	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	3	3	4	0.04%	9.15%	GSFSEQGINEFLR	3.94	1,483.72
ATP	6011	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	3	3	4	0.04%	9.15%	GSTAPVGGGAFPTISTR	4.62	1,575.81
ATP	6011	Deoxyribonuclease I-like 1	gi|151553571	35,175.30	99.80%	2	3	3	0.03%	8.86%	IVLHGEHLQSLLR	2.06	1,514.88
ATP	6011	Deoxyribonuclease I-like 1	gi|151553571	35,175.30	99.80%	2	3	3	0.03%	8.86%	VLPSLVLVPLHTTPK	3.87	1,614.00
ATP	6018	TIMM23 protein	gi|134025149,gi|139947578,gi|215274655	21,809.90	99.80%	2	2	2	0.02%	27.80%	TTGGLAGFFGAGGAGYSHADLAGVPLTGMNPLSPYLNVDPR	4.3	4,034.97
ATP	6018	TIMM23 protein	gi|134025149,gi|139947578,gi|215274655	21,809.90	99.80%	2	2	2	0.02%	27.80%	YLVQDTDEFILPTGANK	2.57	1,923.97

ATP	6018	TMEM115 protein	gi|133777923,gi|134085844,gi|146186960,gi|218551717	38,121.60	99.80%	2	2	3	0.03%	6.84%	RYDVGAPSSITISLPGTDPQDAER	3.92	2,545.25
ATP	6018	TMEM115 protein	gi|133777923,gi|134085844,gi|146186960,gi|218551717	38,121.60	99.80%	2	2	3	0.03%	6.84%	YDVGAPSSITISLPGTDPQDAER	4.14	2,389.15
ATP	6018	similar to translationally controlled tumor protein	gi|28189813,gi|59858437,gi|62177164,gi|62901141,gi|74356483	19,564.00	99.80%	2	3	3	0.03%	15.70%	DLISHDEMFSDIYK	2.67	1,728.78
ATP	6018	similar to translationally controlled tumor protein	gi|28189813,gi|59858437,gi|62177164,gi|62901141,gi|74356483	19,564.00	99.80%	2	3	3	0.03%	15.70%	VKPFMTGAAEQIK	2.68	1,435.76
ATP	6018	Chain B, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591027,gi|110591030,gi|114686,gi|27807305,gi|599873,gi|74356487	18,544.10	99.80%	2	3	4	0.03%	19.40%	IQEYEKELEK	3.44	1,308.67
ATP	6018	Chain B, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591027,gi|110591030,gi|114686,gi|27807305,gi|599873,gi|74356487	18,544.10	99.80%	2	3	4	0.03%	19.40%	NIIPFDQMTIEDLNEVFPETK	3.01	2,509.22
ATP	6018	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	10	18	0.15%	13.20%	AQILLDCGEDNICVPDLQLEVFGEQNHVYLGDK	3.79	3,687.77
ATP	6018	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	10	18	0.15%	13.20%	DLDGNGYPDLIVGSFGVDK	4.19	1,980.96

ATP	6018	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	10	18	0.15%	13.20%	LAGMEPTPTLTLTGQDEFGR	6.06	2,150.04
ATP	6018	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	10	18	0.15%	13.20%	QASSIYDDSYLGYSVAVGEFSGDDREDFVAGVPK	3.07	3,643.67
ATP	6018	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	10	18	0.15%	13.20%	QATLTQTLLIQNGAR	4.27	1,627.91
ATP	6018	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	10	18	0.15%	13.20%	TIQFDFQILSK	3.62	1,339.73
ATP	6018	PREDICTED: integrin, alpha 5 (fibronectin receptor, alpha polypeptide) isoform 3	gi|194667041	119,589.00	100.00%	7	10	18	0.15%	13.20%	VTAPPEAEYSGLVR	2.96	1,488.77
ATP	6018	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	3	5	11	0.09%	19.70%	ASFTTFTVTK	2.48	1,102.58
ATP	6018	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	3	5	11	0.09%	19.70%	YVDSEGHLYTVPIR	4.78	1,648.83

ATP	6018	caveolin-1	gi|1840144,gi|2493547,gi|27806715,gi|38322701,gi|56181138	20,577.50	100.00%	3	5	11	0.09%	19.70%	YVDSEGHLYTVPIREQGNIYKPNNK	4.84	2,934.47
ATP	6018	RTN3 protein	gi|115305093,gi|122132179,gi|146231798,gi|151554368,gi|32880223,gi|38327594	25,478.60	99.80%	2	4	4	0.03%	5.49%	TQIDHYVGIAR	2.22	1,272.67
ATP	6018	RTN3 protein	gi|115305093,gi|122132179,gi|146231798,gi|151554368,gi|32880223,gi|38327594	25,478.60	99.80%	2	4	4	0.03%	5.49%	YKTQIDHYVGIAR	2.69	1,563.83
ATP	6018	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	5	7	11	0.09%	20.30%	DNFHGLAIFLDTYPNDETTER	4.2	2,468.14
ATP	6018	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	5	7	11	0.09%	20.30%	DNVDDPTGNFR	3.22	1,249.54
ATP	6018	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	5	7	11	0.09%	20.30%	DRLVPGPVFGSK	1.97	1,271.71
ATP	6018	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	5	7	11	0.09%	20.30%	LPTGYYFGASAGTGDLSDNHDIISMK	5.24	2,746.27
ATP	6018	LMAN2 protein	gi|151553875,gi|155372333	40,385.10	100.00%	5	7	11	0.09%	20.30%	SPKDNVDDPTGNFR	4.16	1,561.72
ATP	6018	LOC789567 protein	gi|148878411,gi|155372329	34,911.10	99.80%	2	3	3	0.03%	4.81%	SQDKLNQVSSEIR	4.33	1,503.78
ATP	6018	LOC789567 protein	gi|148878411,gi|155372329	34,911.10	99.80%	2	3	3	0.03%	4.81%	SQDKLNQVSSEIREK	3.27	1,760.91

ATP	6018	PREDICTED: similar to Splicing factor, proline- and glutamine-rich (Polypyrimidine tract-binding protein-associated-splicing factor) (PTB-associated-splicing factor) (PSF) (DNA-binding p52/p100 complex,	gi|194665922	76,230.60	99.80%	2	2	2	0.02%	3.96%	FATHAAALSVR	3.57	1,143.63
ATP	6018	PREDICTED: similar to Splicing factor, proline- and glutamine-rich (Polypyrimidine tract-binding protein-associated-splicing factor) (PTB-associated-splicing factor) (PSF) (DNA-binding p52/p100 complex,	gi|194665922	76,230.60	99.80%	2	2	2	0.02%	3.96%	LFVGNLPADITEDEFKR	2.49	1,964.01
ATP	6018	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	3	3	4	0.03%	8.41%	EIILVDDYSNDPEDGALLGK	3.83	2,176.07
ATP	6018	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	3	3	4	0.03%	8.41%	NKFNQVESDKLR	2.91	1,477.78

ATP	6018	PREDICTED: similar to polypeptide N-acetylgalactosaminyltransferase 2	gi|119918373	64,740.20	100.00%	3	3	4	0.03%	8.41%	QHPYTFPGGSGTVFAR	3.88	1,721.84
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	ADIGVAMGIAGSDVSK	4.61	1,506.75
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	AVAGDASESALLK	4.11	1,231.65
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	AVFQANQDNLPILK	4.18	1,570.86
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	AVFQANQDNLPILKR	3.9	1,726.96
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	DKYEPAAVSEHGDK	4.47	1,545.72
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	DMTPEQLDDILK	2.3	1,417.69
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	EQPLDEELKDAFQNAYLELGGLGER	3.83	2,834.38
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	GGDRIPADLR	2.47	1,069.58

ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	GVGIISEGNETVEDIAAR	5.29	1,829.92
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	IVEIPFNSTNK	2.6	1,261.68
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	KADIGVAMGIAGSDVSK	6.11	1,634.84
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	LNIPVSQVNPR	3.39	1,236.71
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	LSLDELHR	2.62	982.5317
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	MSINAEEVVVGDLVEVK	3.27	1,846.95
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	NMVPQQALVIR	3.86	1,284.71
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	QAADMILLDDNFASIVTGVEEGR	3.81	2,480.20
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	QGAIVAVTGDGVNDSPALK	4.17	1,811.95
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	QGAIVAVTGDGVNDSPALKK	3.2	1,940.05

ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	SPDFTNENPLETR	4.48	1,519.70
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	VDNSSLTGESEPQTR	4.18	1,619.75
ATP	6018	ATPase, Na+/K+ transporting, alpha 1 polypeptide	gi|115305284,gi|116003819,gi|122132194	112,627.60	100.00%	21	31	65	0.56%	26.00%	VIMVTGDHPITAK	4.08	1,397.75
ATP	6018	PTPLAD1 protein	gi|154425645,gi|157074148,gi|166199295	43,116.60	99.80%	2	3	4	0.03%	8.56%	FSFTLPYPVK	2.18	1,198.65
ATP	6018	PTPLAD1 protein	gi|154425645,gi|157074148,gi|166199295	43,116.60	99.80%	2	3	4	0.03%	8.56%	VELSDVQNPAISITENVLHFK	3.65	2,353.24
ATP	6018	COL18A1 protein	gi|133778103,gi|134085613,gi|157742960	135,049.70	100.00%	2	2	2	0.02%	2.33%	LFVAQAGGADPEKFQGLISELR	5.74	2,346.25
ATP	6018	COL18A1 protein	gi|133778103,gi|134085613,gi|157742960	135,049.70	100.00%	2	2	2	0.02%	2.33%	LQDLYSIVR	2.96	1,106.62
ATP	6018	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	3	4	4	0.03%	27.30%	AFDLLVDRPVTLVR	2.06	1,613.94
ATP	6018	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	3	4	4	0.03%	27.30%	DYKVDQEIVNIIQER	4.21	1,861.97
ATP	6018	NADH dehydrogenase	gi|256,gi|28461255,gi|400533,gi|73587329	20,946.90	100.00%	3	4	4	0.03%	27.30%	TPAPSPQTSLPNPITYLTK	4.29	2,026.09
ATP	6018	ribosomal protein L18	gi|59858459,gi|62752012,gi|75060915,gi|75775560,gi|89573893	21,518.10	100.00%	3	3	7	0.06%	18.10%	ILTFDQLALDSPK	4.11	1,460.80
ATP	6018	ribosomal protein L18	gi|59858459,gi|62752012,gi|75060915,gi|75775560,gi|89573893	21,518.10	100.00%	3	3	7	0.06%	18.10%	TNRPPLSLSR	3.38	1,140.65
ATP	6018	ribosomal protein L18	gi|59858459,gi|62752012,gi|75060915,gi|75775560,gi|89573893	21,518.10	100.00%	3	3	7	0.06%	18.10%	TNSTFNQVVLK	2.95	1,250.67

ATP	6018	RecName: Full=Isocitrate dehydrogenase [NADP], mitochondrial; Short=IDH; AltName: Full=Oxalosuccinate decarboxylase; AltName: Full=NADP(+)-specific ICDH; AltName: Full=IDP; AltName:	gi|109891934,gi|28461205,gi|430,gi|73587323	50,807.00	100.00%	3	4	4	0.03%	8.85%	LIDDMVAQVLK	3.48	1,260.69
ATP	6018	RecName: Full=Isocitrate dehydrogenase [NADP], mitochondrial; Short=IDH; AltName: Full=Oxalosuccinate decarboxylase; AltName: Full=NADP(+)-specific ICDH; AltName: Full=IDP; AltName:	gi|109891934,gi|28461205,gi|430,gi|73587323	50,807.00	100.00%	3	4	4	0.03%	8.85%	LNEHFLNTSDFLDTIK	4.42	1,906.95

ATP	6018	RecName: Full=Isocitrate dehydrogenase [NADP], mitochondrial; Short=IDH; AltName: Full=Oxalosuccinate decarboxylase; AltName: Full=NADP(+)-specific ICDH; AltName: Full=IDP; AltName:	gi|109891934,gi|28461205,gi|430,gi|73587323	50,807.00	100.00%	3	4	4	0.03%	8.85%	TIEAEAAHGTVTR	4.2	1,355.69
ATP	6018	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	8	14	23	0.20%	16.20%	AFEESLSTLK	2.76	1,124.58
ATP	6018	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	8	14	23	0.20%	16.20%	ELDKVFNDYTAVPDLYFENAMR	5.28	2,666.24
ATP	6018	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	8	14	23	0.20%	16.20%	HTLGENIADNGGLK	4.15	1,438.73
ATP	6018	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	8	14	23	0.20%	16.20%	NEIVFPAGILQAPFYTR	4.99	1,936.03

ATP	6018	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	8	14	23	0.20%	16.20%	SSPNALNFGGIGVVVGHELTHAFDDQGR	3.2	2,894.42
ATP	6018	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	8	14	23	0.20%	16.20%	TPESSHEGLITDPHSPSR	4.63	1,946.92
ATP	6018	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	8	14	23	0.20%	16.20%	VFNDYTAVPDLYFENAMR	2.96	2,181.00
ATP	6018	endothelin-converting enzyme	gi|1092971,gi|124829188,gi|190359620,gi|2299388,gi|2299395,gi|30794312,gi|535075,gi|688290,gi|897602	85,603.70	100.00%	8	14	23	0.20%	16.20%	VLTGYLNYMVQLGK	3.88	1,614.86
ATP	6018	RecName: Full=60S ribosomal protein L5	gi|108862056,gi|119900687,gi|119905361,gi|61552973,gi|75775327,gi|78369655	34,327.50	99.80%	2	3	3	0.03%	8.75%	GAVDGGLSIPHSTK	4.56	1,338.70
ATP	6018	RecName: Full=60S ribosomal protein L5	gi|108862056,gi|119900687,gi|119905361,gi|61552973,gi|75775327,gi|78369655	34,327.50	99.80%	2	3	3	0.03%	8.75%	YLIEEDEDAYKK	2.77	1,515.72
ATP	6018	hydroxyacyl-Coenzyme A dehydrogenase	gi|114052468,gi|194678883,gi|86821535	34,251.40	99.80%	2	2	2	0.02%	7.67%	FAGLHFFNPVPLMK	3.08	1,633.86
ATP	6018	hydroxyacyl-Coenzyme A dehydrogenase	gi|114052468,gi|194678883,gi|86821535	34,251.40	99.80%	2	2	2	0.02%	7.67%	TFESLLDFSR	2.9	1,214.61

ATP	6018	secretory carrier membrane protein 3 isoform 1	gi|61553277,gi|71649517,gi|73586519,gi|78369651	38,348.80	99.80%	2	2	2	0.02%	9.22%	AQQEFAAGVFSNPAVR	2.98	1,691.85
ATP	6018	secretory carrier membrane protein 3 isoform 1	gi|61553277,gi|71649517,gi|73586519,gi|78369651	38,348.80	99.80%	2	2	2	0.02%	9.22%	TAAANAAAGAAENAFR	4.5	1,476.72
ATP	6018	ANO10 protein	gi|154425799,gi|156120985	76,294.20	99.70%	2	2	2	0.02%	3.79%	ETLENQNLYLVGASK	3.34	1,678.86
ATP	6018	ANO10 protein	gi|154425799,gi|156120985	76,294.20	99.70%	2	2	2	0.02%	3.79%	LEFESLEALK	2.38	1,178.63
ATP	6018	PREDICTED: similar to mannose receptor, C type 2	gi|119912531	166,060.80	99.80%	2	2	2	0.02%	1.83%	GTDVREPDVSPQGR	3.44	1,512.74
ATP	6018	PREDICTED: similar to mannose receptor, C type 2	gi|119912531	166,060.80	99.80%	2	2	2	0.02%	1.83%	TLGDQLSLLLGGR	3.33	1,342.77
ATP	6018	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	4	6	9	0.08%	17.70%	LATMLETLR	2.69	1,063.58
ATP	6018	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	4	6	9	0.08%	17.70%	LEANHGLLVAR	3.11	1,192.68
ATP	6018	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	4	6	9	0.08%	17.70%	RIQSNLGALSR	3.24	1,214.70
ATP	6018	PRKCDBP protein	gi|133778193,gi|134085797,gi|187611336	27,468.60	100.00%	4	6	9	0.08%	17.70%	SHDTTSNTLAQLLAK	5.99	1,599.83
ATP	6018	SCAMP2 protein	gi|151554759,gi|156120987	36,685.40	99.80%	2	2	2	0.02%	9.76%	ELQNTVANLHVR	2.08	1,393.75
ATP	6018	SCAMP2 protein	gi|151554759,gi|156120987	36,685.40	99.80%	2	2	2	0.02%	9.76%	TGASFQQAQEEFSQGIFSSR	4.2	2,205.02
ATP	6018	vacuolar system associated protein-60	gi|1215746,gi|152941134,gi|2493459,gi|33340013,gi|41386727,gi|74356454	60,133.40	99.80%	2	3	5	0.04%	4.50%	SLEDQVEVLR	3.63	1,187.63
ATP	6018	vacuolar system associated protein-60	gi|1215746,gi|152941134,gi|2493459,gi|33340013,gi|41386727,gi|74356454	60,133.40	99.80%	2	3	5	0.04%	4.50%	TLKEEAEKPEEAAK	2.45	1,572.81

ATP	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	16	147	1.26%	56.30%	DAVTYTEHAK	2.97	1,134.54
ATP	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	16	147	1.26%	56.30%	DNIQGITKPAIR	2.84	1,325.75
ATP	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	16	147	1.26%	56.30%	DNIQGITKPAIRR	2.71	1,481.85
ATP	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	16	147	1.26%	56.30%	ISGLIYEETR	4.16	1,180.62
ATP	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	16	147	1.26%	56.30%	KTVTAMDVVYALK	5.03	1,454.79
ATP	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	16	147	1.26%	56.30%	KTVTAMDVVYALKR	4.35	1,610.89
ATP	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	16	147	1.26%	56.30%	TVTAMDVVYALK	4.4	1,310.70

ATP	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	16	147	1.26%	56.30%	TVTAMDVVYALKR	3.51	1,482.80
ATP	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	16	147	1.26%	56.30%	VFLENVIR	3.24	989.5778
ATP	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	16	147	1.26%	56.30%	VFLENVIRDAVTYTEHAK	4.61	2,105.10
ATP	6018	PREDICTED: similar to Histone H4 replacement CG3379-PC	gi|119915709,gi|119915719,gi|119915738,gi|76613952,gi|76616306,gi|76631252,gi|76631262,gi|76631717	11,349.70	100.00%	11	16	147	1.26%	56.30%	VLRDNIQGITKPAIR	3.87	1,694.01
ATP	6018	RecName: Full=Cleft lip and palate transmembrane protein 1 homolog	gi|110278913,gi|114051439,gi|84708720	75,864.60	100.00%	3	5	5	0.04%	4.63%	ALNTFIDDLFAFVIK	4.4	1,726.94
ATP	6018	RecName: Full=Cleft lip and palate transmembrane protein 1 homolog	gi|110278913,gi|114051439,gi|84708720	75,864.60	100.00%	3	5	5	0.04%	4.63%	NLLTGETEADPEMIK	4.61	1,676.81
ATP	6018	RecName: Full=Cleft lip and palate transmembrane protein 1 homolog	gi|110278913,gi|114051439,gi|84708720	75,864.60	100.00%	3	5	5	0.04%	4.63%	NLLTGETEADPEMIKR	3.04	1,832.91

ATP	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	14	16	23	0.20%	28.00%	AVDEAADALLK	2.97	1,115.59
ATP	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	14	16	23	0.20%	28.00%	ELDSITPEVLPGWK	3.76	1,583.83
ATP	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	14	16	23	0.20%	28.00%	KVEEVRDAMENEMR	2.06	1,751.81
ATP	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	14	16	23	0.20%	28.00%	LAEQELQFR	2.69	1,133.60
ATP	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	14	16	23	0.20%	28.00%	MKTASADLPTVPLGSAVEAIR	3.7	2,143.14
ATP	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	14	16	23	0.20%	28.00%	QHIALALEK	4.19	1,022.60
ATP	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	14	16	23	0.20%	28.00%	QKGDTSASTTAGDTLSVPAPVVQHEELIK	2.36	2,979.53
ATP	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	14	16	23	0.20%	28.00%	SEIQAEQDRKVEEVR	2.38	1,815.92
ATP	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	14	16	23	0.20%	28.00%	SVIENAKKEEVAGAK	2.63	1,572.86
ATP	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	14	16	23	0.20%	28.00%	TASADLPTVPLGSAVEAIR	4.49	1,868.01
ATP	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	14	16	23	0.20%	28.00%	TDHPETGEGKPKPATSEEASSTSVR	4.66	2,598.23
ATP	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	14	16	23	0.20%	28.00%	TIPYSDKLFEMVLGSPPYTVPLPK	2.94	2,708.43
ATP	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	14	16	23	0.20%	28.00%	VQEQELKYEFEQDLSEKLAEQELQFR	2.93	3,256.60
ATP	6018	inner membrane protein, mitochondrial	gi|152941206	83,035.60	100.00%	14	16	23	0.20%	28.00%	VVSQYHELVVQAR	4.27	1,527.83

ATP	6018	SCARB2 protein	gi|151556135,gi|156120953	53,968.70	100.00%	3	3	3	0.03%	10.30%	GQGSTDEGTADERAPLIR	2.13	1,872.90
ATP	6018	SCARB2 protein	gi|151556135,gi|156120953	53,968.70	100.00%	3	3	3	0.03%	10.30%	HDVSPYFGLFYGK	3.18	1,529.74
ATP	6018	SCARB2 protein	gi|151556135,gi|156120953	53,968.70	100.00%	3	3	3	0.03%	10.30%	NGAPIIMSFPHFYQADEK	3.14	2,080.98
ATP	6018	Endoplasmic reticulum protein 29	gi|109658363,gi|115495555,gi|143811387	28,789.90	100.00%	3	3	3	0.03%	14.30%	GALPLDTITFYK	2.63	1,338.73
ATP	6018	Endoplasmic reticulum protein 29	gi|109658363,gi|115495555,gi|143811387	28,789.90	100.00%	3	3	3	0.03%	14.30%	ILDQGEDFPASEMTR	4.04	1,724.78
ATP	6018	Endoplasmic reticulum protein 29	gi|109658363,gi|115495555,gi|143811387	28,789.90	100.00%	3	3	3	0.03%	14.30%	SLNILTAFQK	3.13	1,134.65
ATP	6018	ATAD1 protein	gi|154426126,gi|76671592	41,750.40	99.80%	2	3	4	0.03%	11.40%	EYVNSTSEESHDEDEIRPVQQQDLHR	4.39	3,140.42
ATP	6018	ATAD1 protein	gi|154426126,gi|76671592	41,750.40	99.80%	2	3	4	0.03%	11.40%	LQPSIIFIDEIDSFLR	3.22	1,906.03
ATP	6018	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	3	5	6	0.05%	13.50%	GLFTGLTPR	2.4	961.5467
ATP	6018	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	3	5	6	0.05%	13.50%	SAATLITHPFHVITLR	3.65	1,777.01
ATP	6018	Mitochondrial carrier homolog 2 (C. elegans)	gi|151554706,gi|28603744,gi|59858227,gi|67461083,gi|7959093	33,276.60	100.00%	3	5	6	0.05%	13.50%	VLIQVGYEPLAPTVGR	4.48	1,711.97
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	AAALRPEEDGAFRPSEAFETLQK	3.3	2,533.27
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	AEESAAHLPEEIR	3.88	1,451.71

ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	AEESAAHLPEEIRR	2.64	1,607.81
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	ASVGQVESDLK	3.55	1,132.58
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	DLSDGIHVVK	2.89	1,082.58
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	EAADSEHHTLQALTEK	4.4	1,779.85
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	EELGQGLQGVEQK	3.31	1,414.72
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	ELVSLKQEQQR	3.1	1,357.74
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	ERDFTSLENTVEER	4.11	1,724.81
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	EVVKEIQTSVK	3.04	1,259.72

ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	FKEAADSEHHTLQALTEK	3.66	2,055.01
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	GLGEAQLSLAGDVDELK	5.25	1,714.89
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	GLGEAQLSLAGDVDELKR	4.04	1,870.99
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	GLGEAQLSLAGDVDELKRR	2.23	2,027.09
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	GLLEDLRNDLDR	2.24	1,428.74
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	GLLEDLRNDLDRLFVK	2.57	1,916.06
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	IETNENNLESAK	3.44	1,361.65
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	ILRAEESAAHLPEEIR	3.49	1,833.98

ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	LEEELGQLK	3.49	1,058.57
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	LQNEILKDLSDGIHVVK	4.89	1,921.08
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	LQSVEDGVQAAR	3.69	1,272.65
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	QREELGQGLQGVEQK	5.46	1,698.88
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	RLEEELGQLK	3.46	1,214.67
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	SINDNIAIFTDVQK	5.23	1,577.82
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	SINDNIAIFTDVQKR	2.93	1,733.92
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	STIQTMESDVYTEVK	3.59	1,746.81

ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	TAVDSLVAYSVK	3.48	1,252.68
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	VQEQVHTLLGR	4.22	1,279.71
ATP	6018	PREDICTED: similar to cytoskeleton-associated protein 4	gi|119892686	64,511.50	100.00%	29	44	101	0.86%	46.50%	VQSLQATFGTFESLVR	4.13	1,782.94
ATP	6018	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	3	4	5	0.04%	20.40%	KQYDSYTFTASK	3.65	1,438.68
ATP	6018	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	3	4	5	0.04%	20.40%	LEDPDGNVLYKEMKK	2.74	1,794.89
ATP	6018	TMED7 protein	gi|134025246,gi|157428116	25,318.00	100.00%	3	4	5	0.04%	20.40%	TVYFDFQVGEDPPLFPSENR	2.04	2,357.11
ATP	6018	similar to peptidylprolyl isomerase A (cyclophilin A)	gi|28189771,gi|58760424,gi|75948300	17,851.80	100.00%	4	5	5	0.04%	16.50%	FDDENFILK	2.52	1,140.56
ATP	6018	similar to peptidylprolyl isomerase A (cyclophilin A)	gi|28189771,gi|58760424,gi|75948300	17,851.80	100.00%	4	5	5	0.04%	16.50%	SIYGEKFDDENFILK	4.12	1,817.90
ATP	6018	similar to peptidylprolyl isomerase A (cyclophilin A)	gi|28189771,gi|58760424,gi|75948300	17,851.80	100.00%	4	5	5	0.04%	16.50%	VSFELFADK	2.37	1,055.54
ATP	6018	similar to peptidylprolyl isomerase A (cyclophilin A)	gi|28189771,gi|58760424,gi|75948300	17,851.80	100.00%	4	5	5	0.04%	16.50%	VSFELFADKVPK	2.66	1,379.76
ATP	6018	Clusterin	gi|109939936,gi|116530,gi|146231734,gi|151555910,gi|163115,gi|27806907	51,096.70	100.00%	4	4	4	0.03%	15.30%	KLLLSSLEEAKK	3.06	1,358.83

ATP	6018	Clusterin	gi|109939936,gi|116530,gi|146231734,gi|151555910,gi|163115,gi|27806907	51,096.70	100.00%	4	4	4	0.03%	15.30%	LFNSFPITVTVPQEVSSPNFMENVAEK	3.3	3,040.50
ATP	6018	Clusterin	gi|109939936,gi|116530,gi|146231734,gi|151555910,gi|163115,gi|27806907	51,096.70	100.00%	4	4	4	0.03%	15.30%	LYDQLLQSYQQK	4.06	1,526.79
ATP	6018	Clusterin	gi|109939936,gi|116530,gi|146231734,gi|151555910,gi|163115,gi|27806907	51,096.70	100.00%	4	4	4	0.03%	15.30%	RPQDTQYYSPFSSFPR	3.42	1,975.93
ATP	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	32	0.27%	58.50%	AAELIANSLATAGDGLIELR	4.01	1,998.09
ATP	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	32	0.27%	58.50%	AATFGLILDDVSLTHLTFGK	2.24	2,119.14
ATP	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	32	0.27%	58.50%	AATFGLILDDVSLTHLTFGKEFTEAVEAK	3.61	3,123.63
ATP	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	32	0.27%	58.50%	DLQNVNITLR	3.95	1,185.66
ATP	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	32	0.27%	58.50%	FDAGELITQR	3.76	1,149.59
ATP	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	32	0.27%	58.50%	FGLALAVAGGVVNSALYNVDAGHR	3.99	2,371.25
ATP	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	32	0.27%	58.50%	IFTSIGEDYDER	3.42	1,444.66
ATP	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	32	0.27%	58.50%	ILFRPVASQLPR	3.05	1,396.84
ATP	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	32	0.27%	58.50%	KLEAAEDIAYQLSR	4.36	1,606.84
ATP	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	32	0.27%	58.50%	NITYLPAGQSVLLQLPQ	4.55	1,855.03
ATP	6018	Prohibitin	gi|74354527,gi|77736091,gi|88909243	29,786.60	100.00%	11	14	32	0.27%	58.50%	VLPSITTEILK	2.41	1,213.74

ATP	6018	ras-related C3 botulinum toxin substrate 1	gi|27806443,gi|51702785,gi|6007014,gi|73587375	21,432.60	99.90%	2	3	3	0.03%	7.81%	KLTPITYPQGLAMAK	2.86	1,647.91
ATP	6018	ras-related C3 botulinum toxin substrate 1	gi|27806443,gi|51702785,gi|6007014,gi|73587375	21,432.60	99.90%	2	3	3	0.03%	7.81%	LTPITYPQGLAMAK	3.36	1,519.82
ATP	6018	heterogeneous nuclear ribonucleoprotein D	gi|146231918,gi|148230364,gi|148878011	32,830.70	99.80%	2	2	2	0.02%	7.19%	GFGFVLFK	2.37	914.5135
ATP	6018	heterogeneous nuclear ribonucleoprotein D	gi|146231918,gi|148230364,gi|148878011	32,830.70	99.80%	2	2	2	0.02%	7.19%	IFVGGLSPDTPEEK	4.1	1,488.76
ATP	6018	Interferon induced transmembrane protein 1 (9-27)	gi|112362418,gi|118151192,gi|118151350,gi|118151354,gi|119919513,gi|14279576,gi|14279578,gi|148744152,gi|32480628,gi|73586549,gi|73587371	13,631.00	99.80%	2	3	5	0.04%	13.70%	KMVGDITGAQSYASTAK	5.2	1,743.86
ATP	6018	Interferon induced transmembrane protein 1 (9-27)	gi|112362418,gi|118151192,gi|118151350,gi|118151354,gi|119919513,gi|14279576,gi|14279578,gi|148744152,gi|32480628,gi|73586549,gi|73587371	13,631.00	99.80%	2	3	5	0.04%	13.70%	MVGDITGAQSYASTAK	5.1	1,615.76
ATP	6018	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	5	6	8	0.07%	51.00%	ALAAAGYDVEK	3.08	1,107.57

ATP	6018	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	5	6	8	0.07%	51.00%	ALAAAGYDVEKNNSR	4.78	1,578.79
ATP	6018	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	5	6	8	0.07%	51.00%	ASGPPVSELITK	2.97	1,198.67
ATP	6018	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	5	6	8	0.07%	51.00%	SETAPAAPAAAPPAEK	3.46	1,478.75
ATP	6018	RecName: Full=Histone H1.1; AltName: Full=CTL-1	gi|121903	10,347.40	100.00%	5	6	8	0.07%	51.00%	SGVSLAALKK	2.89	973.6041
ATP	6018	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	5	5	6	0.05%	23.40%	ILHVNGFNGEGGEEDPQAAR	5.69	2,110.00
ATP	6018	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	5	5	6	0.05%	23.40%	LLLLGAGESGK	3.63	1,057.63
ATP	6018	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	5	5	6	0.05%	23.40%	SKIEDYFPEFAR	2.43	1,501.73
ATP	6018	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	5	5	6	0.05%	23.40%	VDYILSVMNVPDFDFPPEFYEHAK	3.14	2,888.35
ATP	6018	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	5	5	6	0.05%	23.40%	YFIRDEFLR	2.1	1,258.66
ATP	6018	GNAS complex locus	gi|113912207,gi|74268384	45,691.40	100.00%	5	5	6	0.05%	23.40%	YTTPEDATPEPGEDPR	3.16	1,774.78
ATP	6018	PREDICTED: similar to Transmembrane 9 superfamily member 2 precursor (p76), partial	gi|194671915	72,962.00	99.80%	2	2	3	0.03%	4.40%	IYYHVVETGSMGAR	3.65	1,598.76

ATP	6018	PREDICTED: similar to Transmembrane 9 superfamily member 2 precursor (p76), partial	gi|194671915	72,962.00	99.80%	2	2	3	0.03%	4.40%	RPSENLGQVLFGER	3.84	1,601.84
ATP	6018	interferon stimulated gene 17 [Ovis aries]	gi|12082402,gi|57619183	17,482.10	100.00%	4	4	4	0.03%	33.10%	EVLQEGVPLVHQGLK	3.43	1,645.93
ATP	6018	interferon stimulated gene 17 [Ovis aries]	gi|12082402,gi|57619183	17,482.10	100.00%	4	4	4	0.03%	33.10%	INVPAFQQR	2.89	1,072.59
ATP	6018	interferon stimulated gene 17 [Ovis aries]	gi|12082402,gi|57619183	17,482.10	100.00%	4	4	4	0.03%	33.10%	MLGGEEILVPLR	2.69	1,342.74
ATP	6018	interferon stimulated gene 17 [Ovis aries]	gi|12082402,gi|57619183	17,482.10	100.00%	4	4	4	0.03%	33.10%	SSSYEVQLTQTVAVLK	3.97	1,752.94
ATP	6018	PREDICTED: similar to E3 ubiquitin-protein ligase MARCH5 (Membrane-associated RING finger protein 5) (Membrane-associated RING-CH protein V) (MARCH-V) (RING finger	gi|119917492,gi|122064341,gi|73586675,gi|77736375	29,755.90	99.80%	2	2	2	0.02%	13.70%	ADPLFLLIGLPTIPVMLILGK	2.96	2,250.36

ATP	6018	PREDICTED: similar to E3 ubiquitin-protein ligase MARCH5 (Membrane-associated RING finger protein 5) (Membrane-associated RING-CH protein V) (MARCH-V) (RING finger	gi|119917492,gi|122064341,gi|73586675,gi|77736375	29,755.90	99.80%	2	2	2	0.02%	13.70%	IPAEANPLADHVSATR	2.61	1,661.86
ATP	6018	RecName: Full=60S acidic ribosomal protein P0; AltName: Full=L10E	gi|108935888,gi|2293577,gi|59858525,gi|60592767	34,353.40	99.80%	2	2	2	0.02%	6.92%	IIQLLDDYPK	3.69	1,217.68
ATP	6018	RecName: Full=60S acidic ribosomal protein P0; AltName: Full=L10E	gi|108935888,gi|2293577,gi|59858525,gi|60592767	34,353.40	99.80%	2	2	2	0.02%	6.92%	TSFFQALGITTK	2.82	1,313.71
ATP	6018	RPL12 protein	gi|148744191,gi|42564206,gi|45430019,gi|47117092,gi|74354972	17,801.10	99.80%	2	2	2	0.02%	15.20%	IGPLGLSPK	2.24	881.5457
ATP	6018	RPL12 protein	gi|148744191,gi|42564206,gi|45430019,gi|47117092,gi|74354972	17,801.10	99.80%	2	2	2	0.02%	15.20%	QAQIEVVPSASALIIK	4.24	1,666.97
ATP	6018	Nucleobindin 2	gi|113912161,gi|115496067	49,171.70	99.80%	2	2	3	0.03%	8.19%	LHDVNSDGFLDEQELEALFTK	4.24	2,420.16
ATP	6018	Nucleobindin 2	gi|113912161,gi|115496067	49,171.70	99.80%	2	2	3	0.03%	8.19%	QVIDVLETDSHFR	3.63	1,558.79

ATP	6018	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	gi|111304648,gi|115496338,gi|121957506	27,838.90	99.80%	2	4	6	0.05%	11.20%	FKGPFTDVVTTNLK	4.16	1,566.85
ATP	6018	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	gi|111304648,gi|115496338,gi|121957506	27,838.90	99.80%	2	4	6	0.05%	11.20%	GPFTDVVTTNLK	4.12	1,291.69
ATP	6018	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	gi|111304648,gi|115496338,gi|121957506	27,838.90	99.80%	2	4	6	0.05%	11.20%	HEQILVLDPPTDLK	4.33	1,617.89
ATP	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	17	19	26	0.22%	31.60%	AEVQNLGGELVVSGVDSAMSLIQAAK	5.48	2,602.34
ATP	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	17	19	26	0.22%	31.60%	AHVLAASVEQATENFLEK	3.83	1,957.00
ATP	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	17	19	26	0.22%	31.60%	AIMAQLPQEQK	3.84	1,272.66
ATP	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	17	19	26	0.22%	31.60%	ALKPEVDKLNIMAAK	2.78	1,656.94
ATP	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	17	19	26	0.22%	31.60%	ESQFLKEELVAAVEDVRK	4.85	2,090.11
ATP	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	17	19	26	0.22%	31.60%	FTEQVEAAVEALSSDPAQPMDENEFIDASR	5.1	3,312.49
ATP	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	17	19	26	0.22%	31.60%	HVNPVQALSEFK	2.89	1,368.73

ATP	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	17	19	26	0.22%	31.60%	IAEQVASFQEEK	3.92	1,378.68
ATP	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	17	19	26	0.22%	31.60%	LLILADMADVYK	3.12	1,380.74
ATP	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	17	19	26	0.22%	31.60%	NAGTEQDLGIQYK	3.65	1,436.70
ATP	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	17	19	26	0.22%	31.60%	NLMNAVVQTVK	3.98	1,232.67
ATP	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	17	19	26	0.22%	31.60%	QALQDLLSEYMGNAGR	3.99	1,781.85
ATP	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	17	19	26	0.22%	31.60%	QIIVDPLSFSEER	3.7	1,532.80
ATP	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	17	19	26	0.22%	31.60%	SDALNSAIDKMTK	3.56	1,409.69
ATP	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	17	19	26	0.22%	31.60%	TSVQTEDDQLIAGQSAR	4.52	1,818.88
ATP	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	17	19	26	0.22%	31.60%	VIHVVTSEMDNYEPGVYTEK	3.76	2,326.09
ATP	6018	RecName: Full=Catenin alpha-1	gi|114149256,gi|75773615,gi|78369272	100,117.00	100.00%	17	19	26	0.22%	31.60%	VLTDAVDDITSIDDFLAVSENHILEDVNK	4.29	3,200.58
ATP	6018	RecName: Full=Transmembrane and coiled-coil domain-containing protein 1	gi|109895213,gi|74354058,gi|77736477	21,158.30	99.80%	2	3	3	0.03%	15.40%	LPFTPLSYIQGLSHR	3.66	1,728.94

ATP	6018	RecName: Full=Transmembrane and coiled-coil domain-containing protein 1	gi|109895213,gi|74354058,gi|77736477	21,158.30	99.80%	2	3	3	0.03%	15.40%	QAGGFLGPPPPSGK	2.51	1,309.69
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	AKFEELNMDLFR	4.68	1,528.75
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	DAGTIAGLNVMR	3.84	1,233.63
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	DNHLLGTFDLTGIPPAPR	2.8	1,934.01
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	EFFNGKEPSR	2.3	1,210.59
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	ELEEIVQPIISK	3.58	1,397.79
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	FEELNMDLFR	2.93	1,329.61
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	GVPQIEVTFEIDVNGILR	3.14	1,999.09

ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	IDTRNELESYAYSLK	4.24	1,801.90
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	IEIESFYEGEDFSETLTR	3.61	2,164.99
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	IINEPTAAAIAYGLDK	4.25	1,659.90
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	IINEPTAAAIAYGLDKR	4.45	1,816.00
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	ITPSYVAFTPEGER	3.41	1,566.78
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	KKELEEIVQPIISK	4.93	1,653.98
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	KSQIFSTASDNQPTVTIK	3.59	1,965.03
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	KVTHAVVTVPAYFNDAQR	2.36	2,016.07

ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	MKETAEAYLGKK	3.67	1,384.71
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	MVNDAEKFAEEDKK	3.58	1,669.77
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	NELESYAYSLK	3.65	1,316.64
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	NQLTSNPENTVFDAK	5.03	1,677.81
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	SDIDEIVLVGGSTR	2.28	1,460.76
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	SQIFSTASDNQPTVTIK	4.14	1,836.93
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	TFAPEEISAMVLTK	4.23	1,552.79
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	TKPYIQVDVGGGQTK	4.09	1,590.85

ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	VLEDSDLKKSDIDEIVLVGGSTR	5.46	2,488.31
ATP	6018	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	gi|111308468,gi|115495027,gi|152941210	72,383.60	100.00%	25	33	58	0.50%	42.10%	VTHAVVTVPAYFNDAQR	5.17	1,887.97
ATP	6018	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	4	5	6	0.05%	11.30%	LNTIPLFVQLLYSSVENIQR	4.09	2,347.30
ATP	6018	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	4	5	6	0.05%	11.30%	MLSSPVESVLFYAITTLHNLLLYQEGAK	3.49	3,153.65
ATP	6018	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	4	5	6	0.05%	11.30%	SAIVHLINYQDDAELATR	3.27	2,029.04
ATP	6018	Junction plakoglobin	gi|109658166,gi|157391363,gi|158065994,gi|20336613,gi|211637709,gi|218103015,gi|51316492,gi|51591897	81,804.10	100.00%	4	5	6	0.05%	11.30%	TLVTQNSGVEALIHAILR	2.57	1,935.10
ATP	6018	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	100.00%	3	3	3	0.03%	39.00%	AALVDLEPGTMDSVR	3.75	1,589.78
ATP	6018	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	100.00%	3	3	3	0.03%	39.00%	ALTVPELTQQMFDAK	3.29	1,707.86
ATP	6018	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	100.00%	3	3	3	0.03%	39.00%	FPGQLNADLR	2.72	1,130.60

ATP	6018	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	100.00%	3	3	3	0.03%	39.00%	FPGQLNADLRK	2.7	1,258.69
ATP	6018	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	100.00%	3	3	3	0.03%	39.00%	GHYTEGAELVDSVLDVVR	4.05	1,958.98
ATP	6018	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	100.00%	3	3	3	0.03%	39.00%	GHYTEGAELVDSVLDVVRK	4.32	2,087.08
ATP	6018	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	100.00%	3	3	3	0.03%	39.00%	LAVNMVPFPR	4.05	1,159.63
ATP	6018	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	100.00%	3	3	3	0.03%	39.00%	LHFFMPGFAPLTAR	3.76	1,620.84
ATP	6018	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	100.00%	3	3	3	0.03%	39.00%	LTTPTYGDLNHLVSATMSGVTTSLR	2.77	2,651.33
ATP	6018	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	100.00%	3	3	3	0.03%	39.00%	MSATFIGNSTAIQELFK	4.88	1,873.94
ATP	6018	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	100.00%	3	3	3	0.03%	39.00%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	4.3	4,479.06
ATP	6018	tubulin, beta 6	gi|114052148,gi|87578360	49,882.10	100.00%	3	3	3	0.03%	39.00%	YLTVAAVFR	2.97	1,039.59
ATP	6018	RecName: Full=Rab GDP dissociation inhibitor beta; Short=Rab GDI beta; AltName: Full=Guanosine diphosphate dissociation inhibitor 2; Short=GDI-2	gi|109939713,gi|146231738,gi|75773612,gi|76253900	50,472.30	99.80%	2	2	2	0.02%	6.74%	FVSISDLLVPK	2.5	1,217.71

ATP	6018	RecName: Full=Rab GDP dissociation inhibitor beta; Short=Rab GDI beta; AltName: Full=Guanosine diphosphate dissociation inhibitor 2; Short=GDI-2	gi|109939713,gi|146231738,gi|75773612,gi|76253900	50,472.30	99.80%	2	2	2	0.02%	6.74%	SPYLYPLYGLGELPQGFAR	4.58	2,141.11
ATP	6018	RecName: Full=60S ribosomal protein L11	gi|108860925,gi|115497634,gi|74268362	20,235.20	99.80%	2	2	2	0.02%	12.90%	VLEQLTGQTPVFSK	3.49	1,546.85
ATP	6018	RecName: Full=60S ribosomal protein L11	gi|108860925,gi|115497634,gi|74268362	20,235.20	99.80%	2	2	2	0.02%	12.90%	YDGIILPGK	2.43	975.5512
ATP	6018	syntaxin 7	gi|118150840,gi|122140829,gi|73586654	29,638.60	99.80%	2	2	4	0.03%	10.70%	EFGSLPTTPSDQR	3.69	1,434.69
ATP	6018	syntaxin 7	gi|118150840,gi|122140829,gi|73586654	29,638.60	99.80%	2	2	4	0.03%	10.70%	TLNQLGTPQDSPELR	5.15	1,668.86
ATP	6018	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	5	6	8	0.07%	19.60%	GDLLFLTNR	2.49	1,048.58
ATP	6018	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	5	6	8	0.07%	19.60%	GDLLFLTNRVEDPIR	3.03	1,757.95
ATP	6018	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	5	6	8	0.07%	19.60%	MLSLDFLDDVR	2.56	1,339.66
ATP	6018	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	5	6	8	0.07%	19.60%	MLSLDFLDDVRR	2.38	1,495.76
ATP	6018	SEC11 homolog A (S. cerevisiae)	gi|151554619,gi|27806149,gi|54039632,gi|6979934	20,607.80	100.00%	5	6	8	0.07%	19.60%	VGEIVVFR	2.74	918.5407

ATP	6018	CAND1 protein	gi|154426008,gi|155372073,gi|182627583	136,363.10	100.00%	4	4	4	0.03%	5.20%	IDLRPVLGEGVPILASFLR	2.86	2,065.22
ATP	6018	CAND1 protein	gi|154426008,gi|155372073,gi|182627583	136,363.10	100.00%	4	4	4	0.03%	5.20%	ISGSILNELIGLVR	4.7	1,483.88
ATP	6018	CAND1 protein	gi|154426008,gi|155372073,gi|182627583	136,363.10	100.00%	4	4	4	0.03%	5.20%	MLTGPVYSQSTALTHK	3.04	1,749.88
ATP	6018	CAND1 protein	gi|154426008,gi|155372073,gi|182627583	136,363.10	100.00%	4	4	4	0.03%	5.20%	SVILEAFSSPSEEVK	3.35	1,621.83
ATP	6018	RecName: Full=Acyl-protein thioesterase 1; AltName: Full=Lysophospholipase 1; AltName: Full=Lysophospholipase I	gi|115311636,gi|75948308,gi|77736321	24,578.40	99.80%	2	2	2	0.02%	10.40%	ASFPQGPIGGVNR	1.99	1,299.68
ATP	6018	RecName: Full=Acyl-protein thioesterase 1; AltName: Full=Lysophospholipase 1; AltName: Full=Lysophospholipase I	gi|115311636,gi|75948308,gi|77736321	24,578.40	99.80%	2	2	2	0.02%	10.40%	TLVNPANVTFR	2.43	1,231.68
ATP	6018	PREDICTED: brain protein 44	gi|119889010,gi|194665199	14,264.40	99.80%	2	4	6	0.05%	18.90%	LRPLYNHPAGPR	2.57	1,390.77
ATP	6018	PREDICTED: brain protein 44	gi|119889010,gi|194665199	14,264.40	99.80%	2	4	6	0.05%	18.90%	VLDKVELLLPEK	3.92	1,395.85
ATP	6018	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	8	9	16	0.14%	20.30%	FLVVLNFGDVGQLAR	4.95	1,647.92
ATP	6018	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	8	9	16	0.14%	20.30%	FTGLSKEELLK	3.63	1,264.71

ATP	6018	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	8	9	16	0.14%	20.30%	LLIAGTDSSDLQQILR	5.05	1,742.97
ATP	6018	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	8	9	16	0.14%	20.30%	NQEDDLTETNLEQIDPIFGSK	5.02	2,406.13
ATP	6018	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	8	9	16	0.14%	20.30%	NQEDDLTETNLEQIDPIFGSKEDFESLLHSAK	4.72	3,662.73
ATP	6018	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	8	9	16	0.14%	20.30%	SLLHGDFYDLSSGPDLFSYIR	3.8	2,402.17
ATP	6018	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	8	9	16	0.14%	20.30%	VDLLLSTQPGR	3.37	1,198.68
ATP	6018	SLC3A2 protein	gi|115304925,gi|164448600,gi|59857795,gi|74354296	63,166.50	100.00%	8	9	16	0.14%	20.30%	VILDLTPNYK	3.07	1,175.67
ATP	6018	MHC class I antigen	gi|84095083	40,657.50	100.00%	7	9	111	0.95%	24.00%	DYIALNEDLR	3.09	1,221.61
ATP	6018	MHC class I antigen	gi|84095083	40,657.50	100.00%	7	9	111	0.95%	24.00%	FIAVGYVDDTQFVR	5.33	1,629.83
ATP	6018	MHC class I antigen	gi|84095083	40,657.50	100.00%	7	9	111	0.95%	24.00%	IYTQAASSDSAQGSDVSLTVPK	6.27	2,225.09
ATP	6018	MHC class I antigen	gi|84095083	40,657.50	100.00%	7	9	111	0.95%	24.00%	IYTQAASSDSAQGSDVSLTVPKV	5.15	2,324.16
ATP	6018	MHC class I antigen	gi|84095083	40,657.50	100.00%	7	9	111	0.95%	24.00%	SWTAADTAAQITK	4.15	1,363.69
ATP	6018	MHC class I antigen	gi|84095083	40,657.50	100.00%	7	9	111	0.95%	24.00%	VQHEGLQEPLTLR	3.86	1,519.82
ATP	6018	MHC class I antigen	gi|84095083	40,657.50	100.00%	7	9	111	0.95%	24.00%	WAALVVPSGEEQR	2.68	1,441.74

ATP	6018	RecName: Full=Serine palmitoyltransferase 1; AltName: Full=Serine-palmitoyl-CoA transferase 1; Short=SPT 1; Short=SPT1; AltName: Full=Long chain base biosynthesis protein 1; Short=L	gi|122139929,gi|75948211,gi|77736443	52,771.80	100.00%	3	3	3	0.03%	8.88%	LLKEQEIEDQKNPR	4.36	1,739.93
ATP	6018	RecName: Full=Serine palmitoyltransferase 1; AltName: Full=Serine-palmitoyl-CoA transferase 1; Short=SPT 1; Short=SPT1; AltName: Full=Long chain base biosynthesis protein 1; Short=L	gi|122139929,gi|75948211,gi|77736443	52,771.80	100.00%	3	3	3	0.03%	8.88%	VVVTVEQTEEDLEK	4.66	1,617.82

ATP	6018	RecName: Full=Serine palmitoyltransferase 1; AltName: Full=Serine-palmitoyl-CoA transferase 1; Short=SPT 1; Short=SPT1; AltName: Full=Long chain base biosynthesis protein 1; Short=L	gi|122139929,gi|75948211,gi|77736443	52,771.80	100.00%	3	3	3	0.03%	8.88%	VVVTVEQTEEDLEKAASTISEVAQTVLL	3.24	3,001.58
ATP	6018	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	5	6	6	0.05%	9.44%	ALLELQLEPEELYQTFQR	4.75	2,220.15
ATP	6018	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	5	6	6	0.05%	9.44%	ARPFPDGLAEDIDKGEVSAR	4.8	2,143.08
ATP	6018	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	5	6	6	0.05%	9.44%	EGIPALDNFLDKL	3.26	1,444.77
ATP	6018	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	5	6	6	0.05%	9.44%	STAISLFYELSENDLNFIK	5.2	2,204.11
ATP	6018	eukaryotic translation elongation factor 2	gi|115497900,gi|74353984,gi|88909609	95,352.20	100.00%	5	6	6	0.05%	9.44%	VFSGLVSTGLK	2.64	1,107.64

ATP	6018	RecName: Full=Synaptic glycoprotein SC2; AltName: Full=Trans-2,3-enoyl-CoA reductase; Short=TER	gi|122140918,gi|73586600,gi|77736441	36,056.10	100.00%	3	3	3	0.03%	11.70%	DYPPLRMPIIPFLL	2.84	1,700.94
ATP	6018	RecName: Full=Synaptic glycoprotein SC2; AltName: Full=Trans-2,3-enoyl-CoA reductase; Short=TER	gi|122140918,gi|73586600,gi|77736441	36,056.10	100.00%	3	3	3	0.03%	11.70%	LPVGTTATLYFR	4.01	1,338.74
ATP	6018	RecName: Full=Synaptic glycoprotein SC2; AltName: Full=Trans-2,3-enoyl-CoA reductase; Short=TER	gi|122140918,gi|73586600,gi|77736441	36,056.10	100.00%	3	3	3	0.03%	11.70%	SLKDEDVLQK	2.58	1,174.63
ATP	6018	RecName: Full=Galectin-9	gi|122145068,gi|59858325,gi|62751460,gi|75775171,gi|87044899	39,329.70	99.80%	2	2	3	0.03%	9.30%	NLPAINNLEVGGDIQLTHVQT	5.76	2,246.18
ATP	6018	RecName: Full=Galectin-9	gi|122145068,gi|59858325,gi|62751460,gi|75775171,gi|87044899	39,329.70	99.80%	2	2	3	0.03%	9.30%	SGSDIAFHLNPR	3.06	1,313.66
ATP	6018	PREDICTED: similar to Calpain-5 (nCL-3) (htra-3) isoform 1	gi|76636134	72,988.00	100.00%	3	3	3	0.03%	8.12%	ANADDLQALHTLHLR	3.24	1,687.89

ATP	6018	PREDICTED: similar to Calpain-5 (nCL-3) (htra-3) isoform 1	gi|76636134	72,988.00	100.00%	3	3	3	0.03%	8.12%	VLFEDPNFPATDDSLYYK	3.26	2,134.00
ATP	6018	PREDICTED: similar to Calpain-5 (nCL-3) (htra-3) isoform 1	gi|76636134	72,988.00	100.00%	3	3	3	0.03%	8.12%	YVIIPTTFEPGHTGEFLLR	2.42	2,190.16
ATP	6018	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	5	5	10	0.09%	29.20%	GVDLQENNPASR	2.94	1,299.63
ATP	6018	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	5	5	10	0.09%	29.20%	KLPKNEPQNAAGAPGR	2.96	1,647.89
ATP	6018	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	5	5	10	0.09%	29.20%	LVLLGESAVGK	3.81	1,085.66
ATP	6018	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	5	5	10	0.09%	29.20%	QASPNIVIALAGNK	3.29	1,395.80
ATP	6018	RAB5C, member RAS oncogene family	gi|109659170,gi|61553191,gi|75052596,gi|77736431	23,448.70	100.00%	5	5	10	0.09%	29.20%	YHSLAPMYYR	2.6	1,316.61
ATP	6018	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	6	12	0.10%	27.40%	ELNVMFIETSAK	3.32	1,397.70
ATP	6018	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	6	12	0.10%	27.40%	GSDVIIMLVGNK	2.86	1,261.68
ATP	6018	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	6	12	0.10%	27.40%	GSDVIIMLVGNKTDLADKR	4.17	2,061.10

ATP	6018	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	6	12	0.10%	27.40%	LVFLGEQSVGK	2.84	1,176.66
ATP	6018	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	6	12	0.10%	27.40%	RVAAALPGMESTQDR	2.63	1,617.80
ATP	6018	PREDICTED: similar to RAB6A, member RAS oncogene family isoform 2	gi|119907595,gi|119907597	23,545.30	100.00%	6	6	12	0.10%	27.40%	VAAALPGMESTQDR	2.49	1,461.70
ATP	6018	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	5	0.04%	27.40%	DLTDYLMK	2.57	1,014.48
ATP	6018	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	5	0.04%	27.40%	GYSFTTTAER	3.25	1,132.53
ATP	6018	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	5	0.04%	27.40%	HQGVMVGMGQKDCYVGDEAQSK	2.67	2,383.05
ATP	6018	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	5	0.04%	27.40%	HQGVMVGMGQKDCYVGDEAQSKR	3.39	2,539.15
ATP	6018	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	5	0.04%	27.40%	IKIIAPPERK	3.12	1,164.75

ATP	6018	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	5	0.04%	27.40%	LDLAGRDLTDYLMK	3.35	1,639.84
ATP	6018	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	5	0.04%	27.40%	SYELPDGQVITIGNER	3.84	1,790.89
ATP	6018	PREDICTED: similar to Actin, cytoplasmic 2 (Beta-actin-2)	gi|194676388	41,854.80	99.80%	2	3	5	0.04%	27.40%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	6.77	3,199.61
ATP	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	gi|27806197,gi|3676399,gi|71153779,gi|73586683	29,157.00	100.00%	4	5	7	0.06%	29.80%	AAFDDAIAELDTLSEESYKDSTLIMQLLR	5.09	3,274.60
ATP	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	gi|27806197,gi|3676399,gi|71153779,gi|73586683	29,157.00	100.00%	4	5	7	0.06%	29.80%	EAAENSLVAYK	2.15	1,194.60
ATP	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	gi|27806197,gi|3676399,gi|71153779,gi|73586683	29,157.00	100.00%	4	5	7	0.06%	29.80%	LICCDILDVLDKHLIPAANTGESK	2.25	2,581.34

ATP	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	gi|27806197,gi|3676399,gi|71153779,gi|73586683	29,157.00	100.00%	4	5	7	0.06%	29.80%	YLAEFATGNDRK	3.07	1,384.69
ATP	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	gi|118151330,gi|152941256,gi|154426168,gi|74354028,gi|82592596	27,747.40	99.80%	2	2	2	0.02%	17.60%	AVTEQGAELSNEER	4.99	1,532.72
ATP	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	gi|118151330,gi|152941256,gi|154426168,gi|74354028,gi|82592596	27,747.40	99.80%	2	2	2	0.02%	17.60%	TAFDEAIAELDTLNEDSYKDSTLIMQLLR	4.69	3,331.63
ATP	6018	Transducin (beta)-like 2	gi|112362303,gi|115495815	49,894.00	100.00%	3	3	3	0.03%	7.85%	APIVNIGIADTGK	3.45	1,268.72
ATP	6018	Transducin (beta)-like 2	gi|112362303,gi|115495815	49,894.00	100.00%	3	3	3	0.03%	7.85%	LFHNTPGYR	2.3	1,104.56
ATP	6018	Transducin (beta)-like 2	gi|112362303,gi|115495815	49,894.00	100.00%	3	3	3	0.03%	7.85%	LQQQLTQAQEALK	4.96	1,498.82
ATP	6018	proteasome activator 28 alpha subunit	gi|63139650,gi|73921836,gi|86821522,gi|91680535	28,675.80	100.00%	4	4	4	0.03%	19.30%	APLDIPVPDPVKEK	2.75	1,517.86
ATP	6018	proteasome activator 28 alpha subunit	gi|63139650,gi|73921836,gi|86821522,gi|91680535	28,675.80	100.00%	4	4	4	0.03%	19.30%	LEGFHTQISK	1.98	1,159.61
ATP	6018	proteasome activator 28 alpha subunit	gi|63139650,gi|73921836,gi|86821522,gi|91680535	28,675.80	100.00%	4	4	4	0.03%	19.30%	NAYAVLYDIILK	2.81	1,395.79
ATP	6018	proteasome activator 28 alpha subunit	gi|63139650,gi|73921836,gi|86821522,gi|91680535	28,675.80	100.00%	4	4	4	0.03%	19.30%	QLVHELDEAEYR	1.86	1,501.73

ATP	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	14	17	0.15%	14.10%	FNTSDVSAIEK	2.74	1,210.60
ATP	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	14	17	0.15%	14.10%	GDFIALDLGGSSFR	3.56	1,454.73
ATP	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	14	17	0.15%	14.10%	GKFNTSDVSAIEK	3.11	1,395.71
ATP	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	14	17	0.15%	14.10%	HIDLVEGDEGR	3.59	1,239.60
ATP	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	14	17	0.15%	14.10%	ITPELLTR	1.95	942.562
ATP	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	14	17	0.15%	14.10%	LSDETLLDIMNR	3.99	1,435.71
ATP	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	14	17	0.15%	14.10%	QIEETLAHFSLTK	3.35	1,516.80
ATP	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	14	17	0.15%	14.10%	SANLVAATLGAILSR	3.57	1,456.85
ATP	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	14	17	0.15%	14.10%	TIYDKLVDEFSLNSGK	2.32	1,828.93
ATP	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	14	17	0.15%	14.10%	TTVGVDGSLYK	2.83	1,139.59
ATP	6018	Hexokinase 1	gi|154426122,gi|33332343,gi|60592784	102,191.60	100.00%	11	14	17	0.15%	14.10%	YLSQIESDRLALLQVR	3.71	1,904.06
ATP	6018	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	5	6	8	0.07%	8.56%	DIQGSLQDIFK	3.33	1,263.66
ATP	6018	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	5	6	8	0.07%	8.56%	INENTGSVSVTR	3.89	1,276.65
ATP	6018	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	5	6	8	0.07%	8.56%	RSIVVSPILIPENQR	2.79	1,721.01

ATP	6018	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	5	6	8	0.07%	8.56%	SIVVSPILIPENQR	2.51	1,564.91
ATP	6018	RecName: Full=Cadherin-13; Flags: Precursor	gi|110832787,gi|77567834,gi|78369244	78,179.40	100.00%	5	6	8	0.07%	8.56%	TLEGPVPLEVIVIDQNDNRPIFR	1.96	2,634.43
ATP	6018	alpha-actinin 1	gi|145286437,gi|77567675,gi|78369242	102,966.00	100.00%	3	3	4	0.03%	8.18%	FAIQDISVEETSAK	3.91	1,537.77
ATP	6018	alpha-actinin 1	gi|145286437,gi|77567675,gi|78369242	102,966.00	100.00%	3	3	4	0.03%	8.18%	IDQLEGDHQLIQEALIFDNK	4.69	2,339.19
ATP	6018	alpha-actinin 1	gi|145286437,gi|77567675,gi|78369242	102,966.00	100.00%	3	3	4	0.03%	8.18%	LLETIDQLYLEYAK	4.81	1,711.92
ATP	6018	alpha-actinin 1	gi|145286437,gi|77567675,gi|78369242	102,966.00	100.00%	3	3	4	0.03%	8.18%	LSNRPAFMPSEGR	3	1,477.72
ATP	6018	alpha-actinin 1	gi|145286437,gi|77567675,gi|78369242	102,966.00	100.00%	3	3	4	0.03%	8.18%	TINEVENQILTR	2.69	1,429.76
ATP	6018	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein H (hnRNP H) isoform 26	gi|194668611	49,211.80	100.00%	3	3	4	0.03%	11.10%	ATENDIYNFFSPLNPVR	4.09	1,996.98
ATP	6018	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein H (hnRNP H) isoform 26	gi|194668611	49,211.80	100.00%	3	3	4	0.03%	11.10%	HTGPNSPDTANDGFVR	4.45	1,684.77

ATP	6018	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein H (hnRNP H) isoform 26	gi|194668611	49,211.80	100.00%	3	3	4	0.03%	11.10%	STGEAFVQFASQEIAEK	3.27	1,841.89
ATP	6018	PREDICTED: similar to programmed cell death 8 isoform 2	gi|76658657	66,854.50	100.00%	4	4	4	0.03%	10.60%	ASGTEVIQLFPEKGNMGK	3.55	1,921.97
ATP	6018	PREDICTED: similar to programmed cell death 8 isoform 2	gi|76658657	66,854.50	100.00%	4	4	4	0.03%	10.60%	ATSSALEGEPEPQVR	2.84	1,570.77
ATP	6018	PREDICTED: similar to programmed cell death 8 isoform 2	gi|76658657	66,854.50	100.00%	4	4	4	0.03%	10.60%	ISGLGLTPEEK	3.22	1,143.63
ATP	6018	PREDICTED: similar to programmed cell death 8 isoform 2	gi|76658657	66,854.50	100.00%	4	4	4	0.03%	10.60%	KVETDHIVAAVGLEPNVELAK	2.74	2,232.22
ATP	6018	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	7	9	13	0.11%	18.80%	FAIQTDPNSNDGLVTVVKPIDFETNR	3.08	2,890.46

ATP	6018	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	7	9	13	0.11%	18.80%	FLEAGIYEVPIIITDSGNPPK	4.08	2,273.21
ATP	6018	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	7	9	13	0.11%	18.80%	QLLIDPEDDVRDNILK	2.18	1,896.01
ATP	6018	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	7	9	13	0.11%	18.80%	RLDERPIHAEPQYPVR	2.47	1,976.05

ATP	6018	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	7	9	13	0.11%	18.80%	SAAPHPGDIGDFINEGLK	5.3	1,837.91
ATP	6018	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	7	9	13	0.11%	18.80%	YDEEGGGEEDQDYDLSQLQQPDTVEPDAIKPVGIR	5.21	3,905.78
ATP	6018	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD325; Flags: Precursor	gi|115421,gi|194678068,gi|664894	96,830.40	100.00%	7	9	13	0.11%	18.80%	YSVTGPGADQPPTGIFIINPISGQLSVTKPLDR	4.91	3,438.83
ATP	6018	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	99.80%	2	2	10	0.09%	35.20%	ELAEAQEDTILK	4.34	1,359.70
ATP	6018	F1-F0-ATPase	gi|162701,gi|231615,gi|28603752,gi|74268301	8,303.10	99.80%	2	2	10	0.09%	35.20%	YSALFLGMAYGAK	4.08	1,407.70

ATP	6018	PREDICTED: similar to ATP-binding cassette, sub-family B, member 7	gi|194680502	83,040.70	100.00%	4	4	5	0.04%	13.30%	ADNDAGNAAIDSLLNYETVK	4.62	2,094.00
ATP	6018	PREDICTED: similar to ATP-binding cassette, sub-family B, member 7	gi|194680502	83,040.70	100.00%	4	4	5	0.04%	13.30%	AMASPLQITPQTATVAFDNVHFEYIEGQK	3.74	3,222.58
ATP	6018	PREDICTED: similar to ATP-binding cassette, sub-family B, member 7	gi|194680502	83,040.70	100.00%	4	4	5	0.04%	13.30%	AVGVVPQDAVLFHNTIYYNLLYGNISASPEEVYAVAK	5.39	4,025.07
ATP	6018	PREDICTED: similar to ATP-binding cassette, sub-family B, member 7	gi|194680502	83,040.70	100.00%	4	4	5	0.04%	13.30%	QALIDMNTLFTLLK	3.33	1,636.90
ATP	6018	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	17	0.15%	33.50%	FLESGGQDGAGDDDDLEDLEEAEEPDLEEDDDQKAVKDEL	5.23	4,394.84
ATP	6018	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	17	0.15%	33.50%	GNFDEALAAHK	3.47	1,172.57
ATP	6018	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	17	0.15%	33.50%	HNQLPLVIEFTEQTAPK	3.66	1,965.04
ATP	6018	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	17	0.15%	33.50%	ILEFFGLK	2.57	966.566
ATP	6018	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	17	0.15%	33.50%	LITLEEEMTK	2.8	1,222.62
ATP	6018	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	17	0.15%	33.50%	NFEEVAFDEKK	3.75	1,355.65
ATP	6018	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	17	0.15%	33.50%	QFLLAAEAIDDIPFGITSNSDVFSK	4.91	2,698.36
ATP	6018	P4HB protein	gi|148878430,gi|152941196	57,187.70	100.00%	11	14	17	0.15%	33.50%	THILLFLPK	2.58	1,081.68

ATP	6018	P4HB protein	gi|148878430,gi|15294196	57,187.70	100.00%	11	14	17	0.15%	33.50%	VDATEESDLAQQYGVR	4.28	1,780.83
ATP	6018	P4HB protein	gi|148878430,gi|15294196	57,187.70	100.00%	11	14	17	0.15%	33.50%	YKPESDELTAEK	4.44	1,409.68
ATP	6018	P4HB protein	gi|148878430,gi|15294196	57,187.70	100.00%	11	14	17	0.15%	33.50%	YQLDKDGVVLFK	3.53	1,424.78
ATP	6018	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	4	4	7	0.06%	24.80%	GAVGALLVYDIAK	4.1	1,289.75
ATP	6018	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	4	4	7	0.06%	24.80%	HLTYENVER	2.46	1,160.57
ATP	6018	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	4	4	7	0.06%	24.80%	NNLSFIETSALDSTNVEEAFK	3.95	2,329.12
ATP	6018	RecName: Full=Ras-related protein Rab-11B	gi|108860922,gi|75773827,gi|78369332	24,471.00	100.00%	4	4	7	0.06%	24.80%	VVLIGDSGVGK	3.29	1,043.61
ATP	6018	SEPT11 protein	gi|126010811,gi|126723403,gi|162416046	48,974.60	100.00%	3	3	4	0.03%	9.88%	AAAQLLQSQAQQSGAQQTK	5.8	1,957.01
ATP	6018	SEPT11 protein	gi|126010811,gi|126723403,gi|162416046	48,974.60	100.00%	3	3	4	0.03%	9.88%	FESDPATHNEPGVR	2.16	1,555.71
ATP	6018	SEPT11 protein	gi|126010811,gi|126723403,gi|162416046	48,974.60	100.00%	3	3	4	0.03%	9.88%	VNIIPIIAK	2.45	980.6504
ATP	6018	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	4	4	4	0.03%	15.00%	IPDEFDNDPILVQQLR	4.44	1,911.98
ATP	6018	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	4	4	4	0.03%	15.00%	QNLFFSSLTSR	2.47	1,299.67
ATP	6018	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	4	4	4	0.03%	15.00%	TVLEHYALEEDPLEAFK	2.58	2,004.00

ATP	6018	translocase of inner mitochondrial membrane 50 homolog	gi|110665640,gi|74268127,gi|78042512,gi|83305921	40,747.80	100.00%	4	4	4	0.03%	15.00%	VLLDLSAFLK	3.03	1,118.68
ATP	6018	PREDICTED: ATP-binding cassette, sub-family B (MDR/TAP), member 1	gi|194685301	144,522.00	100.00%	5	6	6	0.05%	6.31%	GNELELENTPGESLSK	4.44	1,716.83
ATP	6018	PREDICTED: ATP-binding cassette, sub-family B (MDR/TAP), member 1	gi|194685301	144,522.00	100.00%	5	6	6	0.05%	6.31%	ILLLDEATSALDTESEAVVQAALDK	5.05	2,615.37
ATP	6018	PREDICTED: ATP-binding cassette, sub-family B (MDR/TAP), member 1	gi|194685301	144,522.00	100.00%	5	6	6	0.05%	6.31%	LPNKFDTLVGER	2.61	1,388.75
ATP	6018	PREDICTED: ATP-binding cassette, sub-family B (MDR/TAP), member 1	gi|194685301	144,522.00	100.00%	5	6	6	0.05%	6.31%	LYDPTEGMVSIDGQDIR	3.41	1,924.90
ATP	6018	PREDICTED: ATP-binding cassette, sub-family B (MDR/TAP), member 1	gi|194685301	144,522.00	100.00%	5	6	6	0.05%	6.31%	YGREDVTMDEIQK	3.36	1,599.73
ATP	6018	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	6	6	7	0.06%	9.44%	GLGYAQYLPR	3.16	1,137.61

ATP	6018	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	6	6	7	0.06%	9.44%	GMGGLFSVGETTAK	3.45	1,370.66
ATP	6018	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	6	6	7	0.06%	9.44%	NLETLQQELGIEGENR	3.47	1,842.92
ATP	6018	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	6	6	7	0.06%	9.44%	VGQISFDLPR	3.31	1,131.62
ATP	6018	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	6	6	7	0.06%	9.44%	VSEEIFFGR	3.13	1,083.55
ATP	6018	AFG3 ATPase family gene 3-like 2	gi|114051125,gi|118572819,gi|86820707	89,372.80	100.00%	6	6	7	0.06%	9.44%	VTQSAYAQIVQFGMNEK	3.79	1,929.94
ATP	6018	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	3	3	5	0.04%	28.30%	NYQEYSLANIIYYSLK	4.42	1,981.99
ATP	6018	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	3	3	5	0.04%	28.30%	RPPTFGDASVIALELLNSGYEFDEGSIIFNR	4.31	3,427.72
ATP	6018	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	gi|115495411,gi|158428988,gi|158428995,gi|158429005,gi|158429012,gi|158429019,gi|158429026,gi|158431072,gi|543874,gi|74268047	30,124.50	100.00%	3	3	5	0.04%	28.30%	TEEKPIFSLDTISSAESMSIYDDIDADVLR	7.18	3,376.60
ATP	6018	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	3	4	6	0.05%	18.60%	QMEQISQFLQAAER	3.74	1,694.82

ATP	6018	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	3	4	6	0.05%	18.60%	TLMNLGGLAVAR	4.02	1,231.68
ATP	6018	transgelin 2	gi|59858295,gi|61888874,gi|73919851	22,408.90	100.00%	3	4	6	0.05%	18.60%	YFSDNQLQEGK	3.16	1,328.61
ATP	6018	PREDICTED: similar to Heparan sulfate 2-O-sulfotransferase 1 (2-O-sulfotransferase) (2OST), partial	gi|119889909	37,063.70	100.00%	3	3	4	0.03%	12.10%	EKDGDLYILAQNFFYEK	4.12	2,093.02
ATP	6018	PREDICTED: similar to Heparan sulfate 2-O-sulfotransferase 1 (2-O-sulfotransferase) (2OST), partial	gi|119889909	37,063.70	100.00%	3	3	4	0.03%	12.10%	LVSYYYFLR	2.97	1,223.65
ATP	6018	PREDICTED: similar to Heparan sulfate 2-O-sulfotransferase 1 (2-O-sulfotransferase) (2OST), partial	gi|119889909	37,063.70	100.00%	3	3	4	0.03%	12.10%	NNPVMSLQDQVR	3.53	1,416.69
ATP	6018	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	5	5	7	0.06%	7.28%	IMKVEYHLLSPYVSPR	3.75	1,948.04
ATP	6018	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	5	5	7	0.06%	7.28%	LAADEEENVDSNMR	3.93	1,608.68
ATP	6018	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	5	5	7	0.06%	7.28%	SSVGTSLLLTLAR	3	1,317.77

ATP	6018	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	5	5	7	0.06%	7.28%	VEYHLLSPYVSPR	3	1,559.82
ATP	6018	PREDICTED: similar to transferrin receptor	gi|119879652	85,420.40	100.00%	5	5	7	0.06%	7.28%	VSASPLLYSLIEK	2.66	1,419.81
ATP	6018	Leucine rich repeat containing 8 family, member A	gi|115304767,gi|116003833	93,997.70	100.00%	4	4	4	0.03%	8.64%	ALSETVVEESDPKPAFSK	2.65	1,933.98
ATP	6018	Leucine rich repeat containing 8 family, member A	gi|115304767,gi|116003833	93,997.70	100.00%	4	4	4	0.03%	8.64%	IEAPALAFLR	2.33	1,100.65
ATP	6018	Leucine rich repeat containing 8 family, member A	gi|115304767,gi|116003833	93,997.70	100.00%	4	4	4	0.03%	8.64%	MANLTELELIR	3.33	1,318.70
ATP	6018	Leucine rich repeat containing 8 family, member A	gi|115304767,gi|116003833	93,997.70	100.00%	4	4	4	0.03%	8.64%	YLDLSHNNLTFLPADIGLLQSLQNLAVTANR	2.93	3,424.82
ATP	6018	TM9SF1 protein	gi|134025888,gi|139949144,gi|162416063	69,145.70	99.90%	2	2	2	0.02%	3.47%	SLSLGEVLDGDR	3.22	1,260.64
ATP	6018	TM9SF1 protein	gi|134025888,gi|139949144,gi|162416063	69,145.70	99.90%	2	2	2	0.02%	3.47%	SLSLGEVLDGDRMAESLYEIR	4.88	2,369.17
ATP	6018	Caveolin 2	gi|157279219,gi|38322700,gi|51512145,gi|56119130,gi|66774044	18,142.30	100.00%	3	3	6	0.05%	27.20%	ADVQLFMDDDSYSR	3.23	1,677.71
ATP	6018	Caveolin 2	gi|157279219,gi|38322700,gi|51512145,gi|56119130,gi|66774044	18,142.30	100.00%	3	3	6	0.05%	27.20%	SFSSVSLQLSHD	3.18	1,306.63

ATP	6018	Caveolin 2	gi|157279219,gi|38322700,gi|51512145,gi|56119130,gi|66774044	18,142.30	100.00%	3	3	6	0.05%	27.20%	VGFEDVIAEPVSTHSFDK	2.93	1,976.96
ATP	6018	solute carrier family 29 (nucleoside transporters), member 1	gi|110331885,gi|73587285,gi|77735743	49,866.60	99.80%	2	3	3	0.03%	6.80%	DIQASASPLAPSPER	3.72	1,538.78
ATP	6018	solute carrier family 29 (nucleoside transporters), member 1	gi|110331885,gi|73587285,gi|77735743	49,866.60	99.80%	2	3	3	0.03%	6.80%	LEGPGEQTKLDLISK	4.15	1,756.93
ATP	6018	calcium binding protein P22	gi|115497570,gi|122142989,gi|152941188,gi|74354201	22,425.20	100.00%	3	3	3	0.03%	16.40%	ASTLLRDEELEEIKK	3.45	1,773.96
ATP	6018	calcium binding protein P22	gi|115497570,gi|122142989,gi|152941188,gi|74354201	22,425.20	100.00%	3	3	3	0.03%	16.40%	EDFQRIPELAINPLGDR	4.51	1,983.03
ATP	6018	calcium binding protein P22	gi|115497570,gi|122142989,gi|152941188,gi|74354201	22,425.20	100.00%	3	3	3	0.03%	16.40%	IPELAINPLGDR	3.58	1,307.73
ATP	6018	ACTN4 protein	gi|146186472,gi|148238040,gi|162416099	104,913.30	100.00%	9	10	11	0.09%	16.50%	ETTDTDTADQVIASFK	3.46	1,741.81
ATP	6018	ACTN4 protein	gi|146186472,gi|148238040,gi|162416099	104,913.30	100.00%	9	10	11	0.09%	16.50%	FAIQDISVEETSAK	3.91	1,537.77
ATP	6018	ACTN4 protein	gi|146186472,gi|148238040,gi|162416099	104,913.30	100.00%	9	10	11	0.09%	16.50%	KDDPVTNLNNAFEVAEK	3.86	1,903.94
ATP	6018	ACTN4 protein	gi|146186472,gi|148238040,gi|162416099	104,913.30	100.00%	9	10	11	0.09%	16.50%	LSNRPAFMPSEGK	3.44	1,449.72
ATP	6018	ACTN4 protein	gi|146186472,gi|148238040,gi|162416099	104,913.30	100.00%	9	10	11	0.09%	16.50%	MAPYQGPDAVPGALDYK	2.93	1,808.85
ATP	6018	ACTN4 protein	gi|146186472,gi|148238040,gi|162416099	104,913.30	100.00%	9	10	11	0.09%	16.50%	MLDAEDIVNTARPDEK	4.32	1,832.87

ATP	6018	ACTN4 protein	gi|146186472,gi|148238040,gi|162416099	104,913.30	100.00%	9	10	11	0.09%	16.50%	SIVDYKPNLDLLEQQHQLIQEALIFDNK	5.14	3,324.75
ATP	6018	ACTN4 protein	gi|146186472,gi|148238040,gi|162416099	104,913.30	100.00%	9	10	11	0.09%	16.50%	TINEVENQILTR	2.69	1,429.76
ATP	6018	ACTN4 protein	gi|146186472,gi|148238040,gi|162416099	104,913.30	100.00%	9	10	11	0.09%	16.50%	VLAVNQENEHLMEDYER	2.24	2,104.96
ATP	6018	Chromosome 9 open reading frame 46 ortholog	gi|74354529,gi|77735799	17,091.30	99.80%	2	3	4	0.03%	15.60%	GMITFESLEK	3.12	1,170.57
ATP	6018	Chromosome 9 open reading frame 46 ortholog	gi|74354529,gi|77735799	17,091.30	99.80%	2	3	4	0.03%	15.60%	MKGEAENILETEK	4.2	1,507.73
ATP	6018	STAT1 protein	gi|154426144	86,914.50	99.80%	2	2	2	0.02%	3.35%	ELSAVTFPDIIR	2.77	1,360.75
ATP	6018	STAT1 protein	gi|154426144	86,914.50	99.80%	2	2	2	0.02%	3.35%	VMAAENIPENPLK	3.84	1,441.74
ATP	6018	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	99.80%	2	2	3	0.03%	21.90%	DYLALNEDLR	3.09	1,221.61
ATP	6018	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	99.80%	2	2	3	0.03%	21.90%	NGEDQTQDMELVETRPSGDGTFQK	3.05	2,698.19
ATP	6018	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	99.80%	2	2	3	0.03%	21.90%	SWTAADTAAQITK	4.15	1,363.69
ATP	6018	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	99.80%	2	2	3	0.03%	21.90%	VQHEGLQEPLTLR	3.86	1,519.82
ATP	6018	non-classical MHC class I antigen	gi|157785629,gi|83638606	38,884.20	99.80%	2	2	3	0.03%	21.90%	YFLTAVSRPGLGEPR	3.3	1,662.90
ATP	6018	LOC539976 protein	gi|133778097,gi|157074098	83,155.80	99.80%	2	2	2	0.02%	4.62%	AVGFSSGTENPHGVK	2.67	1,486.73
ATP	6018	LOC539976 protein	gi|133778097,gi|157074098	83,155.80	99.80%	2	2	2	0.02%	4.62%	LYSEEQPQEAVPHLEAALR	2.74	2,180.10
ATP	6018	v-ral simian leukemia viral oncogene homolog B	gi|146231722,gi|147900776,gi|148878477	23,421.00	99.80%	2	3	3	0.03%	13.60%	AEEDKIPLLVVGNK	3.38	1,524.86

ATP	6018	v-ral simian leukemia viral oncogene homolog B	gi|146231722,gi|147900776,gi|148878477	23,421.00	99.80%	2	3	3	0.03%	13.60%	ANVDKVFFDLMR	4.05	1,470.74
ATP	6018	v-ral simian leukemia viral oncogene homolog B	gi|146231722,gi|147900776,gi|148878477	23,421.00	99.80%	2	3	3	0.03%	13.60%	VFFDLMR	2.1	943.4707
ATP	6018	v-ral simian leukemia viral oncogene homolog B	gi|146231722,gi|147900776,gi|148878477	23,421.00	99.80%	2	3	3	0.03%	13.60%	VKAEEDKIPLLVVGNK	2.9	1,752.03
ATP	6018	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	6	6	8	0.07%	21.00%	DTILQLNLK	2.48	1,057.63

ATP	6018	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	6	6	8	0.07%	21.00%	IATSGYLPTQQDVLR	4.11	1,661.89
ATP	6018	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	6	6	8	0.07%	21.00%	ILHSHLVDYFPEFDGPQR	4.19	2,170.07

ATP	6018	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	6	6	8	0.07%	21.00%	LLLLGTGESGK	3.11	1,087.64
ATP	6018	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	6	6	8	0.07%	21.00%	VPTTGIIEYPFDLENIIFR	4.9	2,237.19

ATP	6018	RecName: Full=Guanine nucleotide-binding protein subunit alpha-11; Short=G-protein subunit alpha-11; Short=G alpha-11; AltName: Full=G-protein subunit GL2 alpha	gi|1169852,gi|133777482,gi|217568,gi|27805795	41,360.90	100.00%	6	6	8	0.07%	21.00%	VRVPTTGIIEYPFDLENIIFR	4.97	2,492.36
ATP	6018	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	3	4	5	0.04%	26.40%	IALMPLLQAEK	2.39	1,242.71
ATP	6018	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	3	4	5	0.04%	26.40%	LQIEDFEAR	2.81	1,120.56
ATP	6018	mitochondrial NADH:ubiquinone oxidoreductase B16.6 subunit	gi|15864616,gi|20139062,gi|28603804,gi|74268330	16,655.90	100.00%	3	4	5	0.04%	26.40%	VKQDMPPVGGYGPIDYKR	4.75	2,036.03
ATP	6018	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	gi|111307057,gi|115432055,gi|2852383,gi|71153774	28,065.10	99.80%	2	3	3	0.03%	19.90%	QTTVSNSQQAYQEAFEISKK	3.21	2,287.12

ATP	6018	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	gi|111307057,gi|115432055,gi|2852383,gi|71153774	28,065.10	99.80%	2	3	3	0.03%	19.90%	TAFDEAIAELDTLNEESYKDSTLIMQLLR	5.49	3,345.64
ATP	6018	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	5	6	8	0.07%	21.80%	FFVVSSESR	3.14	1,057.53
ATP	6018	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	5	6	8	0.07%	21.80%	RKPDEVLDDEDIGSAPLK	5.15	1,997.02
ATP	6018	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	5	6	8	0.07%	21.80%	TELHIPNVDLK	2.81	1,278.71
ATP	6018	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	5	6	8	0.07%	21.80%	VLKEDALPDLK	2.9	1,240.72
ATP	6018	basigin	gi|115496127,gi|120419551,gi|154425710,gi|156713141,gi|73587049	29,754.80	100.00%	5	6	8	0.07%	21.80%	VLKEDALPDLKTEYEVDSEDR	5.68	2,464.21
ATP	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	14	15	26	0.22%	40.20%	ALTVPELTQQMFDAK	3.29	1,707.86
ATP	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	14	15	26	0.22%	40.20%	AVLVDLEPGTMDSVR	3.37	1,617.82
ATP	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	14	15	26	0.22%	40.20%	FPGQLNADLR	2.72	1,130.60
ATP	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	14	15	26	0.22%	40.20%	FPGQLNADLRK	2.7	1,258.69
ATP	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	14	15	26	0.22%	40.20%	GHYTEGAELVDSVLDVVR	4.05	1,958.98
ATP	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	14	15	26	0.22%	40.20%	GHYTEGAELVDSVLDVVRK	4.32	2,087.08
ATP	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	14	15	26	0.22%	40.20%	IMNTFSVVPSPK	3.92	1,335.70

ATP	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	14	15	26	0.22%	40.20%	IREEYPDRIMNTFSVVPSPK	2.87	2,394.21
ATP	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	14	15	26	0.22%	40.20%	ISEQFTAMFR	2.79	1,245.59
ATP	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	14	15	26	0.22%	40.20%	LAVNMVPFPR	4.05	1,159.63
ATP	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	14	15	26	0.22%	40.20%	LHFFMPGFAPLTSR	3.36	1,636.83
ATP	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	14	15	26	0.22%	40.20%	MSATFIGNSTAIQELFK	4.88	1,873.94
ATP	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	14	15	26	0.22%	40.20%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	4.3	4,479.06
ATP	6018	Tubulin, beta 2C	gi|75773583,gi|77736271	49,812.70	100.00%	14	15	26	0.22%	40.20%	YLTVAAVFR	2.97	1,039.59
ATP	6018	RecName: Full=Peptidyl-prolyl cis-trans isomerase B; Short=PPIase; Short=Rotamase; AltName: Full=Cyclophilin B; AltName: Full=S-cyclophilin; Short=SCYLP; Flags: Precursor	gi|215274238,gi|27806469,gi|529242,gi|59858297,gi|74268324	23,726.00	100.00%	2	2	4	0.03%	12.50%	TVDNFVALATGEK	4.06	1,364.71

ATP	6018	RecName: Full=Peptidyl-prolyl cis-trans isomerase B; Short=PPIase; Short=Rotamase; AltName: Full=Cyclophilin B; AltName: Full=S-cyclophilin; Short=SCYLP; Flags: Precursor	gi|215274238,gi|27806469,gi|529242,gi|59858297,gi|74268324	23,726.00	100.00%	2	2	4	0.03%	12.50%	VIKDFMIQGGDFTR	3.51	1,642.83
ATP	6018	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	8	9	10	0.09%	25.70%	DVYDKVDYLSSLGK	3.76	1,601.81
ATP	6018	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	8	9	10	0.09%	25.70%	LLAELPASVHALTGVDLSK	4.16	1,934.10
ATP	6018	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	8	9	10	0.09%	25.70%	MALVLDALPR	3.7	1,114.63
ATP	6018	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	8	9	10	0.09%	25.70%	NVVLQTLEGHLR	2.11	1,378.78
ATP	6018	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	8	9	10	0.09%	25.70%	QVLLAQAEAEK	3.05	1,199.66
ATP	6018	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	8	9	10	0.09%	25.70%	SILGTLTVEQIYQDRDQFAK	2.85	2,325.21
ATP	6018	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	8	9	10	0.09%	25.70%	TAEAQLAYELQGAR	3.06	1,520.77
ATP	6018	FLOT2 protein	gi|151553623,gi|164452939	46,976.90	100.00%	8	9	10	0.09%	25.70%	TDKELIATVR	2.43	1,145.65
ATP	6018	RecName: Full=GPI transamidase component PIG-S; AltName: Full=Phosphatidylinositol-glycan biosynthesis class S protein	gi|116248578,gi|74268100,gi|77735383	61,769.20	100.00%	3	4	4	0.03%	11.90%	APLPYSQISGLNSLK	4.2	1,587.87

ATP	6018	RecName: Full=GPI transamidase component PIG-S; AltName: Full=Phosphatidylinositol-glycan biosynthesis class S protein	gi|116248578,gi|74268100,gi|77735383	61,769.20	100.00%	3	4	4	0.03%	11.90%	LMVPVTVVFTQESVPLDDQEKLPFTVVHER	3.82	3,468.81
ATP	6018	RecName: Full=GPI transamidase component PIG-S; AltName: Full=Phosphatidylinositol-glycan biosynthesis class S protein	gi|116248578,gi|74268100,gi|77735383	61,769.20	100.00%	3	4	4	0.03%	11.90%	SVENLATATTTLTSLAQLLGK	4.62	2,132.18
ATP	6018	PREDICTED: similar to ADAM metallopeptidase domain 17 isoform 1	gi|76630298	92,981.40	99.80%	2	2	2	0.02%	5.09%	GYGIQIEQIR	3.57	1,176.64
ATP	6018	PREDICTED: similar to ADAM metallopeptidase domain 17 isoform 1	gi|76630298	92,981.40	99.80%	2	2	2	0.02%	5.09%	MDTIQEDPSTDSHADEDGFEKDPFPNSSAAAK	2.6	3,468.47
ATP	6018	PREDICTED: similar to Solute carrier family 12 member 7 (Electroneutral potassium-chloride cotransporter 4) (K-Cl cotransporter 4)	gi|194676429	128,599.80	99.80%	2	2	2	0.02%	2.61%	DLQTFLYHLR	2.89	1,305.70

ATP	6018	PREDICTED: similar to Solute carrier family 12 member 7 (Electroneutral potassium-chloride cotransporter 4) (K-Cl cotransporter 4)	gi|194676429	128,599.80	99.80%	2	2	2	0.02%	2.61%	LANYTNLSQGVVEHEEAEDSR	4.05	2,361.10
ATP	6018	YWHAG protein	gi|157279400,gi|157744500,gi|2852385,gi|71153781	28,235.10	99.80%	2	2	2	0.02%	17.40%	NVTELNEPLSNEER	4	1,643.79
ATP	6018	YWHAG protein	gi|157279400,gi|157744500,gi|2852385,gi|71153781	28,235.10	99.80%	2	2	2	0.02%	17.40%	TAFDDAIAELDTLNEDSYKDSTLIMQLLR	4.23	3,317.61
ATP	6018	Chain C, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591028,gi|110591031,gi|114687,gi|163036,gi|27807291,gi|55670489,gi|73586602	12,514.70	99.80%	2	2	2	0.02%	43.50%	ADMNTFPNFTFEDPKFEVVEKPQS	3.01	2,833.30
ATP	6018	Chain C, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591028,gi|110591031,gi|114687,gi|163036,gi|27807291,gi|55670489,gi|73586602	12,514.70	99.80%	2	2	2	0.02%	43.50%	QTSGGPVDAGPEYQQDLDRELFK	3.52	2,550.21
ATP	6018	heterogeneous nuclear ribonucleoprotein A2/B1	gi|114051756,gi|122145945,gi|87578315	35,988.50	99.80%	2	3	3	0.03%	13.20%	GFGFVTFDDHDPVDKIVLQK	2.67	2,277.16
ATP	6018	heterogeneous nuclear ribonucleoprotein A2/B1	gi|114051756,gi|122145945,gi|87578315	35,988.50	99.80%	2	3	3	0.03%	13.20%	NMGGPYGGGNYGPGGSGGSGGYGGR	4.58	2,205.90

ATP	6018	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	7	10	11	0.09%	7.24%	AFMTADLPNELIELLEK	2.78	1,963.01
ATP	6018	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	7	10	11	0.09%	7.24%	ISGETIFVTAPHEATAGIIGVNR	3.77	2,353.25
ATP	6018	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	7	10	11	0.09%	7.24%	KFDVNTSAVQVLIEHIGNLDR	5.41	2,368.26
ATP	6018	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	7	10	11	0.09%	7.24%	NNLAGAEELFAR	3.42	1,304.66
ATP	6018	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	7	10	11	0.09%	7.24%	RPISADSAIMNPASK	3.44	1,573.80

ATP	6018	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	7	10	11	0.09%	7.24%	SVNESLNNLFITEEDYQALR	4.64	2,355.15
ATP	6018	RecName: Full=Clathrin heavy chain 1	gi|1705915,gi|27806689,gi|56554548,gi|56554549,gi|56554550,gi|56554551,gi|56554552,gi|56554553,gi|56554554,gi|56554555,gi|56554556	186,919.60	100.00%	7	10	11	0.09%	7.24%	TLQIFNIEMK	2.49	1,252.66
ATP	6018	PREDICTED: similar to Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase 4) (CCK-4) isoform 2	gi|119915291	126,668.70	99.80%	2	2	2	0.02%	2.52%	HPASEAAIQPLTQVTLR	3.51	1,832.00
ATP	6018	PREDICTED: similar to Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase 4) (CCK-4) isoform 2	gi|119915291	126,668.70	99.80%	2	2	2	0.02%	2.52%	VVLAPQDVVVAR	2.51	1,265.76
ATP	6018	coiled-coil domain containing 47	gi|146231852,gi|73586661,gi|78369308,gi|97045772	55,725.10	100.00%	3	3	3	0.03%	10.60%	ELLESNFTLVGDDGTNKEATSTGK	3.39	2,526.22
ATP	6018	coiled-coil domain containing 47	gi|146231852,gi|73586661,gi|78369308,gi|97045772	55,725.10	100.00%	3	3	3	0.03%	10.60%	RQDLLNVLAR	3.05	1,197.71

ATP	6018	coiled-coil domain containing 47	gi|146231852,gi|73586661,gi|78369308,gi|97045772	55,725.10	100.00%	3	3	3	0.03%	10.60%	TLLFTFNVPGSGNTYPK	2.26	1,855.96
ATP	6018	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	4	5	6	0.05%	14.20%	FDAVIGYK	2.54	912.4826
ATP	6018	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	4	5	6	0.05%	14.20%	KSVTGEIVLITGAGHGIGR	3.61	1,865.06
ATP	6018	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	4	5	6	0.05%	14.20%	NPSTSLGPTLEPEEVVNK	5.22	1,910.97
ATP	6018	hydroxysteroid (17-beta) dehydrogenase 11	gi|114052807,gi|86438493	35,077.20	100.00%	4	5	6	0.05%	14.20%	SVTGEIVLITGAGHGIGR	4.69	1,736.97
ATP	6018	pre-B-cell leukemia transcription factor interacting protein 1	gi|110331795,gi|115497324,gi|151554897,gi|158706093	80,239.50	99.80%	2	2	2	0.02%	3.85%	ALESELQQLR	3.15	1,186.64
ATP	6018	pre-B-cell leukemia transcription factor interacting protein 1	gi|110331795,gi|115497324,gi|151554897,gi|158706093	80,239.50	99.80%	2	2	2	0.02%	3.85%	LLQAQLQAQKEELQSLMR	3.69	2,143.15
ATP	6018	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	4	4	4	0.03%	24.70%	AELNEFLTR	2.75	1,092.57
ATP	6018	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	4	4	4	0.03%	24.70%	DEILPTTPISEQK	3.46	1,470.77
ATP	6018	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	4	4	4	0.03%	24.70%	FVDGLMIHSGDPVNYYVDTAVR	5.3	2,484.19
ATP	6018	Ribosomal protein S3	gi|74268226,gi|77404290,gi|91207641	26,670.50	100.00%	4	4	4	0.03%	24.70%	GGKPEPPAMPQPVPTA	2.97	1,589.80
ATP	6018	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	8	8	0.07%	15.60%	ADDKLIAEEGVDSLNVK	3.59	1,815.93

ATP	6018	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	8	8	0.07%	15.60%	AMYLPETLSPADQLK	3.54	1,692.85
ATP	6018	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	8	8	0.07%	15.60%	FLQDTIEEMALK	3.46	1,453.72
ATP	6018	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	8	8	0.07%	15.60%	IRETGERPSNEEIMR	2.06	1,832.89
ATP	6018	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	8	8	0.07%	15.60%	KLEEGGPVYSPPAQAAVR	3.17	1,868.99
ATP	6018	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	8	8	0.07%	15.60%	LLELQSIGTNNFLR	4.33	1,617.90
ATP	6018	Leucine zipper-EF-hand containing transmembrane protein 1	gi|111308604,gi|115497920	81,801.70	100.00%	7	8	8	0.07%	15.60%	LLSLASALDDNKDGKVDIDDLVK	1.97	2,457.31
ATP	6018	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	8	9	47	0.40%	37.80%	LTFDSSFSPNTGK	3.91	1,400.67
ATP	6018	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	8	9	47	0.40%	37.80%	LTFDSSFSPNTGKK	3.67	1,528.76
ATP	6018	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	8	9	47	0.40%	37.80%	LTLSALLDGK	3.89	1,030.61
ATP	6018	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	8	9	47	0.40%	37.80%	LTLSALLDGKNVNAGGHK	3.17	1,808.00
ATP	6018	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	8	9	47	0.40%	37.80%	TDEFQLHTNVNDGTEFGGSIYQK	5.53	2,600.19

ATP	6018	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	8	9	47	0.40%	37.80%	TKSENGLEFTSSGSANTETTK	4.67	2,189.02
ATP	6018	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	8	9	47	0.40%	37.80%	VNNSSLIGLGYTQTLKPGIK	5.28	2,103.18
ATP	6018	voltage-dependent anion channel 1	gi|8810220,gi|90111863	30,723.80	100.00%	8	9	47	0.40%	37.80%	VTQSNFAVGYK	3.83	1,213.62
ATP	6018	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	7	8	24	0.21%	29.60%	GFGFGLVK	1.99	824.4666
ATP	6018	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	7	8	24	0.21%	29.60%	LTFDTTFSPNTGK	3.83	1,428.70
ATP	6018	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	7	8	24	0.21%	29.60%	LTFDTTFSPNTGKK	3.74	1,556.80
ATP	6018	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	7	8	24	0.21%	29.60%	LTLSALVDGK	3.39	1,016.60
ATP	6018	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	7	8	24	0.21%	29.60%	TGDFQLHTNVNDGTEFGGSIYQK	5.61	2,528.17
ATP	6018	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	7	8	24	0.21%	29.60%	VNNSSLIGVGYTQTLRPGVK	4.68	2,103.16
ATP	6018	voltage-dependent anion channel 2	gi|59858401,gi|62177148,gi|73586695,gi|8574295,gi|8810222,gi|90111864	31,602.50	100.00%	7	8	24	0.21%	29.60%	YQLDPTASISAK	3.13	1,293.67
ATP	6018	Trx-like protein	gi|109726696,gi|115494922,gi|122145628,gi|126920889,gi|146231808	31,563.90	99.90%	2	2	2	0.02%	8.27%	LLPESSQPLKK	2.09	1,239.73

ATP	6018	Trx-like protein	gi|109726696,gi|115494922,gi|122145628,gi|126920889,gi|146231808	31,563.90	99.90%	2	2	2	0.02%	8.27%	VDVTEQPGLSGR	4.1	1,257.64
ATP	6018	endothelial cell-specific molecule 2	gi|114053335,gi|86438024	20,621.00	99.80%	2	3	6	0.05%	13.20%	ESEDPQKPGSSGLSESGSTANGEK	4.15	2,378.06
ATP	6018	endothelial cell-specific molecule 2	gi|114053335,gi|86438024	20,621.00	99.80%	2	3	6	0.05%	13.20%	NKESEDPQKPGSSGLSESGSTANGEK	3.52	2,620.20
ATP	6018	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	5	6	8	0.07%	7.45%	ANLINNIFELAGLGK	4.63	1,586.89
ATP	6018	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	5	6	8	0.07%	7.45%	GLGEHELDEDEEDYESSAK	4.99	2,151.88
ATP	6018	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	5	6	8	0.07%	7.45%	IFGELSSYEDFLDAR	3.23	1,761.83
ATP	6018	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	5	6	8	0.07%	7.45%	IKRDEQYTALSNMPK	4.19	1,809.92
ATP	6018	PREDICTED: similar to leucyl/cystinyl aminopeptidase	gi|119895933	119,380.70	100.00%	5	6	8	0.07%	7.45%	KYFAATQFEPLAAR	3.46	1,612.85
ATP	6018	PREDICTED: similar to Zinc finger protein basonuclin-1	gi|76647059	111,795.20	99.80%	2	2	2	0.02%	2.48%	IEKETMETADEKR	3.59	1,595.76
ATP	6018	PREDICTED: similar to Zinc finger protein basonuclin-1	gi|76647059	111,795.20	99.80%	2	2	2	0.02%	2.48%	VEPCVPFPDYIK	2.29	1,406.70

ATP	6018	CYB5B protein	gi|158455068,gi|76640228	26,782.70	99.80%	2	2	3	0.03%	22.40%	FLDEHPGGEEVLMEQAGGDATESFEDVGHSSDAR	4.18	3,634.55
ATP	6018	CYB5B protein	gi|158455068,gi|76640228	26,782.70	99.80%	2	2	3	0.03%	22.40%	QYYIGDVHPNDLKPGGGSK	2.66	2,045.01
ATP	6018	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	3	3	4	0.03%	16.20%	EQNGDSLVHAALVAESAAIGSAEANAFSVLQHVLGAGPHVK	3.46	4,065.08
ATP	6018	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	3	3	4	0.03%	16.20%	MALIGLGVSHPVLK	3.36	1,450.85
ATP	6018	Chain B, Crystal Structure Of Bovine Heart Mitochondrial Bc1 With Jg144 Inhibitor	gi|114793902,gi|27807143,gi|300,gi|401248,gi|59858351,gi|73586962,gi|82407277,gi|82407288	46,506.00	100.00%	3	3	4	0.03%	16.20%	TIAQGNLSNPDVQAAK	5.61	1,626.84
ATP	6018	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	gi|111308529,gi|128825,gi|163414,gi|27807355	79,425.10	100.00%	3	3	3	0.03%	6.19%	ILQDIASGSHPFSQVLQEAK	3.01	2,168.13

ATP	6018	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	gi|111308529,gi|128825,gi|163414,gi|27807355	79,425.10	100.00%	3	3	3	0.03%	6.19%	NRLEEVSPNLVR	2.8	1,425.78
ATP	6018	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	gi|111308529,gi|128825,gi|163414,gi|27807355	79,425.10	100.00%	3	3	3	0.03%	6.19%	VALIGSPVDLTYR	3.59	1,403.79
ATP	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	12	16	21	0.18%	41.00%	AQQVAVQEQEIAR	4.4	1,469.77
ATP	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	12	16	21	0.18%	41.00%	DIHDDQDYLHSLGK	3.42	1,655.77
ATP	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	12	16	21	0.18%	41.00%	ISLNTLTLNVK	3.43	1,215.73
ATP	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	12	16	21	0.18%	41.00%	ITLVSSGSGAMGAAK	4.59	1,365.70
ATP	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	12	16	21	0.18%	41.00%	KAEAFQLYQEAAQLDMLLEK	4.08	2,355.19
ATP	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	12	16	21	0.18%	41.00%	LPQVAEEISGPLTSANK	5.48	1,753.93
ATP	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	12	16	21	0.18%	41.00%	LTGVSISQVNHKPLR	2.6	1,648.95

ATP	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	12	16	21	0.18%	41.00%	MRGEAEAFAIGAR	2.62	1,394.68
ATP	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	12	16	21	0.18%	41.00%	SQLIMQAEAEAEAVR	5.1	1,661.82
ATP	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	12	16	21	0.18%	41.00%	TEAEIAHIALETLEGHQR	5.06	2,018.03
ATP	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	12	16	21	0.18%	41.00%	VSAQYLSEIEMAK	3.14	1,484.73
ATP	6018	Flotillin 1	gi|115305033,gi|116004001,gi|118572320,gi|75775078	47,334.80	100.00%	12	16	21	0.18%	41.00%	VTGEVLDILSR	3.24	1,201.68
ATP	6018	PREDICTED: similar to ribosomal protein S24	gi|119914811,gi|194677142,gi|58760477,gi|70778760,gi|74268388,gi|91207637	15,283.40	100.00%	3	3	4	0.03%	29.50%	KQMVIDVLHPGK	3.68	1,380.77
ATP	6018	PREDICTED: similar to ribosomal protein S24	gi|119914811,gi|194677142,gi|58760477,gi|70778760,gi|74268388,gi|91207637	15,283.40	100.00%	3	3	4	0.03%	29.50%	TTGFGMIYDSLDYAK	2.93	1,697.77
ATP	6018	PREDICTED: similar to ribosomal protein S24	gi|119914811,gi|194677142,gi|58760477,gi|70778760,gi|74268388,gi|91207637	15,283.40	100.00%	3	3	4	0.03%	29.50%	TTPDVIFVFGFR	2.54	1,398.74
ATP	6018	glutathione peroxidase 8	gi|114052907,gi|122143886,gi|84708688	23,965.80	99.80%	2	3	3	0.03%	11.00%	ILGSEAEPAFR	3.49	1,189.62
ATP	6018	glutathione peroxidase 8	gi|114052907,gi|122143886,gi|84708688	23,965.80	99.80%	2	3	3	0.03%	11.00%	NNFGVTFPIFHK	3.56	1,420.74

ATP	6018	PREDICTED: similar to Neuroblast differentiation-associated protein AHNAK (Desmoyokin), partial	gi|194687805	140,614.00	100.00%	4	4	4	0.03%	5.01%	FSMPGFKGEGPEVDVNLPK	3.05	2,064.01
ATP	6018	PREDICTED: similar to Neuroblast differentiation-associated protein AHNAK (Desmoyokin), partial	gi|194687805	140,614.00	100.00%	4	4	4	0.03%	5.01%	ISMPDVDLNLKGPK	2.87	1,542.82
ATP	6018	PREDICTED: similar to Neuroblast differentiation-associated protein AHNAK (Desmoyokin), partial	gi|194687805	140,614.00	100.00%	4	4	4	0.03%	5.01%	VDIEAPDVSLEGPEGK	2.89	1,654.82
ATP	6018	PREDICTED: similar to Neuroblast differentiation-associated protein AHNAK (Desmoyokin), partial	gi|194687805	140,614.00	100.00%	4	4	4	0.03%	5.01%	VDVEAPDVSLEGPEGK	3.19	1,640.80
ATP	6018	Tumor protein p53 inducible protein 11	gi|111304979,gi|115496424	20,907.40	99.80%	2	2	2	0.02%	13.80%	ISQVLGNEIK	2.99	1,100.63
ATP	6018	Tumor protein p53 inducible protein 11	gi|111304979,gi|115496424	20,907.40	99.80%	2	2	2	0.02%	13.80%	KILGVGGEDDDGEVHR	4.53	1,695.83
ATP	6018	ANXA6 protein	gi|154426044,gi|157151716,gi|160332337	75,893.80	99.80%	2	2	2	0.02%	4.75%	GLGTDEDTIIDIIAHR	2.05	1,738.90

ATP	6018	ANXA6 protein	gi|154426044,gi|157151716,gi|160332337	75,893.80	99.80%	2	2	2	0.02%	4.75%	GTVRPAGDFNPDADAK	3.03	1,630.78
ATP	6018	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|155155878,gi|155371877,gi|215275740	48,774.90	100.00%	9	10	22	0.19%	35.30%	GFVLTFK	2.08	811.4713
ATP	6018	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|155155878,gi|155371877,gi|215275740	48,774.90	100.00%	9	10	22	0.19%	35.30%	GVGMVADPDNPLVLDILTGSSTSYSFFPDKPITQYPHAVGK	5.36	4,350.16
ATP	6018	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|155155878,gi|155371877,gi|215275740	48,774.90	100.00%	9	10	22	0.19%	35.30%	LPDVYGVFQFK	3.79	1,312.69
ATP	6018	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|155155878,gi|155371877,gi|215275740	48,774.90	100.00%	9	10	22	0.19%	35.30%	SSLNPILFR	2.58	1,046.60
ATP	6018	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|155155878,gi|155371877,gi|215275740	48,774.90	100.00%	9	10	22	0.19%	35.30%	TADDPSLSLIK	2.82	1,159.62
ATP	6018	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|155155878,gi|155371877,gi|215275740	48,774.90	100.00%	9	10	22	0.19%	35.30%	TAVIDHHNYDVSDLGQHTLIVADTENLLK	6.9	3,231.63
ATP	6018	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|155155878,gi|155371877,gi|215275740	48,774.90	100.00%	9	10	22	0.19%	35.30%	TLVLLDNLNLR	4.29	1,283.77
ATP	6018	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|155155878,gi|155371877,gi|215275740	48,774.90	100.00%	9	10	22	0.19%	35.30%	VIFSGSLDFFSDAFFNSAVQK	2.94	2,326.14
ATP	6018	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gi|110665590,gi|155155878,gi|155371877,gi|215275740	48,774.90	100.00%	9	10	22	0.19%	35.30%	YSQTGNYELAVALSR	3.36	1,671.83
ATP	6018	reticulon 4 isoform 2	gi|164259354,gi|92096636	40,940.20	100.00%	3	4	6	0.05%	10.30%	GPLPAAPLAAPER	2.65	1,259.71

ATP	6018	reticulon 4 isoform 2	gi|164259354,gi|92096636	40,940.20	100.00%	3	4	6	0.05%	10.30%	HQAQIDHYLGLANK	4.4	1,607.83
ATP	6018	reticulon 4 isoform 2	gi|164259354,gi|92096636	40,940.20	100.00%	3	4	6	0.05%	10.30%	LFLVDDLVDSLK	3.6	1,376.77
ATP	6018	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	8	10	16	0.14%	21.80%	ALASILLQDHIR	3.51	1,349.79
ATP	6018	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	8	10	16	0.14%	21.80%	DQHSFELEEK	2.81	1,261.57
ATP	6018	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	8	10	16	0.14%	21.80%	EQLQTLILHVLNPANLMEK	3.05	2,220.21
ATP	6018	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	8	10	16	0.14%	21.80%	IYQGEDLPHPK	3.5	1,296.66
ATP	6018	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	8	10	16	0.14%	21.80%	LAMDEIFQKPFQTLMFLVR	4.36	2,343.22
ATP	6018	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	8	10	16	0.14%	21.80%	LKDIASEFKEQLQTLILHVLNPANLMEK	4.91	3,251.77
ATP	6018	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	8	10	16	0.14%	21.80%	SMLQATAEANNLAAAASAK	5.71	1,848.91
ATP	6018	ATL3 protein	gi|148745456,gi|154707918	60,294.70	100.00%	8	10	16	0.14%	21.80%	VAVVLMDTQGAFDSQSTVK	4.51	2,012.00
ATP	6018	RecName: Full=Glutathione S-transferase P; AltName: Full=GST class-pi	gi|121744,gi|29135329,gi|404,gi|74268086	23,595.90	100.00%	3	4	4	0.03%	24.30%	ALPQHLKPFETLLSQNK	2.55	1,964.10
ATP	6018	RecName: Full=Glutathione S-transferase P; AltName: Full=GST class-pi	gi|121744,gi|29135329,gi|404,gi|74268086	23,595.90	100.00%	3	4	4	0.03%	24.30%	FQDGDLTLYQSNAILR	3.17	1,853.94
ATP	6018	RecName: Full=Glutathione S-transferase P; AltName: Full=GST class-pi	gi|121744,gi|29135329,gi|404,gi|74268086	23,595.90	100.00%	3	4	4	0.03%	24.30%	YVSLIYTNYEAGKEDYVK	3.97	2,155.06

ATP	6018	Poliovirus receptor-related 2 (herpesvirus entry mediator B)	gi|109658349,gi|115497936	43,243.10	100.00%	3	3	3	0.03%	9.68%	ETQGSGPLPGTVTVTSR	3.5	1,686.87
ATP	6018	Poliovirus receptor-related 2 (herpesvirus entry mediator B)	gi|109658349,gi|115497936	43,243.10	100.00%	3	3	3	0.03%	9.68%	LLPVILSVR	1.88	1,009.68
ATP	6018	Poliovirus receptor-related 2 (herpesvirus entry mediator B)	gi|109658349,gi|115497936	43,243.10	100.00%	3	3	3	0.03%	9.68%	YTVTPLSEADGVK	2.85	1,379.71
ATP	6018	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	11	11	0.09%	20.30%	AAYEAELGDARK	3.28	1,293.64
ATP	6018	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	11	11	0.09%	20.30%	IRIDSLSAQLSQLQK	3.91	1,699.97
ATP	6018	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	11	11	0.09%	20.30%	LADALQELR	3.12	1,028.57
ATP	6018	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	11	11	0.09%	20.30%	LKDLEALLNSK	3.3	1,243.73
ATP	6018	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	11	11	0.09%	20.30%	LQEKEDLQELNDR	4.73	1,629.81
ATP	6018	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	11	11	0.09%	20.30%	LQTLKEELDFQK	2.42	1,491.81
ATP	6018	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	11	11	0.09%	20.30%	MQQQLDEYQELLDIK	3.68	1,909.92
ATP	6018	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	11	11	0.09%	20.30%	TALINSTGEEVAMRK	3.53	1,635.84
ATP	6018	Lamin A/C	gi|74354719,gi|77404182	65,105.20	100.00%	9	11	11	0.09%	20.30%	VAVEEVDEEGKFVR	3.61	1,605.81
ATP	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	15	27	0.23%	36.80%	AVAISLPK	2.03	798.5084

ATP	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	15	27	0.23%	36.80%	AVLSAEQLRDDEVHAGLGELLR	5.35	2,391.26
ATP	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	15	27	0.23%	36.80%	DQAVENILLSPVVVASSLGLVSLGGK	5.94	2,565.45
ATP	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	15	27	0.23%	36.80%	DTQSGSLLFIGR	2.86	1,293.68
ATP	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	15	27	0.23%	36.80%	GVVEVTHDLQK	3.94	1,224.66

ATP	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	15	27	0.23%	36.80%	HLAGLGLTEAIDKNK	5.36	1,579.88
ATP	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	15	27	0.23%	36.80%	KAVAISLPK	2.97	926.6034
ATP	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	15	27	0.23%	36.80%	LFYADHPFIFLVR	3.4	1,637.88
ATP	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	15	27	0.23%	36.80%	LSSLIIIMPHHVEPLER	3.21	2,000.10

ATP	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	15	27	0.23%	36.80%	LYGPSSVSFAEDFVR	4.34	1,673.82
ATP	6018	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	gi|114051505,gi|116256076,gi|86821084	46,490.00	100.00%	11	15	27	0.23%	36.80%	SAGLAFSLYQAMAK	3.88	1,473.74
ATP	6018	PREDICTED: hypothetical protein	gi|194667311	68,113.30	100.00%	5	8	8	0.07%	9.11%	ELESQISELQEDLESER	4.21	2,033.95
ATP	6018	PREDICTED: hypothetical protein	gi|194667311	68,113.30	100.00%	5	8	8	0.07%	9.11%	IRELESQISELQEDLESER	5.65	2,303.14
ATP	6018	PREDICTED: hypothetical protein	gi|194667311	68,113.30	100.00%	5	8	8	0.07%	9.11%	KLEGDSTDLNDQIAELQAQIAELK	5.35	2,642.35
ATP	6018	PREDICTED: hypothetical protein	gi|194667311	68,113.30	100.00%	5	8	8	0.07%	9.11%	RKLEGDSTDLNDQIAELQAQIAELK	3.81	2,798.45
ATP	6018	PREDICTED: hypothetical protein	gi|194667311	68,113.30	100.00%	5	8	8	0.07%	9.11%	XXXXXXXXXXX	3.4	1,240.02
ATP	6018	PREDICTED: transmembrane emp24 protein transport domain containing 4	gi|194666384	37,465.50	100.00%	3	4	4	0.03%	7.76%	DKLTELQLR	3.36	1,115.64

ATP	6018	PREDICTED: transmembrane emp24 protein transport domain containing 4	gi|194666384	37,465.50	100.00%	3	4	4	0.03%	7.76%	QLLDQVEQIQK	3.78	1,341.74
ATP	6018	PREDICTED: transmembrane emp24 protein transport domain containing 4	gi|194666384	37,465.50	100.00%	3	4	4	0.03%	7.76%	QLLDQVEQIQKEQDYQR	3.55	2,161.09
ATP	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	15	22	0.19%	14.70%	AVVLAANHFGR	2.36	1,154.64
ATP	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	15	22	0.19%	14.70%	DGQVIFPAPTPK	2.61	1,269.68
ATP	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	15	22	0.19%	14.70%	FFTGQITAAGK	3.18	1,140.60
ATP	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	15	22	0.19%	14.70%	GITHIGYTDLPSR	4.61	1,429.74
ATP	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	15	22	0.19%	14.70%	GTVVMKDGQVIFPAPTPK	3.24	1,901.02
ATP	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	15	22	0.19%	14.70%	MATQASTLYSNNITK	5.63	1,658.81
ATP	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	15	22	0.19%	14.70%	SLGAEPLEVDLK	3.26	1,270.69
ATP	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	15	22	0.19%	14.70%	SLGVGYAAVDNPIFYKPNTAMLLGDAK	2.99	2,841.45

ATP	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	15	22	0.19%	14.70%	TSGTLISFIYPAQNPDLLNK	3.2	2,192.16
ATP	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	15	22	0.19%	14.70%	VALSPAGVQALVK	3.59	1,252.76
ATP	6018	NNT protein	gi|133777477,gi|163397,gi|163410,gi|172045566,gi|27806831	113,839.20	100.00%	11	15	22	0.19%	14.70%	VTIAQGYDALSSMANIAGYK	5	2,089.03
ATP	6018	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	8	13	27	0.23%	29.70%	IPDQLVILDMK	4.3	1,300.72
ATP	6018	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	8	13	27	0.23%	29.70%	ITDSAGHILYSK	4.78	1,304.68
ATP	6018	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	8	13	27	0.23%	29.70%	ITDSAGHILYSKEDATK	3.58	1,848.93
ATP	6018	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	8	13	27	0.23%	29.70%	LEDLSESIVNDFAYMK	4.07	1,889.88
ATP	6018	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	8	13	27	0.23%	29.70%	LKPLEVELR	3.43	1,096.67
ATP	6018	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	8	13	27	0.23%	29.70%	NYEEIAKVEK	3.49	1,222.63

ATP	6018	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	8	13	27	0.23%	29.70%	RLEDLSESIVNDFAYMK	4.3	2,045.99
ATP	6018	Transmembrane emp24-like trafficking protein 10 (yeast)	gi|133778187,gi|59858463,gi|62901402,gi|94966895	24,810.80	100.00%	8	13	27	0.23%	29.70%	RLEDLSESIVNDFAYMKK	5.74	2,174.08
ATP	6018	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	100.00%	4	4	5	0.04%	10.00%	LIDGIVLTK	3.71	971.6138
ATP	6018	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	100.00%	4	4	5	0.04%	10.00%	LITVNTPDLVLFVGEALVGNEAVDQLVK	3.23	2,966.65
ATP	6018	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	100.00%	4	4	5	0.04%	10.00%	NQGFDVVLVDTAGR	4.64	1,490.76
ATP	6018	signal recognition particle receptor	gi|115497558,gi|122139924,gi|75773717	69,879.80	100.00%	4	4	5	0.04%	10.00%	VMGTFSTVTSTVK	2.86	1,373.70
ATP	6018	nitrogen fixation protein [Staphylococcus aureus RF122]	gi|82656058,gi|82750527	16,998.60	99.80%	2	2	2	0.02%	28.60%	EGKAEGTTEEE	2.16	1,179.50
ATP	6018	nitrogen fixation protein [Staphylococcus aureus RF122]	gi|82656058,gi|82750527	16,998.60	99.80%	2	2	2	0.02%	28.60%	GVLDNGSMTVDMNNPTCGDRIRLTFDIEDGIIK	3.03	3,609.74
ATP	6018	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	4	4	4	0.03%	5.34%	FLFLLLGPAGK	2.94	1,175.72
ATP	6018	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	4	4	4	0.03%	5.34%	GPDEEAVVDLGK	3.16	1,228.61

ATP	6018	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	4	4	4	0.03%	5.34%	LAPAVLLSGLTEVPVPTR	3.29	1,833.08
ATP	6018	solute carrier family 4, sodium bicarbonate cotransporter, member 7	gi|219282724	135,822.00	100.00%	4	4	4	0.03%	5.34%	MLQAGEDTVHLPFEGGSLLQIPVK	4	2,595.35
ATP	6018	Stromal interaction molecule 1	gi|154426132,gi|61555683,gi|75057528,gi|78369570	77,134.40	100.00%	3	3	3	0.03%	7.47%	ALDTVLFGPPLLTR	3.47	1,512.88
ATP	6018	Stromal interaction molecule 1	gi|154426132,gi|61555683,gi|75057528,gi|78369570	77,134.40	100.00%	3	3	3	0.03%	7.47%	DLTHSDSESSLHMSDR	3.09	1,832.77
ATP	6018	Stromal interaction molecule 1	gi|154426132,gi|61555683,gi|75057528,gi|78369570	77,134.40	100.00%	3	3	3	0.03%	7.47%	KAAAEEDNGSIGEETDSSPGR	4.03	2,119.94
ATP	6018	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	6	7	0.06%	27.20%	FSDLDSASVDSDMYDLPK	3.67	2,020.87
ATP	6018	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	6	7	0.06%	27.20%	FSDLDSASVDSDMYDLPKKEDALLYQSK	4.44	3,196.49
ATP	6018	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	6	7	0.06%	27.20%	GYNDDYYEESYLTTR	3.57	1,888.79
ATP	6018	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	6	7	0.06%	27.20%	LSPPSSSASSFSYR	2.25	1,472.70
ATP	6018	emerin	gi|37781186,gi|42733600,gi|74356375	29,454.80	100.00%	5	6	7	0.06%	27.20%	QYNIPHGPVVGSTR	2.84	1,524.79
ATP	6018	alpha S1 casein	gi|159793209,gi|195973860,gi|30794348	24,425.40	99.80%	2	2	2	0.02%	10.30%	FFVAPFPEVFGK	2.97	1,384.73
ATP	6018	alpha S1 casein	gi|159793209,gi|195973860,gi|30794348	24,425.40	99.80%	2	2	2	0.02%	10.30%	YLGYLEQLLR	2.99	1,267.70
ATP	6018	PREDICTED: nestin	gi|76612380	175,609.70	99.80%	2	2	2	0.02%	2.85%	GPPAPAPEVEELAQR	3.56	1,560.80

ATP	6018	PREDICTED: nestin	gi|76612380	175,609.70	99.80%	2	2	2	0.02%	2.85%	RPGPLLSVLSPTPLSSPLPGTLETPVPTFLK	2.84	3,211.83
ATP	6018	PREDICTED: similar to Rab5B isoform 3	gi|76618732	23,703.00	99.80%	2	2	2	0.02%	22.80%	LVLLGESAVGK	3.81	1,085.66
ATP	6018	PREDICTED: similar to Rab5B isoform 3	gi|76618732	23,703.00	99.80%	2	2	2	0.02%	22.80%	QASPSIVIALAGNK	2.99	1,368.78
ATP	6018	PREDICTED: similar to Rab5B isoform 3	gi|76618732	23,703.00	99.80%	2	2	2	0.02%	22.80%	TAMNVNDLFLAIAK	2.96	1,536.81
ATP	6018	PREDICTED: similar to Rab5B isoform 3	gi|76618732	23,703.00	99.80%	2	2	2	0.02%	22.80%	YHSLAPMYYR	2.6	1,316.61
ATP	6018	RAP2C, member of RAS oncogene family	gi|115305020,gi|115496672,gi|122132271	20,726.50	99.80%	2	2	2	0.02%	33.90%	EIEVDSSPSVLEILDTAGTEQFASMR	5.29	2,840.35
ATP	6018	RAP2C, member of RAS oncogene family	gi|115305020,gi|115496672,gi|122132271	20,726.50	99.80%	2	2	2	0.02%	33.90%	SMVDELFAEIVR	2.88	1,424.71
ATP	6018	RAP2C, member of RAS oncogene family	gi|115305020,gi|115496672,gi|122132271	20,726.50	99.80%	2	2	2	0.02%	33.90%	VPLILVGNKVDLEPEREVMSSEGR	3.51	2,682.41
ATP	6018	Lu-ECAM-1	gi|2623763,gi|2623765,gi|2623767,gi|30794326	100,991.10	100.00%	3	3	3	0.03%	4.53%	QESYDQADVIVANPYLK	4.39	1,952.96
ATP	6018	Lu-ECAM-1	gi|2623763,gi|2623765,gi|2623767,gi|30794326	100,991.10	100.00%	3	3	3	0.03%	4.53%	TSDFKEDKLNIR	3.15	1,465.76
ATP	6018	Lu-ECAM-1	gi|2623763,gi|2623765,gi|2623767,gi|30794326	100,991.10	100.00%	3	3	3	0.03%	4.53%	YGDDPYTLQYGR	3.59	1,447.65
ATP	6018	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	4	4	6	0.05%	21.30%	ATIGADFLTK	2.9	1,036.57
ATP	6018	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	4	4	6	0.05%	21.30%	DPENFPFVVLGNK	4.85	1,475.75

ATP	6018	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	4	4	6	0.05%	21.30%	FQSLGVAFYR	3.06	1,187.62
ATP	6018	RecName: Full=Ras-related protein Rab-7a	gi|108860919,gi|74354082,gi|78045539	23,526.10	100.00%	4	4	6	0.05%	21.30%	VIILGDSGVGK	2.63	1,057.63
ATP	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	13	16	20	0.17%	28.80%	ARFEELNADLFR	4.08	1,480.75
ATP	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	13	16	20	0.17%	28.80%	DAGTIAGLNVLR	2.87	1,199.67
ATP	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	13	16	20	0.17%	28.80%	IINEPTAAAIAYGLDK	4.25	1,659.90
ATP	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	13	16	20	0.17%	28.80%	IINEPTAAAIAYGLDKK	2.93	1,787.99
ATP	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	13	16	20	0.17%	28.80%	LDKSQIHDIVLVGGSTR	3.96	1,838.01
ATP	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	13	16	20	0.17%	28.80%	LLQDFFNGK	2.75	1,081.57
ATP	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	13	16	20	0.17%	28.80%	MVNHFIAEFK	2.64	1,251.62
ATP	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	13	16	20	0.17%	28.80%	NQVAMNPTNTVFDAK	4.7	1,665.79
ATP	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	13	16	20	0.17%	28.80%	NSLESYAFNMK	2.77	1,319.59
ATP	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	13	16	20	0.17%	28.80%	SFYPEEVSSMVLTK	2.63	1,632.78
ATP	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	13	16	20	0.17%	28.80%	SINPDEAVAYGAAVQAAILSGDK	2.78	2,260.15
ATP	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	13	16	20	0.17%	28.80%	STAGDTHLGGEDFDNR	2.93	1,691.73
ATP	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	13	16	20	0.17%	28.80%	TTPSYVAFTDTER	3.42	1,487.70
ATP	6018	heat shock 70kDa protein 8	gi|146231704	71,224.20	100.00%	13	16	20	0.17%	28.80%	TVTNAVVTVPAYFNDSQR	3.18	1,982.00

ATP	6018	ras homolog gene family, member G	gi|122692461,gi|92096969	21,261.90	99.80%	2	2	2	0.02%	19.90%	EYIPTVFDNYSAQSAVDGR	4.39	2,131.99
ATP	6018	ras homolog gene family, member G	gi|122692461,gi|92096969	21,261.90	99.80%	2	2	2	0.02%	19.90%	LKEQGQAPITPQQGQALAK	4.28	2,006.10
ATP	6018	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	7	8	53	0.45%	21.50%	AAYFGIYDTAK	3.86	1,219.60
ATP	6018	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	7	8	53	0.45%	21.50%	DFLAGGIAAAISK	4.8	1,233.68
ATP	6018	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	7	8	53	0.45%	21.50%	GMGGAFVLVLYDELK	5.1	1,627.84
ATP	6018	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	7	8	53	0.45%	21.50%	GMGGAFVLVLYDELKK	3.07	1,755.94
ATP	6018	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	7	8	53	0.45%	21.50%	LLLQVQHASK	2.98	1,136.68
ATP	6018	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	7	8	53	0.45%	21.50%	YFPTQALNFAFK	3.9	1,446.74
ATP	6018	solute carrier family 25, member A6	gi|119936593,gi|151557097,gi|32189336	32,860.40	100.00%	7	8	53	0.45%	21.50%	YFPTQALNFAFKDK	4.15	1,689.86
ATP	6018	PREDICTED: insulin-like growth factor 1 receptor	gi|119913553	135,693.80	99.90%	2	3	3	0.03%	3.24%	ELGQGSFGMVYEGVAK	3.26	1,687.80
ATP	6018	PREDICTED: insulin-like growth factor 1 receptor	gi|119913553	135,693.80	99.90%	2	3	3	0.03%	3.24%	GNNIASELENFMGLIEVVTGYVK	3.55	2,513.26

ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	APLNVQFSSPGPGDAVK	4.1	1,683.87
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	DLDIIDNYDYSHTVK	2.92	1,810.85
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	EAFTNKPNVFTVVTR	2.76	1,722.92
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	FADEHVPGSPFTVK	2.65	1,530.76
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	GAGIGGLGITVEGPSESK	3.35	1,628.85
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	GFQDGVYAFEYYPSTQGK	3.35	2,056.93
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	GGLVGKPAEFTIDTK	2.56	1,532.83

ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	GLVEPVNVVDNGDGTHTVTYTPSQEGPYMVSVK	6.44	3,505.68
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	GQHVTGSPFQFTVGPLGEGGAHK	3.9	2,308.15
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	IFAQDGDGQPIDIQMK	4.1	1,791.86
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	IPEIDSSDMSAHVTSPSGR	3.83	2,001.92
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	IVGPGLGSGVR	2.61	1,011.59
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	LDVTILSPSR	3.07	1,100.63
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	LIALLEVLSQK	2.93	1,226.77

ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	LTVLSLQESGLK	3.19	1,287.75
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	LVSPGSANETSSILVESVTR	4.4	2,046.07
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	RLTVLSLQESGLK	3.63	1,443.85
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	SPFEVQVGPEAGMQK	4.37	1,619.77
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	SPFTVGVAAPLDLSR	4.33	1,529.83
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	VLFASQEIPTSPFR	3.62	1,591.85
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	VTASGPGLSTYGVPASLPVEFAIDAR	4.69	2,575.34

ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	VTEAEIVPVGK	3.5	1,141.65
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	VTVLFAGQHISK	3.57	1,299.74
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	YGGELVPHFPTR	2.5	1,372.70
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	YMGSHIPESPLQFYVNYPNSGSVSAYGPGLVYGVANK	6.03	3,978.90
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	YMIGVTYGGDDIPLSPYR	4.6	2,032.97
ATP	6018	PREDICTED: similar to filamin B, beta (actin binding protein 278) isoform 7	gi|194677296	277,977.20	100.00%	27	31	35	0.30%	17.30%	YTPTQQGNMQVLVTYGGDPIPK	4.65	2,423.19
ATP	6018	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	4	5	5	0.04%	13.20%	ADVGFAMGIAGTDVAK	3.91	1,538.75

ATP	6018	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	4	5	5	0.04%	13.20%	EAGHGTQKEEIPEEELAEDVEEIDHAER	2.68	3,189.45
ATP	6018	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	4	5	5	0.04%	13.20%	EANHDGDFGITLAELR	3.66	1,757.85
ATP	6018	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	4	5	5	0.04%	13.20%	EASDIILTDDNFTSIVK	4.1	1,880.95
ATP	6018	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	4	5	5	0.04%	13.20%	IDESSLTGESDHVKK	4.05	1,644.81
ATP	6018	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	4	5	5	0.04%	13.20%	KADVGFAMGIAGTDVAK	5.33	1,666.85
ATP	6018	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	4	5	5	0.04%	13.20%	QVVAVTGDGTNDGPALK	5.19	1,641.84
ATP	6018	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	4	5	5	0.04%	13.20%	QVVAVTGDGTNDGPALKK	3.73	1,769.94
ATP	6018	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	4	5	5	0.04%	13.20%	SLDKDPLLLSGTHVMEGSGR	3.87	2,128.07
ATP	6018	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	4	5	5	0.04%	13.20%	SSIHNFMTHPEFR	3.86	1,618.74
ATP	6018	plasma membrane calcium-transporting ATPase	gi|14582762,gi|27807255	134,738.10	100.00%	4	5	5	0.04%	13.20%	YGDLLPADGILIQGNDLK	3.86	1,915.02
ATP	6018	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	100.00%	9	9	10	0.09%	9.00%	IGGILANELSVDEAALHAAVIAINEAIDHR	3.13	3,095.65

ATP	6018	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	100.00%	9	9	10	0.09%	9.00%	IIGNLLYYR	2.89	1,124.65
ATP	6018	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	100.00%	9	9	10	0.09%	9.00%	ILAIGLINEALDEGDAQK	4.09	1,883.01
ATP	6018	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	100.00%	9	9	10	0.09%	9.00%	ILQSPALGLR	2.72	1,067.66
ATP	6018	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	100.00%	9	9	10	0.09%	9.00%	NVIFEISPTEEVGDFEVK	2.72	2,052.02
ATP	6018	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	100.00%	9	9	10	0.09%	9.00%	TLINAEDPPMIVVR	4.03	1,583.85
ATP	6018	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	100.00%	9	9	10	0.09%	9.00%	TLQALQIPAAK	3.6	1,153.69
ATP	6018	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	100.00%	9	9	10	0.09%	9.00%	VNLLAALTNIDLALEQGSAPALFK	5.07	2,482.39

ATP	6018	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP1 (p195)	gi|194676712	182,771.10	100.00%	9	9	10	0.09%	9.00%	YQELINDIAR	2.75	1,234.64
ATP	6018	RecName: Full=Vesicle transport protein GOT1B; AltName: Full=Golgi transport 1 homolog B	gi|109939723,gi|114053223,gi|82571709	15,408.60	100.00%	3	3	3	0.03%	20.30%	RVPVLGSLLNLPGIR	3.36	1,604.00
ATP	6018	RecName: Full=Vesicle transport protein GOT1B; AltName: Full=Golgi transport 1 homolog B	gi|109939723,gi|114053223,gi|82571709	15,408.60	100.00%	3	3	3	0.03%	20.30%	SFVDKVGESNNMV	3.98	1,441.66
ATP	6018	RecName: Full=Vesicle transport protein GOT1B; AltName: Full=Golgi transport 1 homolog B	gi|109939723,gi|114053223,gi|82571709	15,408.60	100.00%	3	3	3	0.03%	20.30%	VPVLGSLLNLPGIR	3.96	1,447.90
ATP	6018	UNC84B protein	gi|151553917,gi|156121283	81,429.80	100.00%	4	4	4	0.03%	6.04%	IRPTAVTLEHVPK	3.23	1,460.86
ATP	6018	UNC84B protein	gi|151553917,gi|156121283	81,429.80	100.00%	4	4	4	0.03%	6.04%	LEGQLAGLR	2.73	956.5525
ATP	6018	UNC84B protein	gi|151553917,gi|156121283	81,429.80	100.00%	4	4	4	0.03%	6.04%	LEGQLAGLRQELAALTLK	2.96	1,924.12
ATP	6018	UNC84B protein	gi|151553917,gi|156121283	81,429.80	100.00%	4	4	4	0.03%	6.04%	SEHQQDSEDLFKK	3.83	1,590.74

ATP	6018	heat shock protein beta-1	gi|71037405,gi|74354863,gi|85542053	22,375.10	99.80%	2	2	2	0.02%	12.40%	LFDQAFGLPR	3.66	1,163.62
ATP	6018	heat shock protein beta-1	gi|71037405,gi|74354863,gi|85542053	22,375.10	99.80%	2	2	2	0.02%	12.40%	QLSSGVSEIQQTADR	5.09	1,618.80
ATP	6018	FBL protein	gi|151553842	37,159.30	99.80%	2	2	2	0.02%	9.32%	DHAVVVGVYRPPPK	2.75	1,533.85
ATP	6018	FBL protein	gi|151553842	37,159.30	99.80%	2	2	2	0.02%	9.32%	LAAAILGGVDQIHIKPGAK	2.57	1,872.11
ATP	6018	ribosomal protein L4	gi|61553010,gi|62460480,gi|73917531,gi|74267758	47,395.70	100.00%	3	4	4	0.03%	11.40%	APIRPDIVNFVHTNLR	4.68	1,862.04
ATP	6018	ribosomal protein L4	gi|61553010,gi|62460480,gi|73917531,gi|74267758	47,395.70	100.00%	3	4	4	0.03%	11.40%	IEEVPELPLVVEDKVEGYKK	2.69	2,313.26
ATP	6018	ribosomal protein L4	gi|61553010,gi|62460480,gi|73917531,gi|74267758	47,395.70	100.00%	3	4	4	0.03%	11.40%	NIPGITLLNVSK	2.09	1,268.76
ATP	6018	PREDICTED: similar to carnitine palmitoyl transferase 1C	gi|194679924	80,680.30	100.00%	3	3	3	0.03%	5.23%	LPVPAVQDTVNR	3.24	1,308.73
ATP	6018	PREDICTED: similar to carnitine palmitoyl transferase 1C	gi|194679924	80,680.30	100.00%	3	3	3	0.03%	5.23%	MTALAQDFAVNLGPR	5.26	1,619.82
ATP	6018	PREDICTED: similar to carnitine palmitoyl transferase 1C	gi|194679924	80,680.30	100.00%	3	3	3	0.03%	5.23%	YLAVDSPFLK	2.36	1,152.63
ATP	6018	PREDICTED: similar to UDP-glucuronate decarboxylase 1	gi|76673441	47,730.90	99.80%	2	2	2	0.02%	11.00%	NLVGSGSEIQFLSEAQDDPQK	3.57	2,262.09
ATP	6018	PREDICTED: similar to UDP-glucuronate decarboxylase 1	gi|76673441	47,730.90	99.80%	2	2	2	0.02%	11.00%	VVSNFILQALQGEPLTVYGSGSQTR	3.04	2,664.40

ATP	6018	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	6	6	6	0.05%	8.27%	GAPVGGHILSYLLEK	1.99	1,553.87
ATP	6018	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	6	6	6	0.05%	8.27%	LLGVEGSTLR	2.54	1,044.60
ATP	6018	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	6	6	6	0.05%	8.27%	LLQSNPVLEAFGNAK	4.51	1,600.87
ATP	6018	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	6	6	6	0.05%	8.27%	MSLLELVEILK	3.3	1,303.75
ATP	6018	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	6	6	6	0.05%	8.27%	QLLLTPNAVVIVEDAK	2.62	1,723.00
ATP	6018	MYO1C protein	gi|146186525,gi|147906576,gi|397403,gi|90109868	118,133.10	100.00%	6	6	6	0.05%	8.27%	VLQALGSEPIQYAVPVVK	3.34	1,911.10
ATP	6018	PREDICTED: similar to Ras-interacting protein 1 isoform 2	gi|76642189	103,383.20	100.00%	3	4	4	0.03%	6.85%	AASGGAALASPGPGSGSGTPAGSGGK	4.91	2,026.98
ATP	6018	PREDICTED: similar to Ras-interacting protein 1 isoform 2	gi|76642189	103,383.20	100.00%	3	4	4	0.03%	6.85%	DAVDTGDIFESFSSHPPLILPLGSSR	2.3	2,757.37
ATP	6018	PREDICTED: similar to Ras-interacting protein 1 isoform 2	gi|76642189	103,383.20	100.00%	3	4	4	0.03%	6.85%	LSLTGPVTDDALHR	2.3	1,494.79

ATP	6018	RecName: Full=Aspartyl-tRNA synthetase, cytoplasmic; AltName: Full=Aspartate--tRNA ligase; Short=AspRS	gi|110287976,gi|74267650,gi|78045531	57,018.30	99.80%	2	2	2	0.02%	7.58%	EAGIEMGDEEDLSTPNEK	2.25	1,979.84
ATP	6018	RecName: Full=Aspartyl-tRNA synthetase, cytoplasmic; AltName: Full=Aspartate--tRNA ligase; Short=AspRS	gi|110287976,gi|74267650,gi|78045531	57,018.30	99.80%	2	2	2	0.02%	7.58%	LPLQLDDAVRPEVEGEEEGR	4.1	2,251.12
ATP	6018	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	5	5	5	0.04%	5.81%	EDGSFSFYSLPSGGYTVIPFYR	3.58	2,489.17
ATP	6018	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	5	5	5	0.04%	5.81%	GQPLGPAGVQVSLR	3.59	1,378.78
ATP	6018	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	5	5	5	0.04%	5.81%	ITFDVAPSR	3.02	1,005.54
ATP	6018	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	5	5	5	0.04%	5.81%	SSIDSEPALVLGPLK	2.8	1,525.85
ATP	6018	PREDICTED: NOMO3-like protein isoform 2	gi|119916799,gi|119916801	134,079.40	100.00%	5	5	5	0.04%	5.81%	VQVMVPEAETR	2.79	1,274.64
ATP	6018	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	4	8	10	0.09%	39.40%	ADALQAGASQFETSAAK	5.13	1,665.81

ATP	6018	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	4	8	10	0.09%	39.40%	LQQTQNQVDEVVDIMR	4.46	1,931.95
ATP	6018	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	4	8	10	0.09%	39.40%	LSELDDRADALQAGASQFETSAAK	7.21	2,494.21
ATP	6018	vesicle-associated membrane protein 3	gi|114052342,gi|122136203,gi|86822282	11,517.30	100.00%	4	8	10	0.09%	39.40%	RLQQTQNQVDEVVDIMR	3.65	2,072.06
ATP	6018	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	6	13	0.11%	33.60%	DKLSELQLR	2.92	1,101.63
ATP	6018	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	6	13	0.11%	33.60%	EEYQPATPGLGMFVEVKDPEDKVILAR	2.38	3,047.54
ATP	6018	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	6	13	0.11%	33.60%	FSLFAGGMLR	3.18	1,114.57
ATP	6018	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	6	13	0.11%	33.60%	QLVEQVEQIQK	3.93	1,341.74
ATP	6018	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	6	13	0.11%	33.60%	QREEYQPATPGLGMFVEVKDPEDK	4.56	2,779.32
ATP	6018	transmembrane emp24 protein transport domain containing 9	gi|59858491,gi|74267997,gi|77736600,gi|81175032	27,280.40	100.00%	6	6	13	0.11%	33.60%	VHLDIQVGEHANDYAEIAAK	3.56	2,193.09

ATP	6018	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	5	7	13	0.11%	36.10%	EFADSLGIPFLETSAK	3.74	1,724.87
ATP	6018	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	5	7	13	0.11%	36.10%	GAHGIIVVYDVTDQESFNNVK	2.77	2,305.15
ATP	6018	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	5	7	13	0.11%	36.10%	KVVDYTTAKEFADSLGIPFLETSAK	3.81	2,730.42
ATP	6018	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	5	7	13	0.11%	36.10%	LLLIGDSGVGK	3.07	1,071.64
ATP	6018	RAB1A, member RAS oncogene family	gi|120419448	22,660.40	100.00%	5	7	13	0.11%	36.10%	NATNVEQSFMTMAAEIK	3.67	1,900.88
ATP	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	12	19	32	0.27%	31.40%	ALYETELADAR	2.82	1,251.62
ATP	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	12	19	32	0.27%	31.40%	DQMQQQLNDYEQLLDVK	4	2,123.99
ATP	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	12	19	32	0.27%	31.40%	IQELEDLLAK	3.38	1,171.66
ATP	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	12	19	32	0.27%	31.40%	LALDMEISAYR	2.29	1,297.65
ATP	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	12	19	32	0.27%	31.40%	LAQALHEMREQHDAQVK	2.67	2,020.00
ATP	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	12	19	32	0.27%	31.40%	LREYEAALNSK	3.24	1,293.68
ATP	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	12	19	32	0.27%	31.40%	LSSEMNTSTVNSAR	4.24	1,496.70
ATP	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	12	19	32	0.27%	31.40%	LYKEELEQTYHAK	2.94	1,651.83
ATP	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	12	19	32	0.27%	31.40%	MRIESLSSQLSNLQK	4.14	1,749.92
ATP	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	12	19	32	0.27%	31.40%	NMYEEEINETR	3.64	1,443.61
ATP	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	12	19	32	0.27%	31.40%	SLESDLEDLKDQIAQLEASLAAAK	5.78	2,558.32
ATP	6018	LMNB1 protein	gi|154425605,gi|157074106	66,404.60	100.00%	12	19	32	0.27%	31.40%	TTIPEEEEEEEAAEVAVEEELFHQQGAPR	5.28	3,425.55

ATP	6018	RecName: Full=40S ribosomal protein S20	gi|108860955,gi|61822677,gi|73587131,gi|77735823	13,395.10	100.00%	3	4	4	0.03%	22.70%	DTGKTPVEPEVAIHR	4.22	1,648.87
ATP	6018	RecName: Full=40S ribosomal protein S20	gi|108860955,gi|61822677,gi|73587131,gi|77735823	13,395.10	100.00%	3	4	4	0.03%	22.70%	LIDLHSPSEIVK	2.21	1,350.76
ATP	6018	RecName: Full=40S ribosomal protein S20	gi|108860955,gi|61822677,gi|73587131,gi|77735823	13,395.10	100.00%	3	4	4	0.03%	22.70%	TPVEPEVAIHR	4.15	1,247.67
ATP	6018	SACM1L protein	gi|151554372,gi|156120909,gi|167016544	67,077.30	99.80%	2	2	2	0.02%	4.43%	LSNTSPEFQEMSLLER	3.38	1,896.90
ATP	6018	SACM1L protein	gi|151554372,gi|156120909,gi|167016544	67,077.30	99.80%	2	2	2	0.02%	4.43%	TNVIQSLLAR	2.92	1,114.66
ATP	6018	Interleukin enhancer binding factor 2, 45kDa	gi|83405442,gi|84000347	43,068.60	100.00%	3	4	4	0.03%	14.60%	ILPTLEAVAALGNK	3.35	1,409.84
ATP	6018	Interleukin enhancer binding factor 2, 45kDa	gi|83405442,gi|84000347	43,068.60	100.00%	3	4	4	0.03%	14.60%	INNVIDNLIVAPGTFEVQIEEVR	3.51	2,582.38
ATP	6018	Interleukin enhancer binding factor 2, 45kDa	gi|83405442,gi|84000347	43,068.60	100.00%	3	4	4	0.03%	14.60%	NQDLAPNSAEQASILSLVTK	3.92	2,099.10
ATP	6018	CALM3 protein	gi|111308539,gi|114053089,gi|115305083,gi|157831834,gi|157879669,gi|194671098,gi|28189857,gi|49037473,gi|86822265	19,973.60	99.80%	2	4	4	0.03%	18.10%	EAFSLFDKDGDGTITTK	4.41	1,844.89
ATP	6018	CALM3 protein	gi|111308539,gi|114053089,gi|115305083,gi|157831834,gi|157879669,gi|194671098,gi|28189857,gi|49037473,gi|86822265	19,973.60	99.80%	2	4	4	0.03%	18.10%	VFDKDGNGYISAAELR	5.02	1,754.87

ATP	6018	RecName: Full=Cytochrome c oxidase polypeptide 7A2, mitochondrial; AltName: Full=Cytochrome c oxidase polypeptide VIIa-liver/heart; Short=Cytochrome c oxidase subunit VIIa-L; Short=VIIIC; Flags: Precursor	gi|117120,gi|28461241,gi|488158,gi|74354141	9,305.40	99.80%	2	2	2	0.02%	27.70%	GGIADALLYR	3.26	1,048.58
ATP	6018	RecName: Full=Cytochrome c oxidase polypeptide 7A2, mitochondrial; AltName: Full=Cytochrome c oxidase polypeptide VIIa-liver/heart; Short=Cytochrome c oxidase subunit VIIa-L; Short=VIIIC; Flags: Precursor	gi|117120,gi|28461241,gi|488158,gi|74354141	9,305.40	99.80%	2	2	2	0.02%	27.70%	LFQEDNGIPVHLK	3.72	1,509.81
ATP	6018	SLC25A24 protein	gi|148745486,gi|149642721,gi|167016553	53,268.40	99.80%	2	3	6	0.05%	8.39%	GYVPNLLGIIPYAGIDLAVYELLK	5.69	2,604.47
ATP	6018	SLC25A24 protein	gi|148745486,gi|149642721,gi|167016553	53,268.40	99.80%	2	3	6	0.05%	8.39%	VLPAVGISYVVYENMK	2.68	1,797.95

ATP	6018	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	6	8	8	0.07%	15.10%	ATTPVIMVGPGTGVAPFIGFIQER	4.27	2,474.31
ATP	6018	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	6	8	8	0.07%	15.10%	GMAADPEEYDLADLSSLPEIEK	5.14	2,409.10
ATP	6018	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	6	8	8	0.07%	15.10%	NIIVFYGSQTGTAEEFANR	3.16	2,117.03
ATP	6018	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	6	8	8	0.07%	15.10%	RSDEDYLYREELAGFHK	3.39	2,128.01
ATP	6018	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	6	8	8	0.07%	15.10%	SYENQKPPFDAK	3.58	1,423.69

ATP	6018	RecName: Full=NADPH--cytochrome P450 reductase; Short=CPR; Short=P450R	gi|110287686,gi|146231834,gi|74268199,gi|78369374	77,249.90	100.00%	6	8	8	0.07%	15.10%	YAVFALGNK	2.85	982.5356
ATP	6018	TXNDC10 protein	gi|151554048,gi|156121223	51,713.50	100.00%	3	4	5	0.04%	10.40%	FQNYLTMDGFLLYELGDTGK	4.44	2,341.11
ATP	6018	TXNDC10 protein	gi|151554048,gi|156121223	51,713.50	100.00%	3	4	5	0.04%	10.40%	MDATSYSSIASEFGVR	3.48	1,736.78
ATP	6018	TXNDC10 protein	gi|151554048,gi|156121223	51,713.50	100.00%	3	4	5	0.04%	10.40%	TKDDIIEFAHR	3.74	1,344.69
ATP	6018	MTCH1 protein	gi|154426180,gi|157074126	41,499.70	100.00%	3	3	4	0.03%	11.30%	LLIQVGHEPMPPTIGTNVLGR	2.72	2,258.23
ATP	6018	MTCH1 protein	gi|154426180,gi|157074126	41,499.70	100.00%	3	3	4	0.03%	11.30%	LMSNALSTVTR	3.24	1,208.63
ATP	6018	MTCH1 protein	gi|154426180,gi|157074126	41,499.70	100.00%	3	3	4	0.03%	11.30%	VLYLPSFFTYAK	3.21	1,448.78
ATP	6018	collagen, type II, alpha 1 isoform 2	gi|164414427	134,410.60	99.80%	2	2	2	0.02%	3.53%	GANGEPGKAGEKGLPGAPGLR	2.58	1,933.03
ATP	6018	collagen, type II, alpha 1 isoform 2	gi|164414427	134,410.60	99.80%	2	2	2	0.02%	3.53%	MIRLGAPQTLVLLTLLVAAVLRCHGQDVR	2.77	3,172.82
ATP	6018	RecName: Full=Histone H2A.V; AltName: Full=H2A.F/Z	gi|109940032,gi|163150,gi|27807373,gi|410,gi|81674301,gi|81674755,gi|83288407,gi|84000371	13,535.20	99.80%	2	5	5	0.04%	33.60%	ATIAGGGVIPHIHK	4.61	1,370.79
ATP	6018	RecName: Full=Histone H2A.V; AltName: Full=H2A.F/Z	gi|109940032,gi|163150,gi|27807373,gi|410,gi|81674301,gi|81674755,gi|83288407,gi|84000371	13,535.20	99.80%	2	5	5	0.04%	33.60%	VGATAAVYSAAILEYLTAEVLELAGNASK	3.93	2,895.54
ATP	6018	CD14 protein	gi|151555647,gi|157703512,gi|157703514,gi|157703516,gi|2274810,gi|3913217,gi|41386760,gi|4887170	39,649.70	99.80%	2	2	2	0.02%	8.04%	LGAAQVPAQLLVAVLR	4.11	1,619.00

ATP	6018	CD14 protein	gi|151555647,gi|157703512,gi|157703514,gi|157703516,gi|2274810,gi|3913217,gi|41386760,gi|4887170	39,649.70	99.80%	2	2	2	0.02%	8.04%	VQPQSLDLSHNSLR	2.72	1,593.83
ATP	6018	PREDICTED: vinculin isoform 1	gi|194679457,gi|194679459	123,848.10	99.90%	2	2	2	0.02%	3.79%	AIPDLTAPVAAVQAAVSNLVR	2.65	2,076.18
ATP	6018	PREDICTED: vinculin isoform 1	gi|194679457,gi|194679459	123,848.10	99.90%	2	2	2	0.02%	3.79%	LLAVAATAPPDAPNREEVFDER	2.97	2,381.21
ATP	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	15	18	26	0.22%	33.40%	ALEEAMEQKAELER	2.77	1,662.80
ATP	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	15	18	26	0.22%	33.40%	ALEQQVEEMKTQLEELEDELQATEDAK	4.87	3,163.48
ATP	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	15	18	26	0.22%	33.40%	ANLQIDQLNTDLNLER	5	1,869.97
ATP	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	15	18	26	0.22%	33.40%	ELEDATETADAMNR	3.34	1,581.67
ATP	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	15	18	26	0.22%	33.40%	IAQLEEELEEEQGNTELVNDR	4.97	2,458.16
ATP	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	15	18	26	0.22%	33.40%	IAQLEEELEEEQGNTELVNDRLK	4.37	2,699.34
ATP	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	15	18	26	0.22%	33.40%	IAQLEEQLDNETKER	3.64	1,815.91
ATP	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	15	18	26	0.22%	33.40%	KANLQIDQLNTDLNLER	2.59	1,998.06
ATP	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	15	18	26	0.22%	33.40%	KFDQLLAEEK	3.02	1,220.65
ATP	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	15	18	26	0.22%	33.40%	LKDVLLQVDDERR	2.26	1,598.89

ATP	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	15	18	26	0.22%	33.40%	LQQELDDLLVDLDHQR	2.36	1,949.99
ATP	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	15	18	26	0.22%	33.40%	NAEQYKDQADKASTR	4.44	1,724.82
ATP	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	15	18	26	0.22%	33.40%	QAQQERDELADEIANSSGK	4.07	2,088.98
ATP	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	15	18	26	0.22%	33.40%	QISTLHAQVTDMRK	2.58	1,643.85
ATP	6018	non-muscle myosin heavy chain	gi|3205211	72,354.70	100.00%	15	18	26	0.22%	33.40%	RQLEEAEEEAQR	3.69	1,487.71
ATP	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	22	38	0.33%	38.10%	AASFLLALEPELEAR	4.47	1,629.88
ATP	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	22	38	0.33%	38.10%	ENLVEQHIQDIVVHYTFNK	3.97	2,326.18
ATP	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	22	38	0.33%	38.10%	IDHILDAL	2.47	909.5042
ATP	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	22	38	0.33%	38.10%	ISVIVEAVYTHVLQPYPTQITQSEK	3.61	2,843.52
ATP	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	22	38	0.33%	38.10%	LPVALDPGAK	2.13	980.5777
ATP	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	22	38	0.33%	38.10%	LVDHVFDEQVIDSLTVK	5.45	1,957.03
ATP	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	22	38	0.33%	38.10%	NIQVDSPYEISR	3.8	1,420.71
ATP	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	22	38	0.33%	38.10%	QFVVFEGNHYFYSPYPTK	3.55	2,223.05
ATP	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	22	38	0.33%	38.10%	SEDLLDYGPFR	4.11	1,311.62
ATP	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	22	38	0.33%	38.10%	THYIVGYNLPSYEYLYNLGDQYALK	3.55	2,997.47
ATP	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	22	38	0.33%	38.10%	TILPAAAQDVYYR	2.77	1,480.78
ATP	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	22	38	0.33%	38.10%	TVDLSSHLAK	3.2	1,070.58
ATP	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	22	38	0.33%	38.10%	VHSENNSPFLTITSMTR	5.12	1,949.94

ATP	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	22	38	0.33%	38.10%	VTAEVVLAHAGSGSSPR	6.37	1,637.86
ATP	6018	RPN1 protein	gi|126717391,gi|129277520	68,335.00	100.00%	15	22	38	0.33%	38.10%	YDYQRQPDSGVSSVR	4	1,756.82
ATP	6018	acyl-Coenzyme A dehydrogenase, very long chain isoform 1 precursor	gi|146231822,gi|160332360,gi|27806205,gi|74267810,gi|930358	70,632.20	99.80%	2	2	2	0.02%	5.95%	GQLTTDQVFPYPSVLNEDQTQFLK	2.96	2,768.38
ATP	6018	acyl-Coenzyme A dehydrogenase, very long chain isoform 1 precursor	gi|146231822,gi|160332360,gi|27806205,gi|74267810,gi|930358	70,632.20	99.80%	2	2	2	0.02%	5.95%	VPAENVLGEVGGGFK	4.09	1,472.77
ATP	6018	RecName: Full=60S ribosomal protein L8	gi|108860941,gi|154426156,gi|74267654,gi|77736197	28,006.80	100.00%	3	3	3	0.03%	18.30%	AQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	3.66	3,169.57
ATP	6018	RecName: Full=60S ribosomal protein L8	gi|108860941,gi|154426156,gi|74267654,gi|77736197	28,006.80	100.00%	3	3	3	0.03%	18.30%	ASGNYATVISHNPETK	4.34	1,688.82
ATP	6018	RecName: Full=60S ribosomal protein L8	gi|108860941,gi|154426156,gi|74267654,gi|77736197	28,006.80	100.00%	3	3	3	0.03%	18.30%	ASGNYATVISHNPETKK	2.45	1,816.92
ATP	6018	Karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	gi|74354742,gi|77735853	57,908.80	100.00%	5	5	5	0.04%	17.40%	GINSNNLESQLQATQAAR	3.1	1,914.96
ATP	6018	Karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	gi|74354742,gi|77735853	57,908.80	100.00%	5	5	5	0.04%	17.40%	LLGATELPIVTPALR	3	1,563.95
ATP	6018	Karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	gi|74354742,gi|77735853	57,908.80	100.00%	5	5	5	0.04%	17.40%	NKNPAPPLEAIEQILPTLVR	3	2,213.27

ATP	6018	Karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	gi|74354742,gi|77735853	57,908.80	100.00%	5	5	5	0.04%	17.40%	NVSSFPDDATSPLQENR	3.75	1,876.87
ATP	6018	Karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	gi|74354742,gi|77735853	57,908.80	100.00%	5	5	5	0.04%	17.40%	QDQIQQVVNHGLVPFLVGLLSK	4.24	2,432.37
ATP	6018	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	5	6	7	0.06%	7.41%	ALTLGALTLPLAR	3.11	1,309.82
ATP	6018	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	5	6	7	0.06%	7.41%	GEGSGTLGSLSLPLSELLVADR	4.11	2,171.16
ATP	6018	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	5	6	7	0.06%	7.41%	LHVLEAQDLIAK	3.94	1,349.78
ATP	6018	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	5	6	7	0.06%	7.41%	LLVPLVPDLQDVAQLR	3.51	1,789.06
ATP	6018	Family with sequence similarity 62 (C2 domain containing), member A	gi|117306190,gi|118150984	123,012.90	100.00%	5	6	7	0.06%	7.41%	LTHSDSPPEAPAGPLGQVK	3.74	1,900.98
ATP	6018	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	8	9	0.08%	11.20%	LKVTEGGEPYR	2.75	1,248.66
ATP	6018	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	8	9	0.08%	11.20%	LSFQHDPETSVLILR	3.32	1,754.94

ATP	6018	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	8	9	0.08%	11.20%	LVAIVDPHIK	2.1	1,104.68
ATP	6018	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	8	9	0.08%	11.20%	MALYGSVPVLLAHSPLR	2.87	1,840.02
ATP	6018	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	8	9	0.08%	11.20%	MLDYLQGSGETPQTDVR	4.3	1,925.89
ATP	6018	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	8	9	0.08%	11.20%	VVIIGAGKPATVVLQTK	4.78	1,694.06
ATP	6018	GANAB protein	gi|151553519,gi|194679898	109,455.80	100.00%	7	8	9	0.08%	11.20%	YHGPQTLYLPVTLSSIPVFQR	3.02	2,416.30
ATP	6018	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	4	4	4	0.03%	5.86%	DVIDKQHTEQEASYGR	4.14	1,875.88
ATP	6018	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	4	4	4	0.03%	5.86%	LVSIIAELLSTK	2.99	1,286.79
ATP	6018	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	4	4	4	0.03%	5.86%	SFHSFYQLLQGGSDQMLR	4.92	2,130.01
ATP	6018	Myosin ID	gi|109659303,gi|115497786,gi|122145769	115,924.40	100.00%	4	4	4	0.03%	5.86%	VTDEMFLEALNSK	3.7	1,512.73
ATP	6018	Chromosome 20 open reading frame 3 ortholog	gi|74268319,gi|78369434	46,074.40	100.00%	3	4	4	0.03%	9.95%	GGADVFVENLPGFPDNIR	3.33	1,916.95
ATP	6018	Chromosome 20 open reading frame 3 ortholog	gi|74268319,gi|78369434	46,074.40	100.00%	3	4	4	0.03%	9.95%	LLLSSETPIEGR	2.59	1,314.73
ATP	6018	Chromosome 20 open reading frame 3 ortholog	gi|74268319,gi|78369434	46,074.40	100.00%	3	4	4	0.03%	9.95%	MSFLNDLTVTR	3.23	1,312.66
ATP	6018	RecName: Full=Pyruvate dehydrogenase E1 component subunit beta, mitochondrial; Short=PDHE1-B; Flags: Precursor	gi|116242689,gi|151556071,gi|164420789	39,108.20	99.80%	2	2	2	0.02%	7.52%	ILEDNSVPQVK	2.81	1,241.67

ATP	6018	RecName: Full=Pyruvate dehydrogenase E1 component subunit beta, mitochondrial; Short=PDHE1-B; Flags: Precursor	gi|116242689,gi|151556071,gi|164420789	39,108.20	99.80%	2	2	2	0.02%	7.52%	IMEGPAFNFLDAPAVR	3.25	1,763.88
ATP	6018	PREDICTED: similar to Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A	gi|119896006	130,855.40	100.00%	3	3	4	0.03%	4.19%	IQFGTLSDYFDALEK	3.97	1,746.86
ATP	6018	PREDICTED: similar to Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A	gi|119896006	130,855.40	100.00%	3	3	4	0.03%	4.19%	TTVVLAPLGDDFR	2.73	1,403.75

ATP	6018	PREDICTED: similar to Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A	gi|119896006	130,855.40	100.00%	3	3	4	0.03%	4.19%	YDLYNGNIANEGIFNMNNIK	3.19	2,333.09
ATP	6018	RecName: Full=Mitochondrial fission factor	gi|122140919,gi|148744119,gi|73586594,gi|77735489	25,042.40	99.90%	2	2	2	0.02%	17.90%	RLQLLEEENKER	3.79	1,556.84
ATP	6018	RecName: Full=Mitochondrial fission factor	gi|122140919,gi|148744119,gi|73586594,gi|77735489	25,042.40	99.90%	2	2	2	0.02%	17.90%	VLTLSERPLDFLDLERPAPTPQNEEIR	4.73	3,148.66
ATP	6018	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	5	13	0.11%	20.10%	DYPLPDVAHVK	3.07	1,253.65

ATP	6018	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	5	13	0.11%	20.10%	FKESFAEMNR	3.47	1,274.58
ATP	6018	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	5	13	0.11%	20.10%	SEDYALPSYVDR	2.88	1,414.65

ATP	6018	RecName: Full=Cytochrome c oxidase subunit 4 isoform 1, mitochondrial; AltName: Full=Cytochrome c oxidase subunit IV isoform 1; Short=COX IV-1; AltName: Full=Cytochrome c oxidase polypeptide IV;	gi|117085,gi|149241539,gi|149241552,gi|149241569,gi|149241582,gi|149241599,gi|149241612,gi|47824862,gi|506389,gi|59858423,gi|74354123	19,554.00	100.00%	4	5	13	0.11%	20.10%	SEDYALPSYVDRR	2.22	1,570.75
ATP	6018	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	8	11	27	0.23%	14.30%	APVPTGEVYFADSFDR	4.39	1,770.83
ATP	6018	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	8	11	27	0.23%	14.30%	IPNPDFFEDLEPFK	3.76	1,707.83
ATP	6018	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	8	11	27	0.23%	14.30%	KIPNPDFFEDLEPFK	5.36	1,835.92
ATP	6018	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	8	11	27	0.23%	14.30%	LPGDKGLVLMSR	2.06	1,301.72
ATP	6018	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	8	11	27	0.23%	14.30%	TDAPQPDVKEDEEEKEEEK	3.66	2,245.00
ATP	6018	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	8	11	27	0.23%	14.30%	TPELNLDQFHDK	4.62	1,456.71
ATP	6018	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	8	11	27	0.23%	14.30%	TPELNLDQFHDKTPYTIMFGPDK	5.1	2,723.30
ATP	6018	Canx protein	gi|157279143,gi|157785567	67,759.10	100.00%	8	11	27	0.23%	14.30%	TPYTIMFGPDK	3.38	1,285.61
ATP	6018	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	7	8	16	0.14%	21.50%	AKMDAQQEPNIQLDHLNLLK	4.49	2,335.21
ATP	6018	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	7	8	16	0.14%	21.50%	DLELLIQTATR	2.84	1,272.72
ATP	6018	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	7	8	16	0.14%	21.50%	ELQQAVLQMEQR	2.53	1,488.75
ATP	6018	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	7	8	16	0.14%	21.50%	KQQQQSHNNPAPGPEGQLK	3.97	2,086.04

ATP	6018	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	7	8	16	0.14%	21.50%	LVTLEEFLASTQR	3.28	1,506.82
ATP	6018	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	7	8	16	0.14%	21.50%	VNVPGSQAQLK	2.76	1,140.64
ATP	6018	Nucleobindin 1	gi|112362164,gi|115497814,gi|122142168	54,964.80	100.00%	7	8	16	0.14%	21.50%	YLQEVINVLETDGHFR	2.75	1,932.98
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	DDKESVPISDTIIPAVPPPTDLR	3.95	2,475.30
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	DLQFVEVTDVK	3.69	1,292.67
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	EINLAPDSSSVVVSGLMVATK	4.22	2,133.11
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	GATYNIIVEAVK	3.24	1,277.71
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	GDSPASSKPVSINYR	3.85	1,577.79
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	GFNCESKPEPEETCFDKYTGNTYR	2.83	2,815.20
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	GLRPGVVYEGQLISVQHYGQR	5.73	2,356.25
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	LGVRPSQGGEAPR	3.38	1,323.71
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	NLQPGSEYAVSLVAVK	4.96	1,674.91

ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	NSITLTNLNPGTEYVVSIVALNSK	4.39	2,547.37
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	NTFAEVTGLSPGVTYHFK	5.73	1,967.99
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	QYNVGPAASQYPLR	3.7	1,563.79
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	RPGAEPGNEGSTAHSYNQYSQR	5.5	2,406.08
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	SSPVVIDASTAIDAPSNLR	5.06	1,913.00
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	STTPDITGYR	2.7	1,110.54
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	SYTITGLQPGTDYK	4.19	1,543.76
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	TEIDKPSQMQVTDVQDNSISVR	5.9	2,506.21
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	TETITGFQVDAIPANGQTPIQR	3.8	2,357.21
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	TKTETITGFQVDAIPANGQTPIQR	3.35	2,586.35
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	VDVIPVNLPGEHGQR	3.24	1,629.87

ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	VEYELSEEGDEPQYLDLPSTATSVNIPDLLPGRK	3.68	3,774.86
ATP	6018	embryo-specific fibronectin 1 transcript variant	gi|220028657,gi|76610126	262,401.30	100.00%	22	30	38	0.33%	16.20%	VPGTSASATLTGLTR	4.52	1,431.78
ATP	6018	nicalin	gi|115494944,gi|94534903	63,091.10	100.00%	4	4	5	0.04%	10.30%	AAQLVDKDGTFLSTLEHYLSR	6.19	2,364.22
ATP	6018	nicalin	gi|115494944,gi|94534903	63,091.10	100.00%	4	4	5	0.04%	10.30%	ELETVAAHQFPEVR	3.64	1,625.83
ATP	6018	nicalin	gi|115494944,gi|94534903	63,091.10	100.00%	4	4	5	0.04%	10.30%	MQQYDLQGQPYGTR	3.77	1,700.77
ATP	6018	nicalin	gi|115494944,gi|94534903	63,091.10	100.00%	4	4	5	0.04%	10.30%	TIDADVLSR	2.61	989.5263
ATP	6018	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	5	7	11	0.09%	22.70%	KLPPLPLTLALGAFLNHR	2.86	1,971.19
ATP	6018	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	5	7	11	0.09%	22.70%	LPPLPLTLALGAFLNHR	1.31	1,843.10
ATP	6018	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	5	7	11	0.09%	22.70%	MQDTSVSFGYQLDLPK	4.07	1,844.87
ATP	6018	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	5	7	11	0.09%	22.70%	QLSPTEAFPVLVGDMDNSGSLNAQVIHQLGPGLR	3.74	3,576.81
ATP	6018	translocase of outer mitochondrial membrane 40	gi|115495635,gi|122134275,gi|94534905	37,707.00	100.00%	5	7	11	0.09%	22.70%	RPGEEGAVMSLAGK	3.63	1,417.71
ATP	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	13	14	14	0.12%	14.50%	ADVGFAMGIAGTDVAK	3.91	1,538.75

ATP	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	13	14	14	0.12%	14.50%	EASDIILTDDNFTSIVK	4.1	1,880.95
ATP	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	13	14	14	0.12%	14.50%	GIIDSTVGDQR	3.43	1,160.59
ATP	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	13	14	14	0.12%	14.50%	IDESSLTGESDHVKK	4.05	1,644.81
ATP	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	13	14	14	0.12%	14.50%	KADVGFAMGIAGTDVAK	5.33	1,666.85
ATP	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	13	14	14	0.12%	14.50%	LKTNPVEGLSGNPADLEK	4.88	1,881.99
ATP	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	13	14	14	0.12%	14.50%	NQNSIHNFMTHPEFTIDEEGPR	3.14	2,629.17
ATP	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	13	14	14	0.12%	14.50%	QVVAVTGDGTNDGPALK	5.19	1,641.84

ATP	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	13	14	14	0.12%	14.50%	QVVAVTGDGTNDGPALKK	3.73	1,769.94
ATP	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	13	14	14	0.12%	14.50%	TNPVEGLSGNPADLEK	4.09	1,640.81
ATP	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	13	14	14	0.12%	14.50%	TPLLDEQEEEIFEK	4.91	1,719.83
ATP	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	13	14	14	0.12%	14.50%	TQDGVALEIQPLNSQEGIDSEEKEKK	3.98	2,885.44
ATP	6018	PREDICTED: ATPase, Ca++ transporting, plasma membrane 4 isoform 5	gi|119908026	133,777.70	100.00%	13	14	14	0.12%	14.50%	YGDLLPADGILIQGNDLK	3.86	1,915.02
ATP	6018	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	5	8	27	0.23%	57.70%	AGLQFPVGR	3.43	944.5313
ATP	6018	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	5	8	27	0.23%	57.70%	HLQLAIR	2.29	850.5258

ATP	6018	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	5	8	27	0.23%	57.70%	NDEELNKLLGK	3.7	1,272.68
ATP	6018	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	5	8	27	0.23%	57.70%	VGAGAPVYLAAVLEYLTAEILELAGNAAR	5.71	2,915.59
ATP	6018	PREDICTED: similar to histone cluster 1, H2aj	gi|119915559,gi|119915725,gi|119939855,gi|198282091,gi|76619954,gi|76631269,gi|76633542	14,074.00	100.00%	5	8	27	0.23%	57.70%	VTIAQGGVLPNIQAVLLPK	4.42	1,931.17
ATP	6018	cpn10 protein	gi|1167,gi|27805927,gi|47606334,gi|74354139	10,913.70	99.90%	2	2	2	0.02%	25.50%	VLQATVVAVGSGSK	3.41	1,315.76
ATP	6018	cpn10 protein	gi|1167,gi|27805927,gi|47606334,gi|74354139	10,913.70	99.90%	2	2	2	0.02%	25.50%	VVLDDKDYFLFR	2.69	1,529.80
ATP	6018	RecName: Full=Nucleophosmin; Short=NPM	gi|116248556,gi|74353960,gi|78369456	32,685.20	99.80%	2	3	5	0.04%	11.60%	MSVQPTVSLGGFEITPPVVLR	5.58	2,243.21
ATP	6018	RecName: Full=Nucleophosmin; Short=NPM	gi|116248556,gi|74353960,gi|78369456	32,685.20	99.80%	2	3	5	0.04%	11.60%	VDNDENEHQLSLR	4.08	1,568.73
ATP	6018	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	100.00%	3	3	3	0.03%	8.29%	EIPVLVTQISSTNHPVK	4.46	1,862.04
ATP	6018	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	100.00%	3	3	3	0.03%	8.29%	VGLSDAFVVVHR	3.71	1,298.72
ATP	6018	Plexin domain containing 2	gi|117306639,gi|118150958	59,450.20	100.00%	3	3	3	0.03%	8.29%	VNLSFDFPFYGHFLR	3.2	1,858.93

ATP	6018	RecName: Full=OCIA domain-containing protein 2	gi|122140146,gi|74353966,gi|77735471	16,827.50	99.80%	2	2	2	0.02%	14.30%	FHSFEGQLR	2.9	1,120.55
ATP	6018	RecName: Full=OCIA domain-containing protein 2	gi|122140146,gi|74353966,gi|77735471	16,827.50	99.80%	2	2	2	0.02%	14.30%	VALAGILGFGLGK	4	1,215.75
ATP	6018	RecName: Full=Cathepsin D; Flags: Precursor	gi|13637914,gi|194679949,gi|299522	37,693.30	100.00%	2	2	2	0.02%	9.54%	AQPGGELMLGGTDSK	2.46	1,476.70
ATP	6018	RecName: Full=Cathepsin D; Flags: Precursor	gi|13637914,gi|194679949,gi|299522	37,693.30	100.00%	2	2	2	0.02%	9.54%	QTFGEAIKQPGVVFIAAK	2.87	1,904.06
ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	ASLDRPFTSLESAFYSIVGLSSLGAQVPDVK	4.66	3,254.69

ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	ASLDRPFTSLESAFYSIVGLSSLGAQVPDVKK	4.71	3,382.79
ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	DLLLAAVSEDSSVAQIYHAVAALSGFGLPLASQEALGALTAR	4.34	4,196.22

ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	EETVLATVQALQTASYLSQQADLR	3.35	2,635.36
ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	FSSGYYDFSVK	2.99	1,299.59

ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	GTFIADSHQNFALFFQLVDVNTGAELTPHQTFVR	3.35	3,820.91
ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	ISTEVGITNVDLSTVDKDQSIAPK	5.36	2,530.33

ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	KLEFDSASGTYTLYLIIGDATLK	3.24	2,519.33
ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	KNFESLSEAFSVASAAALSENR	3.85	2,399.18

ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	LDELGGVYLQFEEGLETTALFVAATYK	4.59	2,977.51
ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	LMDHVGTEPSIKEDQVIQLMNAIFSK	5.72	2,959.49

ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	LQVTNVLSQPLTQATVK	4.78	1,840.05
ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	LQVTNVLSQPLTQATVKLEHAK	2.77	2,418.37

ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	LSKEETVLATVQALQTASYLSQQADLR	5.89	2,963.57
ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	NFESLSEAFSVASAAAALSENR	4.08	2,271.09

ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	SIVEEIEDLVAR	4.64	1,372.73
ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	TGQEVVFVAEPDSK	3.87	1,505.75

ATP	6018	RecName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2; AltName: Full=Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit; AltName: Full=Ribophorin-	gi|122140231,gi|146231756,gi|74267729,gi|77736155	69,197.20	100.00%	18	25	39	0.33%	51.70%	YIANTVELR	3.18	1,078.59
ATP	6018	RecName: Full=60S acidic ribosomal protein P2	gi|1173072,gi|27807523,gi|600177,gi|82571755	11,684.40	100.00%	3	3	3	0.03%	56.50%	ILDSVGIEADDDRLNK	4.12	1,772.90
ATP	6018	RecName: Full=60S acidic ribosomal protein P2	gi|1173072,gi|27807523,gi|600177,gi|82571755	11,684.40	100.00%	3	3	3	0.03%	56.50%	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKKEEK	3.31	3,288.71
ATP	6018	RecName: Full=60S acidic ribosomal protein P2	gi|1173072,gi|27807523,gi|600177,gi|82571755	11,684.40	100.00%	3	3	3	0.03%	56.50%	NIEDVIAQGIGK	2.7	1,256.68
ATP	6018	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	3	4	4	0.03%	9.78%	FGQVTPMEVDILFQLADLYEPR	3.13	2,597.30

ATP	6018	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	3	4	4	0.03%	9.78%	GLLPQLLGVAPEK	2.52	1,334.80
ATP	6018	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	3	4	4	0.03%	9.78%	IAPLEEGTLPFNLAEAQR	5.27	1,969.04
ATP	6018	PREDICTED: similar to Calcium-binding mitochondrial carrier protein Aralar2 (Mitochondrial aspartate glutamate carrier 2) (Solute carrier family 25 member 13) (Citrin)	gi|119890734	74,177.70	100.00%	3	4	4	0.03%	9.78%	YLNIFGESQPNPK	3.34	1,506.76

ATP	6018	RecName: Full=DnaJ homolog subfamily B member 11; AltName: Full=ER-associated dnaJ protein 3; AltName: Full=ERj3p; AltName: Full=ERdj3; AltName: Full=ER-associated Hsp40 co-chaperon	gi|122140749,gi|73587163,gi|77735491	40,486.60	99.80%	2	2	2	0.02%	4.75%	FQDLGAAYEVLSDSEK	3.28	1,771.84
ATP	6018	RecName: Full=DnaJ homolog subfamily B member 11; AltName: Full=ER-associated dnaJ protein 3; AltName: Full=ERj3p; AltName: Full=ERdj3; AltName: Full=ER-associated Hsp40 co-chaperon	gi|122140749,gi|73587163,gi|77735491	40,486.60	99.80%	2	2	2	0.02%	4.75%	FQDLGAAYEVLSDSEKR	2.81	1,927.94
ATP	6018	FXYD domain containing ion transport regulator 6	gi|75775070,gi|77735753,gi|91206665	10,447.10	99.80%	2	2	2	0.02%	26.30%	APGDEEAQVENLVTANATEPQK	3.39	2,311.11
ATP	6018	FXYD domain containing ion transport regulator 6	gi|75775070,gi|77735753,gi|91206665	10,447.10	99.80%	2	2	2	0.02%	26.30%	APGDEEAQVENLVTANATEPQKAEN	5.1	2,625.23

ATP	6018	STT3B protein	gi|146186621,gi|148235371	93,202.50	100.00%	3	3	4	0.03%	5.96%	ENPPVEDSSDEDDKRNPGNLYDK	2.55	2,633.16
ATP	6018	STT3B protein	gi|146186621,gi|148235371	93,202.50	100.00%	3	3	4	0.03%	5.96%	FGEMQLDFR	2.46	1,158.53
ATP	6018	STT3B protein	gi|146186621,gi|148235371	93,202.50	100.00%	3	3	4	0.03%	5.96%	HVTEQEKTEEGLGPNIK	3.74	1,908.97
ATP	6018	PREDICTED: similar to Leucine-rich repeat protein SHOC-2 (Ras-binding protein Sur-8)	gi|119890707	98,503.20	99.80%	2	2	2	0.02%	6.84%	DQLTRALTMIGAYEIMDKITALK	3.26	2,611.38
ATP	6018	PREDICTED: similar to Leucine-rich repeat protein SHOC-2 (Ras-binding protein Sur-8)	gi|119890707	98,503.20	99.80%	2	2	2	0.02%	6.84%	KIPPSISNMVSLHVLILCYNKLETFPTEVCTLDNLR	2.59	4,117.15
ATP	6018	Synaptojanin 2 binding protein	gi|74354054,gi|78369420	15,792.00	99.80%	2	4	6	0.05%	19.30%	LQEGDKILSVNGQDLK	3.62	1,756.94
ATP	6018	Synaptojanin 2 binding protein	gi|74354054,gi|78369420	15,792.00	99.80%	2	4	6	0.05%	19.30%	NLLHQDAVDLFR	3.46	1,440.76
ATP	6018	UBA1 protein	gi|126717459,gi|156523068,gi|182702190	117,813.30	100.00%	4	5	5	0.04%	8.51%	IYDDDFFQNLDGVTNALDNVDAR	3.79	2,630.20
ATP	6018	UBA1 protein	gi|126717459,gi|156523068,gi|182702190	117,813.30	100.00%	4	5	5	0.04%	8.51%	KPLLESGTLGTK	2.73	1,243.73
ATP	6018	UBA1 protein	gi|126717459,gi|156523068,gi|182702190	117,813.30	100.00%	4	5	5	0.04%	8.51%	LAELNSYVPVSAYTGPLVEDFLSDFQVVVLTNSPLEDQLR	4.38	4,438.27
ATP	6018	UBA1 protein	gi|126717459,gi|156523068,gi|182702190	117,813.30	100.00%	4	5	5	0.04%	8.51%	LAGTQPLEVLEAVQR	3.45	1,623.91
ATP	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	14	17	34	0.29%	19.70%	DYAKDDPLEFK	2.1	1,340.64
ATP	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	14	17	34	0.29%	19.70%	ENPETEEDVGPVVQHIYELR	2.54	2,353.13

ATP	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	14	17	34	0.29%	19.70%	FDLQIQSSNLFDK	4.16	1,554.78
ATP	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	14	17	34	0.29%	19.70%	FDLQIQSSNLFDKVSPVVSYK	4.03	2,414.26
ATP	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	14	17	34	0.29%	19.70%	FGSAIAPLGDLDQDGFNDIAIAAPYGGEDK	3.26	3,037.44
ATP	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	14	17	34	0.29%	19.70%	FGSAIAPLGDLDQDGFNDIAIAAPYGGEDKK	6.27	3,165.54
ATP	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	14	17	34	0.29%	19.70%	FSVHQQSEMDTSVK	3.98	1,638.74
ATP	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	14	17	34	0.29%	19.70%	GATDIDKNGYPDLIVGAFGVDR	5.48	2,293.15
ATP	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	14	17	34	0.29%	19.70%	GIVYIFNGRPTGLNAVPSQILEGK	3.73	2,543.40
ATP	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	14	17	34	0.29%	19.70%	IYIGDDNPLTLIVK	4.53	1,573.88
ATP	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	14	17	34	0.29%	19.70%	MFLLVGAPK	3.28	991.5647
ATP	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	14	17	34	0.29%	19.70%	SSASFNVIEFPYK	3.64	1,488.74
ATP	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	14	17	34	0.29%	19.70%	VRPPQEEQEREQLQPHENGEGNSET	2.34	2,917.33
ATP	6018	integrin alpha-V subunit	gi|11596385,gi|124056464	116,117.20	100.00%	14	17	34	0.29%	19.70%	YKENPETEEDVGPVVQHIYELR	4.35	2,644.29
ATP	6018	RecName: Full=Transaldolase	gi|110816439,gi|164420731,gi|83638723	37,668.70	99.80%	2	2	2	0.02%	12.20%	LSFDKDAMVAR	2.25	1,268.63
ATP	6018	RecName: Full=Transaldolase	gi|110816439,gi|164420731,gi|83638723	37,668.70	99.80%	2	2	2	0.02%	12.20%	NTGEIKALAGCDFLTISPQLLGELLKDHSK	3.38	3,211.70
ATP	6018	poly(A) binding protein, cytoplasmic 1	gi|41386798,gi|47117093,gi|74268035,gi|8979741	70,653.30	100.00%	3	3	3	0.03%	6.60%	ALDTMNFDVIK	2.65	1,282.64
ATP	6018	poly(A) binding protein, cytoplasmic 1	gi|41386798,gi|47117093,gi|74268035,gi|8979741	70,653.30	100.00%	3	3	3	0.03%	6.60%	IVATKPLYVALAQR	3.28	1,542.94

ATP	6018	poly(A) binding protein, cytoplasmic 1	gi|41386798,gi|47117093,gi|74268035,gi|8979741	70,653.30	100.00%	3	3	3	0.03%	6.60%	SLGYAYVNFQQPADAER	2.42	1,928.91
ATP	6018	RecName: Full=Monocarboxylate transporter 1; Short=MCT 1; AltName: Full=Solute carrier family 16 member 1	gi|122139973,gi|77567740,gi|82617542	54,281.70	100.00%	4	5	5	0.04%	6.99%	ESKDEETNVDVAEKPK	2.32	1,817.88
ATP	6018	RecName: Full=Monocarboxylate transporter 1; Short=MCT 1; AltName: Full=Solute carrier family 16 member 1	gi|122139973,gi|77567740,gi|82617542	54,281.70	100.00%	4	5	5	0.04%	6.99%	GASDANTDLIGGNPK	4.18	1,429.69
ATP	6018	RecName: Full=Monocarboxylate transporter 1; Short=MCT 1; AltName: Full=Solute carrier family 16 member 1	gi|122139973,gi|77567740,gi|82617542	54,281.70	100.00%	4	5	5	0.04%	6.99%	GASDANTDLIGGNPKEEK	4.62	1,815.87

ATP	6018	RecName: Full=Monocarboxylate transporter 1; Short=MCT 1; AltName: Full=Solute carrier family 16 member 1	gi|122139973,gi|77567740,gi|82617542	54,281.70	100.00%	4	5	5	0.04%	6.99%	GASDANTDLIGGNPKEEKK	2.16	1,943.97
ATP	6018	RecName: Full=L-lactate dehydrogenase B chain; Short=LDH-B	gi|118572666,gi|148744825,gi|154425698,gi|27806561,gi|59858383,gi|74353944,gi|8979739	36,606.70	100.00%	2	3	3	0.03%	7.49%	IVADKDYSVTANSK	4.58	1,510.77
ATP	6018	RecName: Full=L-lactate dehydrogenase B chain; Short=LDH-B	gi|118572666,gi|148744825,gi|154425698,gi|27806561,gi|59858383,gi|74353944,gi|8979739	36,606.70	100.00%	2	3	3	0.03%	7.49%	MVVESAYEVIK	2.81	1,283.66
ATP	6018	PREDICTED: similar to programmed cell death 6 interacting protein isoform 1	gi|119914274	96,862.00	100.00%	4	4	4	0.03%	7.54%	EPSAPSIPTPTYQSSPAGGHAPTPPTPAPR	1.87	2,966.46
ATP	6018	PREDICTED: similar to programmed cell death 6 interacting protein isoform 1	gi|119914274	96,862.00	100.00%	4	4	4	0.03%	7.54%	LLDEEEATDNDLR	3.87	1,532.71
ATP	6018	PREDICTED: similar to programmed cell death 6 interacting protein isoform 1	gi|119914274	96,862.00	100.00%	4	4	4	0.03%	7.54%	NIQVSHQEFSK	3.48	1,316.66

ATP	6018	PREDICTED: similar to programmed cell death 6 interacting protein isoform 1	gi|119914274	96,862.00	100.00%	4	4	4	0.03%	7.54%	TMQGSEVVNVLK	3.65	1,320.68
ATP	6018	ACTR2 protein	gi|154425680,gi|156121073,gi|17943200,gi|182627520,gi|56966173,gi|56966193	44,743.70	99.80%	2	2	2	0.02%	6.09%	DLMVGDEASELR	3.01	1,350.62
ATP	6018	ACTR2 protein	gi|154425680,gi|156121073,gi|17943200,gi|182627520,gi|56966173,gi|56966193	44,743.70	99.80%	2	2	2	0.02%	6.09%	ILLTEPPMNPTK	3.14	1,369.74
ATP	6018	Sec61 alpha 1 subunit (S. cerevisiae)	gi|154426140,gi|59857767,gi|75060961,gi|94966817	52,208.90	100.00%	4	6	15	0.13%	17.40%	GMEFEGAIIALFHLLATR	4.63	2,005.06
ATP	6018	Sec61 alpha 1 subunit (S. cerevisiae)	gi|154426140,gi|59857767,gi|75060961,gi|94966817	52,208.90	100.00%	4	6	15	0.13%	17.40%	GTLMELGISPIVTSGLIMQLLAGAK	4.06	2,529.40
ATP	6018	Sec61 alpha 1 subunit (S. cerevisiae)	gi|154426140,gi|59857767,gi|75060961,gi|94966817	52,208.90	100.00%	4	6	15	0.13%	17.40%	LFYTSNIPIILQSALVSNLYVISQMLSAR	4.82	3,270.78
ATP	6018	Sec61 alpha 1 subunit (S. cerevisiae)	gi|154426140,gi|59857767,gi|75060961,gi|94966817	52,208.90	100.00%	4	6	15	0.13%	17.40%	YRGQYNTYPIK	2.79	1,402.71
ATP	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	15	18	27	0.23%	35.50%	AVDSLVPIGR	3.2	1,026.59

ATP	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	15	18	27	0.23%	35.50%	EVAAFAQFGSDLDAATQQLLSR	4.27	2,338.17
ATP	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	15	18	27	0.23%	35.50%	FENAFLSHVISQHQALLSK	2.94	2,169.15
ATP	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	15	18	27	0.23%	35.50%	GIRPAINVGLSVSR	2.62	1,438.85
ATP	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	15	18	27	0.23%	35.50%	GMSLNLEPDNVGVVVFGNDK	4.9	2,120.03
ATP	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	15	18	27	0.23%	35.50%	GYLDKLEPSK	1.94	1,149.62
ATP	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	15	18	27	0.23%	35.50%	HALIIYDLSK	3.44	1,287.69

ATP	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	15	18	27	0.23%	35.50%	ILGADTSVDLEETGR	4.42	1,575.79
ATP	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	15	18	27	0.23%	35.50%	ITKFENAFLSHVISQHQALLSK	4.5	2,511.37
ATP	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	15	18	27	0.23%	35.50%	RTGAIVDVPVGEELLGR	2.74	1,780.99
ATP	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	15	18	27	0.23%	35.50%	TGAIVDVPVGEELLGR	4.19	1,624.89
ATP	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	15	18	27	0.23%	35.50%	TSIAIDTIINQK	3.28	1,316.74
ATP	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	15	18	27	0.23%	35.50%	VLSIGDGIAR	2.25	1,000.58

ATP	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	15	18	27	0.23%	35.50%	VVDALGNAIDGK	3.97	1,171.63
ATP	6018	H(+)-transporting ATP synthase	gi|102,gi|114402,gi|158429020,gi|158429021,gi|158429022,gi|158431066,gi|158431067,gi|158431068,gi|27807237	55,248.00	100.00%	15	18	27	0.23%	35.50%	VVDALGNAIDGKGPIGSK	4.58	1,710.94
ATP	6018	PREDICTED: similar to 60S ribosomal protein L9	gi|119904384,gi|119905715,gi|164420694,gi|76607197,gi|91207745	21,858.70	99.80%	2	2	2	0.02%	15.10%	FLDGIYVSEK	2.73	1,170.60
ATP	6018	PREDICTED: similar to 60S ribosomal protein L9	gi|119904384,gi|119905715,gi|164420694,gi|76607197,gi|91207745	21,858.70	99.80%	2	2	2	0.02%	15.10%	TILSNQTVDIPENVDINLK	3.4	2,126.13
ATP	6018	Actin related protein 2/3 complex, subunit 4, 20kDa	gi|109939945,gi|115495705,gi|119361249,gi|149243014,gi|149243029,gi|149243036,gi|149243043,gi|149243050,gi|149243057,gi|149243064,gi|56966197	19,649.40	99.80%	2	2	2	0.02%	11.30%	AENFFILR	2.41	1,009.55
ATP	6018	Actin related protein 2/3 complex, subunit 4, 20kDa	gi|109939945,gi|115495705,gi|119361249,gi|149243014,gi|149243029,gi|149243036,gi|149243043,gi|149243050,gi|149243057,gi|149243064,gi|56966197	19,649.40	99.80%	2	2	2	0.02%	11.30%	VLIEGSINSVR	2.98	1,186.68

ATP	6018	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	6	7	14	0.12%	30.30%	IMVANIEEVLQR	4.13	1,430.77
ATP	6018	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	6	7	14	0.12%	30.30%	KLAFAYLEDLHSEFDEQHGK	3.58	2,377.15
ATP	6018	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	6	7	14	0.12%	30.30%	NLGSINTELQDVQR	5.31	1,586.81
ATP	6018	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	6	7	14	0.12%	30.30%	RNLGSINTELQDVQR	4.24	1,742.91
ATP	6018	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	6	7	14	0.12%	30.30%	VADGLPLAASMQEDEQSGR	4.33	1,989.92
ATP	6018	SEC22 vesicle trafficking protein homolog B	gi|115496488,gi|74354583	28,710.00	100.00%	6	7	14	0.12%	30.30%	VADGLPLAASMQEDEQSGRDLQQYQSQAK	4.05	3,179.49
ATP	6018	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	5	7	10	0.09%	27.70%	INVNEIFYDLVR	3.89	1,494.80
ATP	6018	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	5	7	10	0.09%	27.70%	LVVLGSGGVGK	2.86	985.6042
ATP	6018	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	5	7	10	0.09%	27.70%	SKINVNEIFYDLVR	3.46	1,709.92
ATP	6018	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	5	7	10	0.09%	27.70%	VKDTDDVPMILVGNK	4	1,659.86
ATP	6018	GTP-binding protein (smg p21B)	gi|163722,gi|28461271,gi|47117722,gi|74354581	20,806.90	100.00%	5	7	10	0.09%	27.70%	YDPTIEDSYRK	2.94	1,386.65
ATP	6018	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	7	8	9	0.08%	14.60%	EEAAAAAPAPAADDQGVLK	3.6	1,794.89
ATP	6018	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	7	8	9	0.08%	14.60%	KREEAAAAAPAPAADDQGVLK	3.82	2,079.08

ATP	6018	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	7	8	9	0.08%	14.60%	LQEMLSVGLGFLR	3.16	1,478.80
ATP	6018	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	7	8	9	0.08%	14.60%	NKGDSHLNVQVSNFK	3.87	1,686.86
ATP	6018	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	7	8	9	0.08%	14.60%	TELGLDLGLEPK	3.32	1,284.70
ATP	6018	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	7	8	9	0.08%	14.60%	TIEVAEEEVVR	2.82	1,273.66
ATP	6018	metadherin	gi|114051299,gi|89994114	64,037.90	100.00%	7	8	9	0.08%	14.60%	TISTSDPADALIK	3.2	1,331.71
ATP	6018	RecName: Full=Aconitate hydratase, mitochondrial; Short=Aconitase; AltName: Full=Citrate hydro-lyase; Flags: Precursor	gi|110282935,gi|1364216,gi|27806769,gi|74268076,gi|90970312	85,342.00	99.80%	2	2	2	0.02%	3.72%	FKLEAPDADELPR	3.27	1,500.77
ATP	6018	RecName: Full=Aconitate hydratase, mitochondrial; Short=Aconitase; AltName: Full=Citrate hydro-lyase; Flags: Precursor	gi|110282935,gi|1364216,gi|27806769,gi|74268076,gi|90970312	85,342.00	99.80%	2	2	2	0.02%	3.72%	IVYGHLDDPANQEIER	4.75	1,868.91
ATP	6018	RecName: Full=ATP synthase subunit g, mitochondrial; Short=ATPase subunit g	gi|2493093,gi|74354012,gi|7579922,gi|94400870	11,604.00	100.00%	3	4	5	0.04%	37.50%	APALVNAAVTYSKPR	3.8	1,557.87

ATP	6018	RecName: Full=ATP synthase subunit g, mitochondrial; Short=ATPase subunit g	gi|2493093,gi|74354012,gi|7579922,gi|94400870	11,604.00	100.00%	3	4	5	0.04%	37.50%	NLAEKAPALVNAAVTYSKPR	4.87	2,113.18
ATP	6018	RecName: Full=ATP synthase subunit g, mitochondrial; Short=ATPase subunit g	gi|2493093,gi|74354012,gi|7579922,gi|94400870	11,604.00	100.00%	3	4	5	0.04%	37.50%	VELVPPTPAEIPTAIQSLK	2.62	2,003.14
ATP	6018	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	100.00%	4	4	4	0.03%	19.20%	DTILQLNLK	2.48	1,057.63
ATP	6018	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	100.00%	4	4	4	0.03%	19.20%	LLLLGTGESGK	3.11	1,087.64
ATP	6018	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	100.00%	4	4	4	0.03%	19.20%	VADPAYLPTQQDVLR	3.86	1,685.89
ATP	6018	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	100.00%	4	4	4	0.03%	19.20%	VPTTGIIEYPFDLQSVIFR	4.59	2,195.17
ATP	6018	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	100.00%	4	4	4	0.03%	19.20%	VRVPTTGIIEYPFDLQSVIFR	4.31	2,450.34

ATP	6018	guanine nucleotide binding protein (G protein), q polypeptide	gi|158508558	42,125.60	100.00%	4	4	4	0.03%	19.20%	VSAFENPYVDAIK	3.17	1,452.74
ATP	6018	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	100.00%	4	4	4	0.03%	8.23%	LPVPASAPIPFFHR	3.47	1,548.87
ATP	6018	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	100.00%	4	4	4	0.03%	8.23%	NAELEAIPNSGMDHTHR	2.7	1,907.87
ATP	6018	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	100.00%	4	4	4	0.03%	8.23%	NLPFTPILASVNR	3.03	1,441.82
ATP	6018	PREDICTED: similar to CDW92 antigen isoform 1	gi|119900917,gi|119900919	72,875.80	100.00%	4	4	4	0.03%	8.23%	VLMEFVENSR	3.58	1,239.60
ATP	6018	RecName: Full=60S ribosomal protein L7a	gi|108860939,gi|146231828,gi|83638795,gi|94966839	30,008.40	99.80%	2	2	3	0.03%	10.20%	LKVPPAINQFTQALDR	4.91	1,811.02
ATP	6018	RecName: Full=60S ribosomal protein L7a	gi|108860939,gi|146231828,gi|83638795,gi|94966839	30,008.40	99.80%	2	2	3	0.03%	10.20%	NFGIGQDIQPK	2.7	1,216.63
ATP	6018	RecName: Full=Transgelin; AltName: Full=Smooth muscle protein 22-alpha; Short=SM22-alpha; AltName: Full=25 kDa F-actin-binding protein	gi|109940320,gi|114051586,gi|86823808	22,580.80	100.00%	4	5	5	0.04%	27.90%	EFTESQLQEGK	2.49	1,295.61

ATP	6018	RecName: Full=Transgelin; AltName: Full=Smooth muscle protein 22-alpha; Short=SM22-alpha; AltName: Full=25 kDa F-actin-binding protein	gi|109940320,gi|114051586,gi|86823808	22,580.80	100.00%	4	5	5	0.04%	27.90%	LVNSLYPDGSKPVKVPENPPSMVFK	3.9	2,758.45
ATP	6018	RecName: Full=Transgelin; AltName: Full=Smooth muscle protein 22-alpha; Short=SM22-alpha; AltName: Full=25 kDa F-actin-binding protein	gi|109940320,gi|114051586,gi|86823808	22,580.80	100.00%	4	5	5	0.04%	27.90%	TDMFQTVDLFEGK	2.67	1,546.71
ATP	6018	RecName: Full=Transgelin; AltName: Full=Smooth muscle protein 22-alpha; Short=SM22-alpha; AltName: Full=25 kDa F-actin-binding protein	gi|109940320,gi|114051586,gi|86823808	22,580.80	100.00%	4	5	5	0.04%	27.90%	TDMFQTVDLFEGKDLAAVQR	2.89	2,300.12

ATP	6018	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	6	8	8	0.07%	22.20%	GFKDQIYDIFQK	4.17	1,501.77
ATP	6018	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	6	8	8	0.07%	22.20%	GIYAYGFEKPSAIQQR	5.13	1,827.94
ATP	6018	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	6	8	8	0.07%	22.20%	GYDVIAQAQSGTGK	4.05	1,394.69

ATP	6018	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	6	8	8	0.07%	22.20%	LNSNTQVVLLSATMPSDVLEVTK	3.78	2,475.30
ATP	6018	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	6	8	8	0.07%	22.20%	LQMEAPHIIVGTPGR	3.24	1,634.87
ATP	6018	RecName: Full=Eukaryotic initiation factor 4A-I; Short=eIF-4A-I; Short=eIF4A-I; AltName: Full=ATP-dependent RNA helicase eIF4A-1	gi|109892471,gi|74268155,gi|77735407	46,137.30	100.00%	6	8	8	0.07%	22.20%	VLITTDLLAR	3.12	1,114.68
ATP	6018	CDGSH iron sulfur domain 2	gi|115545422,gi|122131734,gi|122692399	15,260.70	99.80%	2	2	2	0.02%	9.63%	LPVPESITGFAR	2.29	1,286.71
ATP	6018	CDGSH iron sulfur domain 2	gi|115545422,gi|122131734,gi|122692399	15,260.70	99.80%	2	2	2	0.02%	9.63%	RLPVPESITGFAR	2.73	1,442.81

ATP	6018	RecName: Full=Mitochondrial Rho GTPase 1; Short=MIRO-1; AltName: Full=Ras homolog gene family member T1	gi|108860795,gi|114051724,gi|88682961	72,061.70	100.00%	3	4	4	0.03%	10.10%	ISDQDNDGTLNDAELNFFQR	4.4	2,312.04
ATP	6018	RecName: Full=Mitochondrial Rho GTPase 1; Short=MIRO-1; AltName: Full=Ras homolog gene family member T1	gi|108860795,gi|114051724,gi|88682961	72,061.70	100.00%	3	4	4	0.03%	10.10%	NISELFYYAQK	3.32	1,375.69
ATP	6018	RecName: Full=Mitochondrial Rho GTPase 1; Short=MIRO-1; AltName: Full=Ras homolog gene family member T1	gi|108860795,gi|114051724,gi|88682961	72,061.70	100.00%	3	4	4	0.03%	10.10%	TSLIMSLVSEEFPEEVPPRAEEITIPADVTPER	2.96	3,697.85
ATP	6018	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	12	15	0.13%	27.20%	DVYVQLYLQHLTAR	3.74	1,718.92
ATP	6018	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	12	15	0.13%	27.20%	GAAGRPLELSDFR	2.06	1,388.73
ATP	6018	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	12	15	0.13%	27.20%	GPPDFSSDEEREPTPVLGSGAAVAGR	5.6	2,598.24
ATP	6018	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	12	15	0.13%	27.20%	HAAPILPITEFSDIPR	3.36	1,776.96
ATP	6018	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	12	15	0.13%	27.20%	LKSELVANNVTLPAGEQR	6.01	1,939.06

ATP	6018	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	12	15	0.13%	27.20%	LKSELVANNVTLPAGEQRK	4.17	2,067.16
ATP	6018	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	12	15	0.13%	27.20%	SELVANNVTLPAGEQR	3.96	1,697.88
ATP	6018	TMPO protein	gi|146186841,gi|147902328	42,927.20	100.00%	8	12	15	0.13%	27.20%	SSTPLPTISSSVENTR	3.64	1,675.85
ATP	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	15	17	17	0.15%	9.92%	AVSSAIAQLLGEVAQGNENYAGIAAR	5.77	2,573.33
ATP	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	15	17	17	0.15%	9.92%	GISMSSSKLLLAAKALSTDPAAPTLK	3.29	2,571.44
ATP	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	15	17	17	0.15%	9.92%	GLAGAVSELLR	3.8	1,085.63
ATP	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	15	17	17	0.15%	9.92%	GVGAAATAVTQALNELLQHVR	3.72	2,119.16
ATP	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	15	17	17	0.15%	9.92%	ILAQATSDLVNAIK	4.19	1,456.84
ATP	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	15	17	17	0.15%	9.92%	LAQAAQSSVATITR	3.71	1,416.78
ATP	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	15	17	17	0.15%	9.92%	LLAALLEDEGGSGRPLLQAAK	3.8	2,122.19
ATP	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	15	17	17	0.15%	9.92%	LNEAAAGLNQAATELVQASR	5.12	2,027.05
ATP	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	15	17	17	0.15%	9.92%	NLGTALAELR	2.49	1,057.60
ATP	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	15	17	17	0.15%	9.92%	TLAESALQLLYTAK	3.24	1,521.85
ATP	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	15	17	17	0.15%	9.92%	TLSHPQQMALLDQTK	3.99	1,726.88
ATP	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	15	17	17	0.15%	9.92%	TMLESAGGLIQTAR	3.81	1,463.75
ATP	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	15	17	17	0.15%	9.92%	VLGEAMTGISQNAK	4.08	1,434.73
ATP	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	15	17	17	0.15%	9.92%	VMVTNVTSLLK	2.5	1,220.69
ATP	6018	PREDICTED: talin 1	gi|119900517	269,759.80	100.00%	15	17	17	0.15%	9.92%	VSQMAQYFEPLTLAAVGAASK	4.7	2,198.12
ATP	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	11	12	0.10%	21.80%	DLGLFGLYK	2.48	1,025.57
ATP	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	11	12	0.10%	21.80%	FGLYLPK	2.77	837.487

ATP	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	11	12	0.10%	21.80%	FKPPSVAVVQPK	2.86	1,296.77
ATP	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	11	12	0.10%	21.80%	FTLGSVAGAVGATAVYPIDLVK	3.68	2,149.19
ATP	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	11	12	0.10%	21.80%	GLIPQLIGVAPEK	2.52	1,334.80
ATP	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	11	12	0.10%	21.80%	HLNYTEFTQFLQELQLEHAR	5	2,517.25
ATP	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	11	12	0.10%	21.80%	IAPLAEGALPYNLAELQR	3.34	1,939.06
ATP	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	11	12	0.10%	21.80%	LTLADIER	2.33	930.5256
ATP	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	11	12	0.10%	21.80%	NIFLQYASTEVDGEHYMTPEDFVQR	3.59	3,005.36
ATP	6018	SLC25A12 protein	gi|151556133,gi|155372111	74,513.90	100.00%	10	11	12	0.10%	21.80%	YLGLYNDPNSNPK	4.26	1,494.72
ATP	6018	RecName: Full=Cytochrome b5	gi|117806,gi|1372997,gi|157830773,gi|27806667,gi|298,gi|79160196	15,311.60	100.00%	3	3	4	0.03%	34.30%	EQAGGDATENFEDVGHSTDAR	2.85	2,205.93
ATP	6018	RecName: Full=Cytochrome b5	gi|117806,gi|1372997,gi|157830773,gi|27806667,gi|298,gi|79160196	15,311.60	100.00%	3	3	4	0.03%	34.30%	FLEEHPGGEEVLR	2.48	1,511.75
ATP	6018	RecName: Full=Cytochrome b5	gi|117806,gi|1372997,gi|157830773,gi|27806667,gi|298,gi|79160196	15,311.60	100.00%	3	3	4	0.03%	34.30%	TFIIGELHPDDR	3.56	1,412.72
ATP	6018	IKK interacting protein	gi|126010633,gi|126165284,gi|193806036	39,199.60	100.00%	3	3	3	0.03%	10.00%	LEPLVNDLTLR	2.56	1,282.74
ATP	6018	IKK interacting protein	gi|126010633,gi|126165284,gi|193806036	39,199.60	100.00%	3	3	3	0.03%	10.00%	METSEFQGLQSK	3.46	1,400.64
ATP	6018	IKK interacting protein	gi|126010633,gi|126165284,gi|193806036	39,199.60	100.00%	3	3	3	0.03%	10.00%	NIGDLLSSSIDR	3.98	1,289.67
ATP	6018	ALDH3A2 protein	gi|151557095,gi|156120617	54,059.30	100.00%	3	3	3	0.03%	7.84%	EKDILAAIGADLSK	2.41	1,443.81
ATP	6018	ALDH3A2 protein	gi|151557095,gi|156120617	54,059.30	100.00%	3	3	3	0.03%	7.84%	IAFGGEMDEATR	3.01	1,312.58
ATP	6018	ALDH3A2 protein	gi|151557095,gi|156120617	54,059.30	100.00%	3	3	3	0.03%	7.84%	NADEAIQFINER	3.22	1,419.69

ATP	6018	defender against cell death 1	gi|59858361,gi|73918963,gi|74354770,gi|77736467,gi|83286811	12,477.50	99.80%	2	2	5	0.04%	19.50%	ADFQGISPER	3.07	1,119.54
ATP	6018	defender against cell death 1	gi|59858361,gi|73918963,gi|74354770,gi|77736467,gi|83286811	12,477.50	99.80%	2	2	5	0.04%	19.50%	FLEEYLSATPQR	3.65	1,453.73
ATP	6018	heterogeneous nuclear ribonucleoprotein A1	gi|114052384,gi|172046785,gi|86823844	34,178.40	100.00%	3	4	4	0.03%	13.10%	IEVIEIMTDR	2.72	1,234.64
ATP	6018	heterogeneous nuclear ribonucleoprotein A1	gi|114052384,gi|172046785,gi|86823844	34,178.40	100.00%	3	4	4	0.03%	13.10%	LFIGGLSFETTDESLR	4.55	1,784.91
ATP	6018	heterogeneous nuclear ribonucleoprotein A1	gi|114052384,gi|172046785,gi|86823844	34,178.40	100.00%	3	4	4	0.03%	13.10%	SSGPYGGGGQYFAKPR	4.25	1,628.78
ATP	6018	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	6	6	6	0.05%	10.60%	DFFTTGSPGETAFR	3.21	1,532.70
ATP	6018	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	6	6	6	0.05%	10.60%	EFDLTKEEDLAALRHEIELR	2.69	2,427.25
ATP	6018	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	6	6	6	0.05%	10.60%	EVLEDFAEDSEK	2.65	1,410.63
ATP	6018	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	6	6	6	0.05%	10.60%	GNSSESIEAIRDYEEEFFQNSK	4.72	2,579.15
ATP	6018	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	6	6	6	0.05%	10.60%	MLAITANTLR	2.97	1,119.62

ATP	6018	PREDICTED: similar to optic atrophy 1 isoform 16	gi|194663697	115,574.20	100.00%	6	6	6	0.05%	10.60%	SLIDMYSEVLDVLSDYDASYNTQDHLPR	4.69	3,275.51
ATP	6018	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	4	4	4	0.03%	12.50%	AFITNIPFDVK	3.25	1,264.69
ATP	6018	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	4	4	4	0.03%	12.50%	GDFFPPERPQQLPHGLGGIGMGLGPGGQPIDANHLNK	3.32	3,834.91
ATP	6018	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	4	4	4	0.03%	12.50%	GNFGGSFAGSFGGAGGHAPGVAR	3.15	2,034.95
ATP	6018	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform 2	gi|119894863	77,466.20	100.00%	4	4	4	0.03%	12.50%	MEEESGAPGVPSGNGAPGPK	2.81	1,883.84
ATP	6018	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	7	9	13	0.11%	18.40%	ELQALTDAMYTNLR	2.95	1,654.81
ATP	6018	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	7	9	13	0.11%	18.40%	EVVADLALPMADGR	3.81	1,472.74
ATP	6018	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	7	9	13	0.11%	18.40%	LLLFPFLSPQK	2.83	1,302.78
ATP	6018	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	7	9	13	0.11%	18.40%	LLLFPFLSPQKDPEIYTDPEVFK	5.3	2,736.45
ATP	6018	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	7	9	13	0.11%	18.40%	LTAAPFITR	2.67	989.5779

ATP	6018	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	7	9	13	0.11%	18.40%	VLDSMPVLDSVLSESLR	3.79	1,875.97
ATP	6018	Prostaglandin I2 (prostacyclin) synthase	gi|112362385,gi|2493372,gi|27806107,gi|538523	56,613.60	100.00%	7	9	13	0.11%	18.40%	YGFGLMQPEHDVPVR	2.26	1,760.84
ATP	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	5	6	0.05%	39.20%	AILVDLEPGTMDSVR	4.42	1,631.83
ATP	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	5	6	0.05%	39.20%	ALTVPELTQQVFDAK	3.52	1,659.90
ATP	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	5	6	0.05%	39.20%	FPGQLNADLR	2.72	1,130.60
ATP	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	5	6	0.05%	39.20%	FPGQLNADLRK	2.7	1,258.69
ATP	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	5	6	0.05%	39.20%	GHYTEGAELVDSVLDVVR	4.05	1,958.98
ATP	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	5	6	0.05%	39.20%	GHYTEGAELVDSVLDVVRK	4.32	2,087.08
ATP	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	5	6	0.05%	39.20%	IMNTFSVVPSPK	3.92	1,335.70
ATP	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	5	6	0.05%	39.20%	IREEYPDRIMNTFSVVPSPK	2.87	2,394.21
ATP	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	5	6	0.05%	39.20%	ISEQFTAMFR	2.79	1,245.59
ATP	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	5	6	0.05%	39.20%	ISVYYNEATGGK	2.7	1,301.64
ATP	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	5	6	0.05%	39.20%	LAVNMVPFPR	4.05	1,159.63
ATP	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	5	6	0.05%	39.20%	LHFFMPGFAPLTSR	3.36	1,636.83
ATP	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	5	6	0.05%	39.20%	VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	4.3	4,479.06
ATP	6018	tubulin, beta	gi|114052731,gi|146231774,gi|86823832	49,652.60	100.00%	3	5	6	0.05%	39.20%	YLTVAAVFR	2.97	1,039.59

ATP	6018	melanoma cell adhesion molecule	gi|2323281	9,468.30	99.80%	2	5	9	0.08%	22.10%	SDKLPEEMGLLQGSSGDK	4.92	1,906.91
ATP	6018	melanoma cell adhesion molecule	gi|2323281	9,468.30	99.80%	2	5	9	0.08%	22.10%	SDKLPEEMGLLQGSSGDKR	4.21	2,063.01
ATP	6018	RecName: Full=Ornithine aminotransferase, mitochondrial; AltName: Full=Ornithine--oxo-acid aminotransferase; Flags: Precursor	gi|122140925,gi|73586966,gi|77735431	48,058.30	100.00%	4	4	4	0.03%	16.20%	GLLNAIVIR	2.83	968.6252
ATP	6018	RecName: Full=Ornithine aminotransferase, mitochondrial; AltName: Full=Ornithine--oxo-acid aminotransferase; Flags: Precursor	gi|122140925,gi|73586966,gi|77735431	48,058.30	100.00%	4	4	4	0.03%	16.20%	SQVDKLTLTSR	2.88	1,247.70
ATP	6018	RecName: Full=Ornithine aminotransferase, mitochondrial; AltName: Full=Ornithine--oxo-acid aminotransferase; Flags: Precursor	gi|122140925,gi|73586966,gi|77735431	48,058.30	100.00%	4	4	4	0.03%	16.20%	TLSAISSSTDPTSYDGFGPFMPGFEIIPYNDLPALER	3.26	4,021.91

ATP	6018	RecName: Full=Ornithine aminotransferase, mitochondrial; AltName: Full=Ornithine--oxo-acid aminotransferase; Flags: Precursor	gi|122140925,gi|73586966,gi|77735431	48,058.30	100.00%	4	4	4	0.03%	16.20%	TVQGPPSSDYIFER	2.48	1,595.77
ATP	6018	dihydropyrimidinase-like 2	gi|115496400,gi|1916227,gi|3122018,gi|88954346	62,259.90	99.80%	2	2	2	0.02%	11.00%	ILDLGITGPEGHVLSRPEEVEAEAVNR	3.24	2,900.51
ATP	6018	dihydropyrimidinase-like 2	gi|115496400,gi|1916227,gi|3122018,gi|88954346	62,259.90	99.80%	2	2	2	0.02%	11.00%	MDENQFVAVTSTNAAK	3.45	1,741.81
ATP	6018	dihydropyrimidinase-like 2	gi|115496400,gi|1916227,gi|3122018,gi|88954346	62,259.90	99.80%	2	2	2	0.02%	11.00%	NLHQSGFSLSGAQIDDNIPR	3.27	2,169.07
ATP	6018	RAP2B protein	gi|134025188,gi|154425870,gi|156523174	20,470.40	99.80%	2	3	3	0.03%	20.80%	ASVDELFAEIVR	2.95	1,348.71
ATP	6018	RAP2B protein	gi|134025188,gi|154425870,gi|156523174	20,470.40	99.80%	2	3	3	0.03%	20.80%	EIEVDSSPSVLEILDTAGTEQFASMR	5.29	2,840.35
ATP	6018	RecName: Full=Transmembrane protein 111	gi|115311872,gi|73587331,gi|78050079	29,903.00	99.80%	2	2	2	0.02%	8.43%	LTQEQVSDSQVLIR	3.86	1,615.87
ATP	6018	RecName: Full=Transmembrane protein 111	gi|115311872,gi|73587331,gi|78050079	29,903.00	99.80%	2	2	2	0.02%	8.43%	VPFPLTLR	2.37	942.5772
ATP	6018	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	3	3	85	0.73%	30.30%	FFESFGDLSSADAILGNPK	2.71	2,014.98
ATP	6018	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	3	3	85	0.73%	30.30%	LLGNVLVVVLAR	4.3	1,265.83

ATP	6018	Hemoglobin, gamma 2	gi|158455008,gi|160333301,gi|393,gi|62460494	15,841.20	100.00%	3	3	85	0.73%	30.30%	VKVDEVGGEALGR	4.01	1,328.72
ATP	6018	vesicle-associated membrane protein 5	gi|114050717,gi|122135927,gi|86826577	12,760.30	99.80%	2	2	3	0.03%	24.10%	QADEVTEIMLNNFDK	3.61	1,782.82
ATP	6018	vesicle-associated membrane protein 5	gi|114050717,gi|122135927,gi|86826577	12,760.30	99.80%	2	2	3	0.03%	24.10%	SDQLLDMSSAFSK	3.53	1,444.66
ATP	6018	Ribosomal protein L6	gi|126717393,gi|58760432,gi|61553343,gi|61553350,gi|67461090,gi|72534798	32,672.90	99.80%	2	2	2	0.02%	11.10%	ASITPGTILIILTGR	3.91	1,525.93
ATP	6018	Ribosomal protein L6	gi|126717393,gi|58760432,gi|61553343,gi|61553350,gi|67461090,gi|72534798	32,672.90	99.80%	2	2	2	0.02%	11.10%	QLGSGLLLVTGPLSLNR	3.28	1,738.02
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	AFGPGLQGGSAGSPAR	4.15	1,429.72
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	ANLPQSFQVDTSK	3	1,434.72
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	ASGPGLNTTGVPASLPVEFTIDAK	3.9	2,342.22
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	AYGPGIEPTGNMVK	3.27	1,449.70

ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	DVDIIDHHDNTYTVK	2.6	1,784.85
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	EGPYSISVLYGDEEVPR	3.44	1,909.92
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	FADQHVPGSPFSVK	3.56	1,515.76
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	GAGTGGLGLAVEGPSEAK	4.5	1,570.81
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	IANLQTDLSDGLR	3.49	1,415.75
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	LIALLEVLSQK	2.93	1,226.77
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	LPQLPITNFSR	2.42	1,285.73
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	LTVSSLQESGLK	3.52	1,261.70

ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	RLTVSSLQESGLK	3.55	1,417.80
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	VAQPAITDNKDGTVTVR	4.5	1,784.95
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	VSGQGLHEGHTFEPAEFIIDTR	2.74	2,440.19
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	VTAQGPGLEPSGNIANK	4.69	1,652.86
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	VTVLFAGQHIAK	3.94	1,283.75
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	VTYTPMAPGSYLISIK	2.77	1,756.92
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	YGGPYHIAGSPFK	2.76	1,393.69
ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	YKGQHVPGSPFQFTVGPLGEGGAHK	2.4	2,595.31

ATP	6018	PREDICTED: filamin A, alpha (actin binding protein 280)	gi|194680254	276,424.10	100.00%	20	22	23	0.20%	12.40%	YTPVQQGPVGINVTYGGDAIPK	5.63	2,274.18
ATP	6018	NRAS protein	gi|146186548,gi|148226664	21,211.30	100.00%	3	3	3	0.03%	24.90%	QGVEDAFYTLVR	2.52	1,397.71
ATP	6018	NRAS protein	gi|146186548,gi|148226664	21,211.30	100.00%	3	3	3	0.03%	24.90%	SALTIQLIQNHFVDEYDPTIEDSYRK	5.09	3,095.53
ATP	6018	NRAS protein	gi|146186548,gi|148226664	21,211.30	100.00%	3	3	3	0.03%	24.90%	SFADINLYR	2.29	1,098.56
ATP	6018	PI4K2A protein	gi|151554868,gi|154152033	54,067.10	100.00%	3	3	4	0.03%	9.19%	ERNEFPEDPEFEAVVR	3.95	1,962.92
ATP	6018	PI4K2A protein	gi|151554868,gi|154152033	54,067.10	100.00%	3	3	4	0.03%	9.19%	ISDPNFVKDLEEDLYELFK	4.32	2,314.15
ATP	6018	PI4K2A protein	gi|151554868,gi|154152033	54,067.10	100.00%	3	3	4	0.03%	9.19%	LVVLDYIIR	2.45	1,103.68
ATP	6018	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	8	11	19	0.16%	41.70%	ANQVTDESLESTR	4.26	1,449.68
ATP	6018	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	8	11	19	0.16%	41.70%	ANQVTDESLESTRR	2.9	1,605.78
ATP	6018	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	8	11	19	0.16%	41.70%	ILGLAIESQDAGIK	3.5	1,427.81
ATP	6018	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	8	11	19	0.16%	41.70%	ITNDAREDEMEDNLTQVGSILGNLK	3.56	2,791.34
ATP	6018	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	8	11	19	0.16%	41.70%	TITMLDEQGEQLK	3.74	1,521.75
ATP	6018	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	8	11	19	0.16%	41.70%	TITMLDEQGEQLKR	2.65	1,677.85
ATP	6018	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	8	11	19	0.16%	41.70%	VTNGQPQQATAGAASGGYIK	4.45	1,918.96
ATP	6018	synaptosomal-associated protein 23	gi|115496868,gi|152941114,gi|83405332	23,209.50	100.00%	8	11	19	0.16%	41.70%	VTNGQPQQATAGAASGGYIKR	4.43	2,075.06

ATP	6018	LBR protein	gi|151557087,gi|154152031	71,240.40	99.80%	2	3	3	0.03%	6.28%	APQDELSPASSGNAIYDFFIGR	4.67	2,355.13
ATP	6018	LBR protein	gi|151557087,gi|154152031	71,240.40	99.80%	2	3	3	0.03%	6.28%	FHLSQESSYIPTQYSLR	2.61	2,056.01
ATP	6018	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	gi|124828540,gi|126158903,gi|145566947	55,991.00	99.80%	2	2	2	0.02%	7.17%	NLFPSNLVVAAFR	2.51	1,447.81
ATP	6018	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	gi|124828540,gi|126158903,gi|145566947	55,991.00	99.80%	2	2	2	0.02%	7.17%	SEEETSPLVTHPNPTGPAASTPESK	4.08	2,563.22
ATP	6018	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	4	7	26	0.22%	8.12%	ESTLHLVLR	3.01	1,067.62
ATP	6018	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	4	7	26	0.22%	8.12%	IQDKEGIPPDQQR	3.69	1,523.78
ATP	6018	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	4	7	26	0.22%	8.12%	TITLEVEPSDTIENVK	4.23	1,787.93
ATP	6018	PREDICTED: ubiquitin C isoform 12	gi|76638716	77,556.00	100.00%	4	7	26	0.22%	8.12%	TITLEVEPSDTIENVKAK	2.29	1,987.06
ATP	6018	TPA: predicted NADPH oxidase-5	gi|151427572,gi|155372001	86,454.40	100.00%	4	5	8	0.07%	8.74%	AIGLQMALDLLAK	4.02	1,372.79
ATP	6018	TPA: predicted NADPH oxidase-5	gi|151427572,gi|155372001	86,454.40	100.00%	4	5	8	0.07%	8.74%	MAALHIVEVNLLPSK	4.27	1,650.92
ATP	6018	TPA: predicted NADPH oxidase-5	gi|151427572,gi|155372001	86,454.40	100.00%	4	5	8	0.07%	8.74%	RPPLFHYRPGDYLYLNIPSIAR	1.98	2,658.43

ATP	6018	TPA: predicted NADPH oxidase-5	gi|151427572,gi|155372001	86,454.40	100.00%	4	5	8	0.07%	8.74%	TIAGEDGEINLQDFKK	3.81	1,777.90
ATP	6018	RecName: Full=Small nuclear ribonucleoprotein Sm D1; Short=Sm-D1; AltName: Full=snRNP core protein D1	gi|109894869,gi|73586929,gi|78050059	13,263.90	99.80%	2	4	6	0.05%	27.70%	NREPVQLETLSIR	4	1,554.86
ATP	6018	RecName: Full=Small nuclear ribonucleoprotein Sm D1; Short=Sm-D1; AltName: Full=snRNP core protein D1	gi|109894869,gi|73586929,gi|78050059	13,263.90	99.80%	2	4	6	0.05%	27.70%	YFILPDSLPLDTLLVDVEPK	5.21	2,287.25
ATP	6018	RecName: Full=Syntaxin-4	gi|122140085,gi|74356383,gi|78050061	34,382.50	100.00%	3	3	5	0.04%	19.20%	AIEPQKEEADENYNSVNTR	4.84	2,207.02
ATP	6018	RecName: Full=Syntaxin-4	gi|122140085,gi|74356383,gi|78050061	34,382.50	100.00%	3	3	5	0.04%	19.20%	QQVTILATPLPEESMKQDLQNLRDEIK	2.51	3,153.65
ATP	6018	RecName: Full=Syntaxin-4	gi|122140085,gi|74356383,gi|78050061	34,382.50	100.00%	3	3	5	0.04%	19.20%	VALVVHPGTAR	2.34	1,119.66
ATP	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	12	15	24	0.21%	15.30%	AKDIVPGDIVEIAVGDKVPADIR	4.24	2,390.33

ATP	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	12	15	24	0.21%	15.30%	DIVPGDIVEIAVGDKVPADIR	3.73	2,191.20
ATP	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	12	15	24	0.21%	15.30%	EEMNLEDSANFIK	2.4	1,555.69
ATP	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	12	15	24	0.21%	15.30%	ISLPVILMDETLK	3.5	1,487.84
ATP	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	12	15	24	0.21%	15.30%	KSEIGIAMGSGTAVAK	5.25	1,535.81
ATP	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	12	15	24	0.21%	15.30%	LDEFGEQLSK	3.12	1,165.57
ATP	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	12	15	24	0.21%	15.30%	MNVFDTELK	2.95	1,112.53

ATP	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	12	15	24	0.21%	15.30%	NAENAIEALKEYEPEMGK	3.77	2,051.96
ATP	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	12	15	24	0.21%	15.30%	NMLFSGTNIAAGK	3.22	1,339.67
ATP	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	12	15	24	0.21%	15.30%	SEIGIAMGSGTAVAK	5.34	1,407.72
ATP	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	12	15	24	0.21%	15.30%	TASEMVLADDNFSTIVAAVEEGR	4.32	2,441.15
ATP	6018	PREDICTED: ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1	gi|76639019	109,762.30	100.00%	12	15	24	0.21%	15.30%	VDQSILTGESVSVIK	3.53	1,574.86
ATP	6018	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	100.00%	3	5	5	0.04%	6.08%	DEEDDDEDMYSDNINAATEEK	5.41	2,463.91

ATP	6018	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	100.00%	3	5	5	0.04%	6.08%	HSLEGNPRDEEDDDEDMYSDNINAATEEK	7.71	3,354.35
ATP	6018	PREDICTED: similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 isoform 2	gi|194679197	71,681.50	100.00%	3	5	5	0.04%	6.08%	NLSLPFIFHEK	2.36	1,344.73
ATP	6018	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	100.00%	3	4	4	0.03%	6.20%	FATLYSTQHR	3.34	1,223.62
ATP	6018	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	100.00%	3	4	4	0.03%	6.20%	ILEVVNQVQDEER	4.77	1,570.81
ATP	6018	ENDOD1 protein	gi|154425575,gi|156523150	54,851.30	100.00%	3	4	4	0.03%	6.20%	IPVYSAFR	2.17	952.525
ATP	6018	PREDICTED: similar to hCG1980844	gi|194674945	298,419.90	99.90%	2	2	2	0.02%	0.87%	QLQPNEEADYLGVR	3.03	1,631.80
ATP	6018	PREDICTED: similar to hCG1980844	gi|194674945	298,419.90	99.90%	2	2	2	0.02%	0.87%	YLLTQELLR	2.76	1,148.67
ATP	6018	PREDICTED: similar to karyopherin beta 1 isoform 2	gi|76644624	97,210.30	100.00%	3	3	4	0.03%	5.25%	AAVENLPTFLVELSR	3.96	1,658.91
ATP	6018	PREDICTED: similar to karyopherin beta 1 isoform 2	gi|76644624	97,210.30	100.00%	3	3	4	0.03%	5.25%	LAATNALLNSLEFTK	4.49	1,605.88
ATP	6018	PREDICTED: similar to karyopherin beta 1 isoform 2	gi|76644624	97,210.30	100.00%	3	3	4	0.03%	5.25%	LLETTDRPDGHQNNLR	2.77	1,878.94

ATP	6018	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	100.00%	4	5	5	0.04%	14.20%	DLLSHENAATLNDVK	4.84	1,639.83
ATP	6018	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	100.00%	4	5	5	0.04%	14.20%	LEDLKEQLAPLEK	4.93	1,525.85
ATP	6018	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	100.00%	4	5	5	0.04%	14.20%	LRDPLQVHLPLR	2.21	1,456.87
ATP	6018	PREDICTED: similar to coiled-coil domain containing 109A	gi|119918565	39,876.70	100.00%	4	5	5	0.04%	14.20%	VAIYSPDGVR	2.57	1,076.57
ATP	6018	sorting and assembly machinery component 50 homolog	gi|114051051,gi|87578317,gi|95769210	52,025.30	99.80%	2	3	3	0.03%	5.33%	ETSYGLSFFKPQPGNFDR	2.97	2,090.00
ATP	6018	sorting and assembly machinery component 50 homolog	gi|114051051,gi|87578317,gi|95769210	52,025.30	99.80%	2	3	3	0.03%	5.33%	LPNLLGR	2.15	782.4884
ATP	6018	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	6	0.05%	7.59%	EKDGEFSVLQLVGMLR	4.16	1,836.95
ATP	6018	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	6	0.05%	7.59%	FADIVSILDK	2.82	1,120.63
ATP	6018	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	6	0.05%	7.59%	IAYSLLGLK	2.54	977.6031

ATP	6018	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	6	0.05%	7.59%	TYVDPHTYEDPNQAVLK	3.04	1,989.96
ATP	6018	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	6	0.05%	7.59%	VIGAGEFGEVYK	3.38	1,268.65
ATP	6018	PREDICTED: similar to ephrin receptor EphA2	gi|119888953	107,900.50	100.00%	6	6	6	0.05%	7.59%	YSEPPLGLTR	2.55	1,132.60
ATP	6018	phospholipase D2	gi|110331871,gi|115304867,gi|115496504,gi|116248582	105,751.20	99.80%	2	2	2	0.02%	3.00%	FAVASSPAPEGDSR	3.17	1,390.66
ATP	6018	phospholipase D2	gi|110331871,gi|115304867,gi|115496504,gi|116248582	105,751.20	99.80%	2	2	2	0.02%	3.00%	FLEDEYLLPSLGSK	3.28	1,610.83
ATP	6018	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	5	5	9	0.08%	23.70%	FYGPEGPYGVFAGR	3.91	1,516.72
ATP	6018	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	5	5	9	0.08%	23.70%	GDQPAASDSDDDEPPPLPR	4.28	1,978.86
ATP	6018	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	5	5	9	0.08%	23.70%	IVRGDQPAASDSDDDEPPPLPR	3.54	2,347.12
ATP	6018	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	5	5	9	0.08%	23.70%	KFYGPEGPYGVFAGR	4.3	1,644.82
ATP	6018	Progesterone receptor membrane component 1	gi|109659385,gi|115495221,gi|116248575,gi|7689365	21,605.30	100.00%	5	5	9	0.08%	23.70%	RDFTPAELR	2.95	1,104.58
ATP	6018	similar to ribosomal protein L27	gi|28189717,gi|47117099,gi|74268027,gi|77404275	15,780.40	100.00%	3	3	3	0.03%	24.30%	NIDDGTSDRPYSHALVAGIDR	4.31	2,272.10

ATP	6018	similar to ribosomal protein L27	gi|28189717,gi|47117099,gi|74268027,gi|77404275	15,780.40	100.00%	3	3	3	0.03%	24.30%	NIDDGTSDRPYSHALVAGIDRYPR	2.89	2,688.31
ATP	6018	similar to ribosomal protein L27	gi|28189717,gi|47117099,gi|74268027,gi|77404275	15,780.40	100.00%	3	3	3	0.03%	24.30%	YSVDIPLDK	2.42	1,049.55
ATP	6018	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	5	8	9	0.08%	11.80%	GVMLAVDAVIAELKK	2.08	1,572.90
ATP	6018	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	5	8	9	0.08%	11.80%	ISSVQSIVPALEIANAHR	2.99	1,905.06
ATP	6018	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	5	8	9	0.08%	11.80%	LVQDVANNTNEEAGDGTTTATVLAR	5.97	2,560.25
ATP	6018	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	5	8	9	0.08%	11.80%	TLNDELEIIEGMKFDR	2.21	1,938.95
ATP	6018	PREDICTED: heat shock 60kDa protein 1 (chaperonin)	gi|119888228	75,015.00	100.00%	5	8	9	0.08%	11.80%	VGLQVVAVK	2.73	912.5877
ATP	6018	LOC535277 protein	gi|151554671,gi|155372051	32,806.80	99.90%	2	2	3	0.03%	19.40%	IQLVEEELDR	3.08	1,243.65
ATP	6018	LOC535277 protein	gi|151554671,gi|155372051	32,806.80	99.90%	2	2	3	0.03%	19.40%	IQLVEEELDRAQER	3.79	1,727.89
ATP	6018	LOC535277 protein	gi|151554671,gi|155372051	32,806.80	99.90%	2	2	3	0.03%	19.40%	KLVILEGELER	4.51	1,298.77
ATP	6018	LOC535277 protein	gi|151554671,gi|155372051	32,806.80	99.90%	2	2	3	0.03%	19.40%	LEEAEKAADESERGMK	3.77	1,808.83
ATP	6018	LOC535277 protein	gi|151554671,gi|155372051	32,806.80	99.90%	2	2	3	0.03%	19.40%	RIQLVEEELDRAQER	2.56	1,883.99
ATP	6018	LOC535277 protein	gi|151554671,gi|155372051	32,806.80	99.90%	2	2	3	0.03%	19.40%	YSEKEDKYEEEIK	3.56	1,689.79

ATP	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	14	30	0.26%	39.30%	FALPSPEHILGLPVGQHIYLSAR	4.65	2,515.38
ATP	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	14	30	0.26%	39.30%	GPNGLLVYQGK	4.09	1,145.63
ATP	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	14	30	0.26%	39.30%	IDGNLVIRPYTPVSSDDDKGFVDLVIK	5.71	2,975.57
ATP	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	14	30	0.26%	39.30%	IGDTIEFR	2.68	950.4943
ATP	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	14	30	0.26%	39.30%	LIDKEVISHDTR	3.14	1,425.77
ATP	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	14	30	0.26%	39.30%	LIDKEVISHDTRR	2.41	1,581.87
ATP	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	14	30	0.26%	39.30%	STPAITLENPDIK	3.32	1,398.75
ATP	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	14	30	0.26%	39.30%	STPAITLENPDIKYPLR	4.98	1,928.05
ATP	6018	CYB5R3 protein	gi|148877441,gi|157151718,gi|162941,gi|1709233	33,973.70	100.00%	9	14	30	0.26%	39.30%	SVGMIAGGTGITPMLQVIR	5.02	1,917.03
ATP	6018	endothelial cell adhesion molecule	gi|118151218,gi|119919027,gi|86823868	41,779.80	100.00%	3	3	4	0.03%	14.90%	ALEEPANDIKEDAIAPR	4.61	1,851.94
ATP	6018	endothelial cell adhesion molecule	gi|118151218,gi|119919027,gi|86823868	41,779.80	100.00%	3	3	4	0.03%	14.90%	LGALTPTPSLSSQVLPSPR	3.16	1,921.08
ATP	6018	endothelial cell adhesion molecule	gi|118151218,gi|119919027,gi|86823868	41,779.80	100.00%	3	3	4	0.03%	14.90%	SPPSSQVFFAPVLDAIHGSLSLK	4.48	2,397.28
ATP	6018	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	9	10	11	0.09%	3.17%	FAPGDFQGFALVNPQR	3.87	1,763.89
ATP	6018	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	9	10	11	0.09%	3.17%	GTLEPVQRPDVVLVGAGHR	3.16	2,000.10

ATP	6018	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	9	10	11	0.09%	3.17%	IPGDQVVSVVFIK	3.76	1,400.81
ATP	6018	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	9	10	11	0.09%	3.17%	IQVVVLPGATTPPVR	3.67	1,546.93
ATP	6018	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	9	10	11	0.09%	3.17%	LDVEFKPLAPDGVLLFSGGK	4.17	2,102.15
ATP	6018	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	9	10	11	0.09%	3.17%	LRPGIVQSGGIVR	3.97	1,351.82
ATP	6018	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	9	10	11	0.09%	3.17%	LRSPVISIDPPSSTVQQGQDASFK	6.54	2,557.33
ATP	6018	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	9	10	11	0.09%	3.17%	SPVISIDPPSSTVQQGQDASFK	4.51	2,288.14
ATP	6018	PREDICTED: heparan sulfate proteoglycan 2	gi|119888979	467,987.40	100.00%	9	10	11	0.09%	3.17%	VVPYFTQTPYSFLPLPTIK	3.05	2,211.21
ATP	6018	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	99.80%	2	2	3	0.03%	3.77%	LASYLDKVR	2.98	1,064.61
ATP	6018	PREDICTED: keratin 19 isoform 8	gi|194676168	51,863.50	99.80%	2	2	3	0.03%	3.77%	VLDELTLAR	3.28	1,029.59
ATP	6018	PTBP1 protein	gi|158454983	47,010.90	99.80%	2	2	3	0.03%	9.87%	IAIPGLAGAGNSVLLVSNLNPER	3.5	2,275.28
ATP	6018	PTBP1 protein	gi|158454983	47,010.90	99.80%	2	2	3	0.03%	9.87%	IIVENLFYPVTLDVLHQIFSK	3.76	2,488.39
ATP	6018	Transmembrane protein 49	gi|111307060,gi|115496266,gi|122133514	46,165.40	99.80%	2	2	7	0.06%	11.30%	EQYNGNFTDPSSVNEK	4.06	1,828.80
ATP	6018	Transmembrane protein 49	gi|111307060,gi|115496266,gi|122133514	46,165.40	99.80%	2	2	7	0.06%	11.30%	LSGAEPDDEEYQEFEEMLEHAETAQDFASR	5.75	3,489.46

ATP	6018	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	4	5	19	0.16%	6.82%	FASFIDKVR	1.87	1,082.60
ATP	6018	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	4	5	19	0.16%	6.82%	LRSEIDNVKK	3.11	1,201.69
ATP	6018	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	4	5	19	0.16%	6.82%	NKYEDEINKR	3.05	1,308.65
ATP	6018	KRT5 protein	gi|146186887,gi|56710317	62,920.60	100.00%	4	5	19	0.16%	6.82%	SLDLDSIIAEVK	3.81	1,302.72
ATP	6018	MHC class I antigen	gi|72536919	40,523.80	99.80%	2	3	9	0.08%	20.90%	GFMQFGYDGR	3.35	1,193.50
ATP	6018	MHC class I antigen	gi|72536919	40,523.80	99.80%	2	3	9	0.08%	20.90%	NGEDQTQDMELVETRPSGDGTFQK	3.05	2,698.19
ATP	6018	MHC class I antigen	gi|72536919	40,523.80	99.80%	2	3	9	0.08%	20.90%	SWTAADTAAQITK	4.15	1,363.69
ATP	6018	MHC class I antigen	gi|72536919	40,523.80	99.80%	2	3	9	0.08%	20.90%	VQHEGLQEPLTLR	3.86	1,519.82
ATP	6018	MHC class I antigen	gi|72536919	40,523.80	99.80%	2	3	9	0.08%	20.90%	YFSTAVSRPGLGEPR	2.55	1,636.84
ATP	6018	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	7	8	8	0.07%	12.50%	ALVQTEDHLLLFLQQLAGR	3.69	2,165.21
ATP	6018	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	7	8	8	0.07%	12.50%	FNVEDGEIVQQVR	2.94	1,532.77
ATP	6018	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	7	8	8	0.07%	12.50%	HLLVGLPSGAILSLPK	3.9	1,614.99
ATP	6018	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	7	8	8	0.07%	12.50%	NFPQAALVSFATTGEK	4.81	1,680.86
ATP	6018	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	7	8	8	0.07%	12.50%	QLHELAPSIFFYLVDADQGR	3.28	2,319.18
ATP	6018	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	7	8	8	0.07%	12.50%	RPEIPTEQSREENLIPYSPDVQIHAER	3.62	3,203.61

ATP	6018	PREDICTED: similar to CG2943 CG2943-PA	gi|119888913	115,925.80	100.00%	7	8	8	0.07%	12.50%	RPVLQSLLLPIMDQDYAK	3.07	2,116.15
ATP	6018	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	100.00%	3	3	3	0.03%	14.00%	AQIQEQNPSIEVVYYNK	4.18	2,023.01
ATP	6018	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	100.00%	3	3	3	0.03%	14.00%	ELQVGIPVTNEQGQR	2.62	1,667.87
ATP	6018	SFXN3 protein	gi|151554123,gi|156120541,gi|206558262	35,690.00	100.00%	3	3	3	0.03%	14.00%	NLLLSGAQLEASR	4.87	1,371.76
ATP	6018	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	100.00%	4	5	8	0.07%	11.10%	LNQAVEFDVLPAFDALGQLTK	5.36	2,289.21
ATP	6018	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	100.00%	4	5	8	0.07%	11.10%	PRPVILDPADPTGNVAGK	2.56	1,816.99
ATP	6018	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	100.00%	4	5	8	0.07%	11.10%	PVILDPADPTGNVAGK	4.12	1,563.84
ATP	6018	2',5'-oligoadenylate synthetase 1, 40/46kDa	gi|158454990,gi|37953332,gi|94967004	45,118.40	100.00%	4	5	8	0.07%	11.10%	QLAKPRPVILDPADPTGNVAGK	2.79	2,257.27
ATP	6018	RecName: Full=Chloride intracellular channel protein 4; AltName: Full=Intracellular chloride ion channel protein p64H1	gi|109877271,gi|122692293,gi|73587123	28,710.60	99.80%	2	2	2	0.02%	14.20%	HPESNTAGMDIFAK	2.26	1,533.70

ATP	6018	RecName: Full=Chloride intracellular channel protein 4; AltName: Full=Intracellular chloride ion channel protein p64H1	gi|109877271,gi|122692293,gi|73587123	28,710.60	99.80%	2	2	2	0.02%	14.20%	LDEYLNSPLPDEIDENSMEDIK	2.74	2,595.17
ATP	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	24	76	0.65%	49.60%	AVFPSIVGRPR	2.88	1,198.71
ATP	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	24	76	0.65%	49.60%	DLTDYLMK	2.57	1,014.48
ATP	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	24	76	0.65%	49.60%	DLYANTVLSGGTTMYPGIADR	5.85	2,231.07
ATP	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	24	76	0.65%	49.60%	EITALAPSTMK	2.84	1,161.62
ATP	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	24	76	0.65%	49.60%	FRCPEALFQPSFLGMESCGIHETTFNSIMK	3.36	3,436.58
ATP	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	24	76	0.65%	49.60%	GYSFTTTAER	3.25	1,132.53
ATP	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	24	76	0.65%	49.60%	IKIIAPPERK	3.12	1,164.75
ATP	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	24	76	0.65%	49.60%	KDLYANTVLSGGTTMYPGIADR	5.4	2,359.16
ATP	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	24	76	0.65%	49.60%	LDLAGRDLTDYLMK	3.35	1,639.84
ATP	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	24	76	0.65%	49.60%	QEYDESGPSIVHR	2.49	1,516.70
ATP	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	24	76	0.65%	49.60%	QEYDESGPSIVHRK	2.32	1,644.80
ATP	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	24	76	0.65%	49.60%	SYELPDGQVITIGNER	3.84	1,790.89

ATP	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	24	76	0.65%	49.60%	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	6.77	3,199.61
ATP	6018	Actin, gamma 1	gi|151554360,gi|74354242,gi|75812932	41,775.90	100.00%	14	24	76	0.65%	49.60%	VAPEEHPVLLTEAPLNPK	4.61	1,954.06
ATP	6018	RecName: Full=40S ribosomal protein S2	gi|108935889,gi|2293579,gi|74267604,gi|75812930	31,218.00	99.80%	2	3	3	0.03%	8.53%	SLEEIYLFSLPIK	2.87	1,551.87
ATP	6018	RecName: Full=40S ribosomal protein S2	gi|108935889,gi|2293579,gi|74267604,gi|75812930	31,218.00	99.80%	2	3	3	0.03%	8.53%	SPYQEFTDHLVK	3.43	1,463.72
ATP	6018	RecName: Full=Peptidyl-tRNA hydrolase 2, mitochondrial; Short=PTH 2; AltName: Full=Bcl-2 inhibitor of transcription; Flags: Precursor	gi|109892883,gi|116292141,gi|60650282,gi|73587109,gi|77735985	19,272.70	99.80%	2	2	2	0.02%	16.20%	APDEETLVELLTHAK	3.61	1,665.87
ATP	6018	RecName: Full=Peptidyl-tRNA hydrolase 2, mitochondrial; Short=PTH 2; AltName: Full=Bcl-2 inhibitor of transcription; Flags: Precursor	gi|109892883,gi|116292141,gi|60650282,gi|73587109,gi|77735985	19,272.70	99.80%	2	2	2	0.02%	16.20%	VLGLTVSLIQDAGR	3.31	1,441.84
ATP	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	16	16	28	0.24%	37.00%	DLFSEAHSEFLK	4.06	1,422.69

ATP	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	16	16	28	0.24%	37.00%	EATNPPVIQEEKPK	3.64	1,579.83
ATP	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	16	16	28	0.24%	37.00%	ELSDFISYLK	1.79	1,214.63
ATP	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	16	16	28	0.24%	37.00%	ELSDFISYLKR	2.47	1,370.73
ATP	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	16	16	28	0.24%	37.00%	FLEDYFDGNLKR	3.46	1,516.74
ATP	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	16	16	28	0.24%	37.00%	FVMQEEFSR	2.8	1,188.54
ATP	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	16	16	28	0.24%	37.00%	GFPTIYFSPANKK	2.99	1,469.78
ATP	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	16	16	28	0.24%	37.00%	IFRDGEESGAYDGPR	4.5	1,668.76
ATP	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	16	16	28	0.24%	37.00%	LRKDPNIVIAK	3.14	1,266.79
ATP	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	16	16	28	0.24%	37.00%	MDATANDVPSPYEVR	4.09	1,680.75
ATP	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	16	16	28	0.24%	37.00%	QAGPASVPLKSEEEFEK	4.05	1,845.92
ATP	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	16	16	28	0.24%	37.00%	REATNPPVIQEEKPK	4.33	1,735.93
ATP	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	16	16	28	0.24%	37.00%	SEPIPESNDGPVK	2.35	1,368.66
ATP	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	16	16	28	0.24%	37.00%	TADGIVSHLKK	2.16	1,168.67
ATP	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	16	16	28	0.24%	37.00%	TFSHELSDFGLESTTGEIPVVAVR	3.42	2,591.30
ATP	6018	PDIA3 protein	gi|146186933,gi|148230374	56,913.80	100.00%	16	16	28	0.24%	37.00%	YGVSGYPTLK	2.81	1,084.57
ATP	6018	MCAM protein	gi|158455045,gi|158519851	48,983.20	99.90%	2	3	5	0.04%	4.55%	EMEEERTDDNGVLVLDPAQK	4.13	2,304.07
ATP	6018	MCAM protein	gi|158455045,gi|158519851	48,983.20	99.90%	2	3	5	0.04%	4.55%	TDDNGVLVLDPAQK	3.2	1,484.76
ATP	6018	PECAM1 protein	gi|111308531	82,597.50	100.00%	7	10	30	0.26%	11.80%	APVHFTIEK	2.75	1,041.57
ATP	6018	PECAM1 protein	gi|111308531	82,597.50	100.00%	7	10	30	0.26%	11.80%	CTVQVTHQAQSFPEIIIQK	4.91	2,170.13
ATP	6018	PECAM1 protein	gi|111308531	82,597.50	100.00%	7	10	30	0.26%	11.80%	EKTSQNQNFVTLEFTVEEQDR	3.05	2,542.21
ATP	6018	PECAM1 protein	gi|111308531	82,597.50	100.00%	7	10	30	0.26%	11.80%	FHIIPEGK	2.85	940.5252
ATP	6018	PECAM1 protein	gi|111308531	82,597.50	100.00%	7	10	30	0.26%	11.80%	GTETVYSEIR	2.82	1,154.57
ATP	6018	PECAM1 protein	gi|111308531	82,597.50	100.00%	7	10	30	0.26%	11.80%	PAVPLLNSNNEK	2.27	1,295.70

ATP	6018	PECAM1 protein	gi|111308531	82,597.50	100.00%	7	10	30	0.26%	11.80%	QMPVEMSRPAVPLLNSNEK	4.17	2,270.13
ATP	6018	PREDICTED: DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 isoform 1	gi|119912544,gi|74354729	69,131.70	99.90%	2	2	3	0.03%	3.58%	APILIATDVASR	3.24	1,226.71
ATP	6018	PREDICTED: DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 isoform 1	gi|119912544,gi|74354729	69,131.70	99.90%	2	2	3	0.03%	3.58%	QVSDLISVLR	2.32	1,129.66
ATP	6018	RecName: Full=40S ribosomal protein S16	gi|108860953,gi|74354274,gi|75812950	16,427.90	100.00%	3	3	3	0.03%	21.90%	EIKDILIQYDR	2.59	1,405.77
ATP	6018	RecName: Full=40S ribosomal protein S16	gi|108860953,gi|74354274,gi|75812950	16,427.90	100.00%	3	3	3	0.03%	21.90%	GPLQSVQVFGR	3.17	1,187.65
ATP	6018	RecName: Full=40S ribosomal protein S16	gi|108860953,gi|74354274,gi|75812950	16,427.90	100.00%	3	3	3	0.03%	21.90%	LLEPVLLLGK	2.31	1,094.72
ATP	6018	PREDICTED: nucleolin isoform 1	gi|76682880	77,835.80	100.00%	3	4	4	0.03%	6.67%	NDLAVVDVR	2.74	1,000.54
ATP	6018	PREDICTED: nucleolin isoform 1	gi|76682880	77,835.80	100.00%	3	4	4	0.03%	6.67%	TLVLSNLSYSATEETLQEVFEK	4.41	2,501.27
ATP	6018	PREDICTED: nucleolin isoform 1	gi|76682880	77,835.80	100.00%	3	4	4	0.03%	6.67%	VTQDELKEVFEDAVEIR	3.41	2,020.02
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	DGQVINETSQHHDDLE	2.9	1,836.80
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	DNLAEDIMR	2.6	1,092.50
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	EEAESTLQSFR	2.87	1,296.61
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	EEAESTLQSFRQDVDNASLAR	4.19	2,366.12
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	EKLQEEMLQREEAESTLQSFR	4.41	2,597.25

ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	EMEENFSVEAANYQDTIGR	3.92	2,218.96
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	ETNLDSLPLVDTHSK	3.83	1,668.84
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	ETNLDSLPLVDTHSKR	3.69	1,824.95
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	EYQDLLNVK	2.18	1,121.58
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	FADLSEAANR	4.37	1,093.53
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	FANYIDKVR	2.54	1,125.61
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	ILLAELEQLK	4.39	1,169.71
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	ILLAELEQLKGQGK	1.85	1,539.91
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	ISLPLPNFSSLNLR	4.53	1,570.90
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	KLHDEEIQELQAQIQEQHVQIDMDVSKPDLTAALR	4.18	4,085.06
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	KVESLQEEIAFLK	5.31	1,533.85
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	KVESLQEEIAFLKK	4.34	1,661.95
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	LHDEEIQELQAQIQEQHVQIDMDVSKPDLTAALR	5.81	3,956.97
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	LLQDSVDFSLADAINTEFK	4.63	2,126.07
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	LQDEIQNMKEEMAR	2.04	1,750.81
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	LQEEMLQREEAESTLQSFR	4.57	2,340.11
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	LQEEMLQREEAESTLQSFRQDVDNASLAR	3.25	3,409.63
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	MALDIEIATYR	3.73	1,311.66
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	RMFGGPGTASRPSSTR	1.68	1,680.82
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	SRLGDLYEEEMR	2.74	1,513.70
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	TLYTSSPGGVYATR	4.2	1,472.74

ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	TNEKVELQELNDR	4.88	1,587.80
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	VELQELNDR	3.31	1,115.57
ATP	6018	vimentin	gi|110347570	53,710.80	100.00%	29	43	110	0.94%	64.20%	VEVERDNLAEDIMR	4.29	1,704.82
ATP	6018	PREDICTED: similar to Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) (GDI-1) isoform 1	gi|119938319,gi|121107,gi|28603774,gi|714,gi|7245833,gi|73587159	23,403.80	100.00%	4	4	4	0.03%	30.40%	AEEYEFLTPMEEAPK	3.14	1,799.80
ATP	6018	PREDICTED: similar to Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) (GDI-1) isoform 1	gi|119938319,gi|121107,gi|28603774,gi|714,gi|7245833,gi|73587159	23,403.80	100.00%	4	4	4	0.03%	30.40%	IDKTDYMVGSYGPR	2.77	1,617.76
ATP	6018	PREDICTED: similar to Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) (GDI-1) isoform 1	gi|119938319,gi|121107,gi|28603774,gi|714,gi|7245833,gi|73587159	23,403.80	100.00%	4	4	4	0.03%	30.40%	SIQEIQELDKDDESLRK	3.64	2,046.04
ATP	6018	PREDICTED: similar to Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) (GDI-1) isoform 1	gi|119938319,gi|121107,gi|28603774,gi|714,gi|7245833,gi|73587159	23,403.80	100.00%	4	4	4	0.03%	30.40%	VAVSADPNVPNVVVTR	4.18	1,636.90

ATP	6018	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	6	9	17	0.15%	17.30%	DKLDGNELDLSLSDLNEVPVK	6.66	2,313.18
ATP	6018	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	6	9	17	0.15%	17.30%	DKLDGNELDLSLSDLNEVPVKELAALPK	5.62	3,035.62
ATP	6018	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	6	9	17	0.15%	17.30%	LDGNELDLSLSDLNEVPVK	4.41	2,070.06
ATP	6018	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	6	9	17	0.15%	17.30%	LDGNELDLSLSDLNEVPVKELAALPK	3.91	2,792.49
ATP	6018	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	6	9	17	0.15%	17.30%	LVNLQHLDLLNNR	2.73	1,561.88
ATP	6018	Leucine rich repeat containing 59	gi|109659325,gi|59857957,gi|75070060,gi|77736103	34,862.40	100.00%	6	9	17	0.15%	17.30%	LVTLPVSFAQLK	3.67	1,315.80
ATP	6018	RecName: Full=CDGSH iron sulfur domain-containing protein 1; AltName: Full=MitoNEET	gi|110825757,gi|73587067,gi|77404223	11,964.80	99.80%	2	2	3	0.03%	26.40%	HNEETGDNVGPLIK	5.04	1,635.83
ATP	6018	RecName: Full=CDGSH iron sulfur domain-containing protein 1; AltName: Full=MitoNEET	gi|110825757,gi|73587067,gi|77404223	11,964.80	99.80%	2	2	3	0.03%	26.40%	VVHAFDMEDLGDK	3.5	1,491.68
ATP	6018	17,000 dalton myosin light chain	gi|578,gi|74268209	16,942.80	100.00%	5	5	5	0.04%	45.00%	ALGQNPTNAEVLK	2.83	1,354.73
ATP	6018	17,000 dalton myosin light chain	gi|578,gi|74268209	16,942.80	100.00%	5	5	5	0.04%	45.00%	EAFQLFDR	2.17	1,025.51

ATP	6018	17,000 dalton myosin light chain	gi|578,gi|74268209	16,942.80	100.00%	5	5	5	0.04%	45.00%	NKDQGTYEDYVEGLR	3.31	1,786.82
ATP	6018	17,000 dalton myosin light chain	gi|578,gi|74268209	16,942.80	100.00%	5	5	5	0.04%	45.00%	VFDKEGNGTVMGAEIR	3.02	1,738.84
ATP	6018	17,000 dalton myosin light chain	gi|578,gi|74268209	16,942.80	100.00%	5	5	5	0.04%	45.00%	VLDFEHFLPMLQTVAK	2.48	1,904.00
ATP	6018	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	9	9	11	0.09%	20.80%	DAGQISGLNVLR	3.07	1,242.68
ATP	6018	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	9	9	11	0.09%	20.80%	EQQIVIQSSGGLSKDDIENMVK	2.25	2,434.21

ATP	6018	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	9	9	11	0.09%	20.80%	ETGVDLTKDNMALQR	2.44	1,706.84
ATP	6018	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	9	9	11	0.09%	20.80%	MKETAENYLGHTAK	3.78	1,608.77

ATP	6018	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	9	9	11	0.09%	20.80%	NAVITVPAYFNDSQR	2.69	1,694.85
ATP	6018	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	9	9	11	0.09%	20.80%	QAVTNPNNTFYATK	3.17	1,568.77

ATP	6018	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	9	9	11	0.09%	20.80%	STNGDTFLGGEDFDQALLR	4.12	2,055.96
ATP	6018	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|122144079,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	9	9	11	0.09%	20.80%	TTPSVVAFTADGER	3.69	1,450.72

ATP	6018	RecName: Full=Stress-70 protein, mitochondrial; AltName: Full=75 kDa glucose-regulated protein; AltName: Full=GRP 75; AltName: Full=Heat shock 70 kDa protein 9; Flags: Precursor	gi|12214479,gi|146231780,gi|73586960,gi|77735995	73,724.40	100.00%	9	9	11	0.09%	20.80%	VINEPTAAALAYGLDK	3.94	1,645.88
ATP	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	9	13	0.11%	45.40%	AVFPSIVGRPR	2.88	1,198.71
ATP	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	9	13	0.11%	45.40%	DLTDYLMK	2.57	1,014.48
ATP	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	9	13	0.11%	45.40%	DLYANNVLSGGTTMYPGIADR	4.13	2,244.06
ATP	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	9	13	0.11%	45.40%	EITALAPSTMK	2.84	1,161.62
ATP	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	9	13	0.11%	45.40%	GYSFVTTAER	3.62	1,130.55
ATP	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	9	13	0.11%	45.40%	IKIIAPPERK	3.12	1,164.75
ATP	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	9	13	0.11%	45.40%	KDLYANNVLSGGTTMYPGIADR	5.25	2,372.16
ATP	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	9	13	0.11%	45.40%	LDLAGRDLTDYLMK	3.35	1,639.84
ATP	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	9	13	0.11%	45.40%	QEYDEAGPSIVHR	3.4	1,500.71
ATP	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	9	13	0.11%	45.40%	SYELPDGQVITIGNER	3.84	1,790.89

ATP	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	9	13	0.11%	45.40%	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	5.69	3,212.60
ATP	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	9	13	0.11%	45.40%	VAPEEHPTLLTEAPLNPK	4.11	1,956.04
ATP	6018	Actin, alpha, cardiac muscle 1	gi|73587039,gi|77736117	42,002.10	100.00%	7	9	13	0.11%	45.40%	YPIEHGIITNWDDMEK	4.08	1,976.91
ATP	6018	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	6	8	11	0.09%	34.00%	GAAGALMVYDITR	4.66	1,353.68
ATP	6018	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	6	8	11	0.09%	34.00%	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	5.06	3,150.56
ATP	6018	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	6	8	11	0.09%	34.00%	KIYQNIQDGSLDLNAAESGVQHKPSAPQGGR	5.65	3,278.65
ATP	6018	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	6	8	11	0.09%	34.00%	NLTNPNTVIILIGNK	4.55	1,623.94
ATP	6018	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	6	8	11	0.09%	34.00%	TGENVEDAFLEAAK	3.38	1,493.71
ATP	6018	RAB14 protein	gi|158455025,gi|195539521	23,879.60	100.00%	6	8	11	0.09%	34.00%	TGENVEDAFLEAAKK	2.83	1,621.81
ATP	6018	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	3	4	7	0.06%	19.00%	EHGLIFMETSAK	2.73	1,378.67
ATP	6018	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	3	4	7	0.06%	19.00%	GAAGALLVYDITR	3.05	1,319.73
ATP	6018	RAB2A, member RAS oncogene family	gi|109939903,gi|116734835	20,833.10	100.00%	3	4	7	0.06%	19.00%	YIIIGDTGVGK	2.6	1,135.64
ATP	6018	RecName: Full=Phosphoglycerate kinase 1	gi|108860885,gi|74353972,gi|77735551	44,520.20	100.00%	4	6	6	0.05%	15.30%	AHSSMVGVNLPK	3.14	1,255.65
ATP	6018	RecName: Full=Phosphoglycerate kinase 1	gi|108860885,gi|74353972,gi|77735551	44,520.20	100.00%	4	6	6	0.05%	15.30%	ALESPERPFLAILGGAK	4.21	1,769.00

<table>
<tr><td>ATP</td><td>6018</td><td>RecName: Full=Phosphoglycerate kinase 1</td><td>gi|108860885,gi|74353972,gi|77735551</td><td>44,520.20</td><td>100.00%</td><td>4</td><td>6</td><td>6</td><td>0.05%</td><td>15.30%</td><td>VDFNVPMKNNQITNNQR</td><td>3.63</td><td>2,048.00</td></tr>
<tr><td>ATP</td><td>6018</td><td>RecName: Full=Phosphoglycerate kinase 1</td><td>gi|108860885,gi|74353972,gi|77735551</td><td>44,520.20</td><td>100.00%</td><td>4</td><td>6</td><td>6</td><td>0.05%</td><td>15.30%</td><td>VLNNMEIGTSLFDEEGSK</td><td>3.61</td><td>1,998.93</td></tr>
<tr><td>ATP</td><td>6018</td><td>RAB5A, member RAS oncogene family</td><td>gi|113911876,gi|115495947,gi|122144200</td><td>23,670.90</td><td>99.80%</td><td>2</td><td>2</td><td>4</td><td>0.03%</td><td>21.90%</td><td>GVDLTEPTQPTR</td><td>2.7</td><td>1,313.67</td></tr>
<tr><td>ATP</td><td>6018</td><td>RAB5A, member RAS oncogene family</td><td>gi|113911876,gi|115495947,gi|122144200</td><td>23,670.90</td><td>99.80%</td><td>2</td><td>2</td><td>4</td><td>0.03%</td><td>21.90%</td><td>LVLLGESAVGK</td><td>3.81</td><td>1,085.66</td></tr>
<tr><td>ATP</td><td>6018</td><td>RAB5A, member RAS oncogene family</td><td>gi|113911876,gi|115495947,gi|122144200</td><td>23,670.90</td><td>99.80%</td><td>2</td><td>2</td><td>4</td><td>0.03%</td><td>21.90%</td><td>TSMNVNEIFMAIAK</td><td>3.9</td><td>1,584.78</td></tr>
<tr><td>ATP</td><td>6018</td><td>RAB5A, member RAS oncogene family</td><td>gi|113911876,gi|115495947,gi|122144200</td><td>23,670.90</td><td>99.80%</td><td>2</td><td>2</td><td>4</td><td>0.03%</td><td>21.90%</td><td>YHSLAPMYYR</td><td>2.6</td><td>1,316.61</td></tr>
<tr><td>ATP</td><td>6018</td><td>FAP protein</td><td>gi|146186488,gi|148233352</td><td>87,719.00</td><td>99.80%</td><td>2</td><td>2</td><td>2</td><td>0.02%</td><td>3.55%</td><td>FMGLPTKDDNLK</td><td>2.7</td><td>1,394.70</td></tr>
<tr><td>ATP</td><td>6018</td><td>FAP protein</td><td>gi|146186488,gi|148233352</td><td>87,719.00</td><td>99.80%</td><td>2</td><td>2</td><td>2</td><td>0.02%</td><td>3.55%</td><td>IFIIDATYPEHIGPR</td><td>3.4</td><td>1,741.93</td></tr>
<tr><td>ATP</td><td>6018</td><td>Chain R, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Reduced State</td><td>gi|149241523,gi|149241540,gi|149241553,gi|149241570,gi|149241583,gi|149241600,gi|149241613,gi|42564216,gi|50872151,gi|60391934,gi|81674705</td><td>16,717.40</td><td>100.00%</td><td>3</td><td>4</td><td>10</td><td>0.09%</td><td>35.50%</td><td>EIYPYVIQELRPTLNELGISTPEELGLDKV</td><td>6.92</td><td>3,428.82</td></tr>
<tr><td>ATP</td><td>6018</td><td>Chain R, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Reduced State</td><td>gi|149241523,gi|149241540,gi|149241553,gi|149241570,gi|149241583,gi|149241600,gi|149241613,gi|42564216,gi|50872151,gi|60391934,gi|81674705</td><td>16,717.40</td><td>100.00%</td><td>3</td><td>4</td><td>10</td><td>0.09%</td><td>35.50%</td><td>GMNTLVGYDLVPEPK</td><td>4.47</td><td>1,648.83</td></tr>
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ATP	6018	Chain R, Cadmium Ion Binding Structure Of Bovine Heart Cytochrome C Oxidase In The Fully Reduced State	gi|149241523,gi|149241540,gi|149241553,gi|149241570,gi|149241583,gi|149241600,gi|149241613,gi|42564216,gi|50872151,gi|60391934,gi|81674705	16,717.40	100.00%	3	4	10	0.09%	35.50%	LNDFASAVR	2.42	992.5159
ATP	6018	nucleoside-diphosphate kinase NBR-A	gi|1064895,gi|1064897,gi|115311823,gi|115496892,gi|119224069,gi|151556410,gi|169658382,gi|169658384,gi|1709243,gi|74354800	17,307.40	99.80%	2	2	2	0.02%	19.10%	TFIAIKPDGVQR	1.82	1,344.76
ATP	6018	nucleoside-diphosphate kinase NBR-A	gi|1064895,gi|1064897,gi|115311823,gi|115496892,gi|119224069,gi|151556410,gi|169658382,gi|169658384,gi|1709243,gi|74354800	17,307.40	99.80%	2	2	2	0.02%	19.10%	VMLGETNPADSKPGTIR	3.85	1,801.91
ATP	6018	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	4	4	4	0.03%	8.79%	GTVGFSGAELENLVNQAALK	4.69	2,018.06
ATP	6018	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	4	4	4	0.03%	8.79%	IKFDQSVDPEIIAR	2.97	1,630.88
ATP	6018	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	4	4	4	0.03%	8.79%	LSPETQSAIEQEIR	3.06	1,600.82
ATP	6018	YME1L1 protein	gi|151557121,gi|156120349	80,044.00	100.00%	4	4	4	0.03%	8.79%	TTTGLDSAVDPVQMK	4.08	1,578.77
ATP	6018	RecName: Full=Vesicle-associated membrane protein 8; Short=VAMP-8	gi|122140420,gi|74353894,gi|77735533	11,339.40	99.80%	2	2	3	0.03%	24.00%	NKTEDLEATSEHFK	4.82	1,648.78

ATP	6018	RecName: Full=Vesicle-associated membrane protein 8; Short=VAMP-8	gi|122140420,gi|74353894,gi|77735533	11,339.40	99.80%	2	2	3	0.03%	24.00%	NLRDEVEGVK	3.24	1,158.61
ATP	6018	RecName: Full=Annexin A1; AltName: Full=Annexin-1; AltName: Full=Annexin I; AltName: Full=Lipocortin I; AltName: Full=Calpactin II; AltName: Full=Chromobindin-9; AltName: Full=p35; AltName: Full=Phospholipase A2	gi|118597373,gi|264182,gi|61553085,gi|73587269,gi|73853762,gi|74	38,881.20	100.00%	3	3	3	0.03%	13.30%	GDRSEELAVNDDLADSDAR	5.49	2,047.92
ATP	6018	RecName: Full=Annexin A1; AltName: Full=Annexin-1; AltName: Full=Annexin I; AltName: Full=Lipocortin I; AltName: Full=Calpactin II; AltName: Full=Chromobindin-9; AltName: Full=p35; AltName: Full=Phospholipase A2	gi|118597373,gi|264182,gi|61553085,gi|73587269,gi|73853762,gi|74	38,881.20	100.00%	3	3	3	0.03%	13.30%	GLGTDEDTLNEILASR	3.87	1,703.84

ATP	6018	RecName: Full=Annexin A1; AltName: Full=Annexin-1; AltName: Full=Annexin I; AltName: Full=Lipocortin I; AltName: Full=Calpactin II; AltName: Full=Chromobindin-9; AltName: Full=p35; AltName: Full=Phospholipase A2	gi|118597373,gi|264182,gi|61553085,gi|73587269,gi|73853762,gi|74	38,881.20	100.00%	3	3	3	0.03%	13.30%	TPAQFDAEELR	3.57	1,276.62
ATP	6018	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	7	10	11	0.09%	13.60%	IEHFISILGK	4.04	1,156.67
ATP	6018	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	7	10	11	0.09%	13.60%	IPQAVVDVSSHLQK	4.49	1,520.84
ATP	6018	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	7	10	11	0.09%	13.60%	LELPLIMLSGLPDTVFEITELQSLK	5.12	2,815.54
ATP	6018	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	7	10	11	0.09%	13.60%	NLEELYLVGSLSHDISR	3.16	1,945.00
ATP	6018	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	7	10	11	0.09%	13.60%	QETGIDDIPDVK	3.24	1,329.65
ATP	6018	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	7	10	11	0.09%	13.60%	SIEEIVSFQHLR	2.71	1,457.77
ATP	6018	LRRC8C protein	gi|148745286,gi|149642813	92,305.20	100.00%	7	10	11	0.09%	13.60%	SNTTQSGPEGSLVNSQSLK	5.24	1,933.95
ATP	6018	PREDICTED: similar to MYB binding protein 1a	gi|119911777	151,796.60	100.00%	3	3	3	0.03%	3.48%	LMGPVNLFSDENIPR	3.28	1,717.86
ATP	6018	PREDICTED: similar to MYB binding protein 1a	gi|119911777	151,796.60	100.00%	3	3	3	0.03%	3.48%	NVAPLTAFTTQQR	3.5	1,446.77
ATP	6018	PREDICTED: similar to MYB binding protein 1a	gi|119911777	151,796.60	100.00%	3	3	3	0.03%	3.48%	QPENPLVLELLEPLLLVIR	2.83	2,198.32

ATP	6018	MGAT1 protein	gi|154426138,gi|59858237,gi|62751783	51,684.70	100.00%	4	4	4	0.03%	11.60%	GIVSFLYR	2.49	954.5407
ATP	6018	MGAT1 protein	gi|154426138,gi|59858237,gi|62751783	51,684.70	100.00%	4	4	4	0.03%	11.60%	LNQHFVPFTQLDLSYLR	4.28	2,091.10
ATP	6018	MGAT1 protein	gi|154426138,gi|59858237,gi|62751783	51,684.70	100.00%	4	4	4	0.03%	11.60%	LPSDSALDDDPASLTR	4.86	1,672.80
ATP	6018	MGAT1 protein	gi|154426138,gi|59858237,gi|62751783	51,684.70	100.00%	4	4	4	0.03%	11.60%	VYGAPLLQVEK	2.42	1,216.69
ATP	6018	ribosomal protein S14	gi|118150778,gi|28189929,gi|74268249	16,758.50	99.80%	2	3	3	0.03%	14.60%	ADRDESSPYAAMLAAQDVAQR	3.41	2,281.05
ATP	6018	ribosomal protein S14	gi|118150778,gi|28189929,gi|74268249	16,758.50	99.80%	2	3	3	0.03%	14.60%	VKADRDESSPYAAMLAAQDVAQR	3.84	2,508.21
ATP	6018	PREDICTED: similar to Thioredoxin domain-containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein ERp46) isoform 1	gi|119915902	45,792.10	100.00%	3	3	5	0.04%	8.37%	FFKPGQEAVK	3.22	1,150.63
ATP	6018	PREDICTED: similar to Thioredoxin domain-containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein ERp46) isoform 1	gi|119915902	45,792.10	100.00%	3	3	5	0.04%	8.37%	GYPTLLLFR	2.63	1,079.62

ATP	6018	PREDICTED: similar to Thioredoxin domain-containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein ERp46) isoform 1	gi|119915902	45,792.10	100.00%	3	3	5	0.04%	8.37%	VDCTQHYELCSGNQVR	3.25	1,851.81
ATP	6018	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	3	4	16	0.14%	25.00%	FFDEESYSLLR	3.59	1,405.66

ATP	6018	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	3	4	16	0.14%	25.00%	NNEDVSVIPPLFTVSVDHR	4.94	2,138.09
ATP	6018	RecName: Full=Translocon-associated protein subunit delta; Short=TRAP-delta; AltName: Full=Signal sequence receptor subunit delta; Short=SSR-delta; Flags: Precursor	gi|122137113,gi|83638548,gi|84370035	18,796.20	100.00%	3	4	16	0.14%	25.00%	VQNMALYADVSGK	4.85	1,411.69

ATP	6018	RecName: Full=Serine hydroxymethyltransferase, mitochondrial; Short=SHMT; Short=Serine methylase; AltName: Full=Glycine hydroxymethyltransferase; Flags: Precursor	gi|108935997,gi|74268173,gi|77735519	55,589.20	100.00%	3	3	3	0.03%	7.94%	LIIAGTSAYAR	3.06	1,135.65
ATP	6018	RecName: Full=Serine hydroxymethyltransferase, mitochondrial; Short=SHMT; Short=Serine methylase; AltName: Full=Glycine hydroxymethyltransferase; Flags: Precursor	gi|108935997,gi|74268173,gi|77735519	55,589.20	100.00%	3	3	3	0.03%	7.94%	LNPQTGLIDYDQLALTAR	4.04	2,002.06

ATP	6018	RecName: Full=Serine hydroxymethyltransferase, mitochondrial; Short=SHMT; Short=Serine methylase; AltName: Full=Glycine hydroxymethyltransferase; Flags: Precursor	gi|108935997,gi|74268173,gi|77735519	55,589.20	100.00%	3	3	3	0.03%	7.94%	VLELVSITANK	4.42	1,186.70
ATP	6018	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	6	7	8	0.07%	14.40%	ASPAPGSGHPDGPGTHLEMNSLDR	2.64	2,416.10
ATP	6018	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	6	7	8	0.07%	14.40%	LRPESALAQAQK	3.39	1,311.74
ATP	6018	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	6	7	8	0.07%	14.40%	NVDLSTFYQNR	3.13	1,356.65
ATP	6018	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	6	7	8	0.07%	14.40%	SDEDKDKEGEALEVK	3.71	1,691.80

ATP	6018	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	6	7	8	0.07%	14.40%	SYFSSFTDDIISQPMLK	2.19	1,994.94
ATP	6018	Translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	gi|115305042,gi|115496634	67,553.40	100.00%	6	7	8	0.07%	14.40%	YMAEALLLR	2.54	1,095.59
ATP	6018	RecName: Full=Probable saccharopine dehydrogenase	gi|122140337,gi|74354153,gi|77735529	47,302.40	99.80%	2	2	2	0.02%	13.30%	LGRPTLSSEVGIIICDITNPASLDEMAKQATVVLNCVGPYR	3.46	4,360.24
ATP	6018	RecName: Full=Probable saccharopine dehydrogenase	gi|122140337,gi|74354153,gi|77735529	47,302.40	99.80%	2	2	2	0.02%	13.30%	LRNESDMKPVPIVGPK	2.42	1,795.97
ATP	6018	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	3	3	5	0.04%	5.16%	IPLNDIFR	3.28	987.5623
ATP	6018	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	3	3	5	0.04%	5.16%	VALKIPLNDIFR	3.61	1,398.85
ATP	6018	lysosomal-associated membrane protein 2 isoform 1	gi|164420738,gi|74353978,gi|77736087	44,524.90	100.00%	3	3	5	0.04%	5.16%	YLDFVFAVK	2.8	1,101.60
ATP	6018	Nicastrin	gi|74267600,gi|77735901	79,055.00	99.80%	2	2	2	0.02%	2.65%	ALAGVATVLAR	3.36	1,041.64
ATP	6018	Nicastrin	gi|74267600,gi|77735901	79,055.00	99.80%	2	2	2	0.02%	2.65%	LLYGFLVR	2.18	980.5928

ATP	6018	RecName: Full=ATP synthase subunit O, mitochondrial; AltName: Full=Oligomycin sensitivity conferral protein; Short=OSCP; Flags: Precursor	gi|143811365,gi|157881386,gi|159164706,gi|163451,gi|27806307,gi|28189911,gi|74268299	13,204.80	99.80%	2	2	3	0.03%	25.80%	FSPLTSNLINLLAENGR	2.76	1,859.00
ATP	6018	RecName: Full=ATP synthase subunit O, mitochondrial; AltName: Full=Oligomycin sensitivity conferral protein; Short=OSCP; Flags: Precursor	gi|143811365,gi|157881386,gi|159164706,gi|163451,gi|27806307,gi|28189911,gi|74268299	13,204.80	99.80%	2	2	3	0.03%	25.80%	LVRPPVQIYGIEGR	3.68	1,596.92
ATP	6018	G-protein gamma-12 subunit	gi|1109682,gi|148743956,gi|1586681,gi|2494918,gi|27807509	8,039.60	99.80%	2	2	2	0.02%	26.40%	NDPLLMGIPTSENPFK	3.09	1,788.88
ATP	6018	G-protein gamma-12 subunit	gi|1109682,gi|148743956,gi|1586681,gi|2494918,gi|27807509	8,039.60	99.80%	2	2	2	0.02%	26.40%	NDPLLMGIPTSENPFKDKK	2.07	2,160.10
ATP	6018	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	4	9	0.08%	18.80%	DFSLEQLR	2.5	1,007.52
ATP	6018	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	4	9	0.08%	18.80%	FYGPAGPYGIFAGR	3.64	1,472.73
ATP	6018	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	4	9	0.08%	18.80%	GLGAGAGAGEESPAASLPR	4.68	1,667.83
ATP	6018	PGRMC2 protein	gi|148744919,gi|149642895	23,693.20	100.00%	4	4	9	0.08%	18.80%	RGLGAGAGAGEESPAASLPR	4.29	1,823.94

ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	AEDIPQMDDAFSQTVK	2.72	1,810.82
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	ALSQIHEAAVR	4.09	1,194.66
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	DQLKPTQLLQNVAR	3.99	1,623.92
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	FGKPDPIVSVIFKDEK	3.63	1,819.00
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	GKSDENEDPSVVGEFK	3.68	1,736.80
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	GNNPFFDELFFYNVHLTPSELMDEIISIR	5	3,473.67
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	IDVGFVYDEPGHAVMR	4.13	1,820.86
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	ILHQHLGPPEER	3.39	1,425.76
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	ILVELSTLLEK	3.72	1,257.77
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	IPAHQVLYSTSGGDASGK	5.31	1,787.89
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	IYRAEDIPQMDDAFSQTVK	3.81	2,243.07

ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	LDAVNTLLVMAER	3.94	1,460.78
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	NDVVGTTYLHLSK	3.98	1,446.76
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	NLGPPGPPFNITPR	3.22	1,476.80
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	NLMALDKDSFSDPYAHVSFLHR	3.75	2,579.23
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	NLVDPFVEVSFAGK	3.37	1,521.79
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	SLLTEADAGHTEFTDEVYQNESR	6.04	2,612.17
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	TLHSSFQPNISQGR	3.93	1,571.79
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	TQGLVPEHVETR	2.68	1,365.71
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	VEMTLEVLNEKEADERPAGK	4.4	2,274.13
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	VFLPKEELYMPPLVIK	3.93	1,932.09
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	VIEDRDNYIPNTLNPVFGR	3.03	2,232.14

ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	VIIELFDNDQVGKDEFLGR	5.77	2,207.13
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	VIVESASNIPK	3.22	1,156.66
ATP	6018	PREDICTED: similar to myoferlin isoform 12	gi|194678941	234,648.00	100.00%	25	33	45	0.38%	19.90%	VSMFVLGTGDEPPPEKQDRDNDSDDVESNLLLPAGIALR	4.06	4,226.06
ATP	6018	TXNDC13 protein	gi|148878448,gi|149642897	38,865.40	100.00%	3	3	3	0.03%	12.10%	FFVTTLPAFFHAK	2.93	1,525.82
ATP	6018	TXNDC13 protein	gi|148878448,gi|149642897	38,865.40	100.00%	3	3	3	0.03%	12.10%	VDVIQEPGLSGR	3.47	1,269.68
ATP	6018	TXNDC13 protein	gi|148878448,gi|149642897	38,865.40	100.00%	3	3	3	0.03%	12.10%	YRGPGVYEDLQNYILEK	5.05	2,057.03
ATP	6018	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	3	4	5	0.04%	23.50%	ADFREPNAEVPRPIPHIGADYIPTEEER	3.25	3,218.59
ATP	6018	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	3	4	5	0.04%	23.50%	NRESYEVTLTHK	3.27	1,476.74
ATP	6018	OCIA domain containing 1	gi|59858509,gi|62751843,gi|75040205	27,811.90	100.00%	3	4	5	0.04%	23.50%	SVPLAATSMLITQGLISK	3.5	1,846.04
ATP	6018	RecName: Full=Myosin-10; AltName: Full=Myosin heavy chain 10; AltName: Full=Myosin heavy chain, non-muscle IIb; AltName: Full=Non-muscle myosin heavy chain IIb; Short=NMMHC II-b;	gi|13431706,gi|27807325,gi|4115748	229,087.40	100.00%	3	3	3	0.03%	3.59%	KFDQLLAEEK	3.02	1,220.65

ATP	6018	RecName: Full=Myosin-10; AltName: Full=Myosin heavy chain 10; AltName: Full=Myosin heavy chain, non-muscle IIb; AltName: Full=Non-muscle myosin heavy chain IIb; Short=NMMHC II-b;	gi|13431706,gi|27807325,gi|4115748	229,087.40	100.00%	3	3	3	0.03%	3.59%	LDPHLVLDQLR	2.29	1,318.75
ATP	6018	RecName: Full=Myosin-10; AltName: Full=Myosin heavy chain 10; AltName: Full=Myosin heavy chain, non-muscle IIb; AltName: Full=Non-muscle myosin heavy chain IIb; Short=NMMHC II-b;	gi|13431706,gi|27807325,gi|4115748	229,087.40	100.00%	3	3	3	0.03%	3.59%	LQQELDDLLVDLDHQR	2.36	1,949.99

ATP	6018	RecName: Full=Myosin-10; AltName: Full=Myosin heavy chain 10; AltName: Full=Myosin heavy chain, non-muscle IIb; AltName: Full=Non-muscle myosin heavy chain IIb; Short=NMMHC II-b;	gi|13431706,gi|27807325,gi|4115748	229,087.40	100.00%	3	3	3	0.03%	3.59%	LQQLFNHTMFILEQEEYQR	3.03	2,483.20
ATP	6018	RecName: Full=Myosin-10; AltName: Full=Myosin heavy chain 10; AltName: Full=Myosin heavy chain, non-muscle IIb; AltName: Full=Non-muscle myosin heavy chain IIb; Short=NMMHC II-b;	gi|13431706,gi|27807325,gi|4115748	229,087.40	100.00%	3	3	3	0.03%	3.59%	SSLQEQQEEEEEARR	1.96	1,847.84
ATP	6018	Na-K-Cl cotransporter	gi|2264408,gi|27807511	130,380.80	99.80%	2	2	2	0.02%	2.83%	LQEGLDISHLQGQEELLSSQEK	4.36	2,481.25
ATP	6018	Na-K-Cl cotransporter	gi|2264408,gi|27807511	130,380.80	99.80%	2	2	2	0.02%	2.83%	TFGHNTMDAVPR	2.51	1,361.63
ATP	6018	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	5	5	8	0.07%	20.70%	GSYGDLGGPIITTQVTIPK	5.56	1,917.03

ATP	6018	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	5	5	8	0.07%	20.70%	IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK	6.05	3,829.95
ATP	6018	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	5	5	8	0.07%	20.70%	IILDLISESPIK	3.89	1,340.80
ATP	6018	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	5	5	8	0.07%	20.70%	RPAEDMEEEQAFKR	4.48	1,751.80
ATP	6018	RecName: Full=Heterogeneous nuclear ribonucleoprotein K; Short=hnRNP K	gi|108860777,gi|74354615,gi|77736071	51,003.40	100.00%	5	5	8	0.07%	20.70%	TDYNASVSVPDSSGPER	2.76	1,780.80
ATP	6018	myristoylated alanine-rich protein kinase C substrate	gi|115495497,gi|148872484,gi|163340,gi|94534743	31,960.80	99.80%	2	3	4	0.03%	6.87%	GEATAERPGEAAVASSPSK	4.59	1,814.89
ATP	6018	myristoylated alanine-rich protein kinase C substrate	gi|115495497,gi|148872484,gi|163340,gi|94534743	31,960.80	99.80%	2	3	4	0.03%	6.87%	TAAKGEATAERPGEAAVASSPSK	3.92	2,186.10
ATP	6018	RecName: Full=DnaJ homolog subfamily C member 11	gi|110808198,gi|114050887,gi|84708894	63,220.40	100.00%	3	3	3	0.03%	12.20%	GTISVGIDATDLFDRYEEEYEDVSGSGFPQIEINK	4.72	3,893.82

ATP	6018	RecName: Full=DnaJ homolog subfamily C member 11	gi|110808198,gi|114050887,gi|84708894	63,220.40	100.00%	3	3	3	0.03%	12.20%	GVLHQVMALDSEALR	3.38	1,654.86
ATP	6018	RecName: Full=DnaJ homolog subfamily C member 11	gi|110808198,gi|114050887,gi|84708894	63,220.40	100.00%	3	3	3	0.03%	12.20%	LFNLVHQAYEVLSDPQTR	4.32	2,130.10
ATP	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	16	24	0.21%	14.20%	FKMLAELYGSDPQEELVY	3.09	2,148.02
ATP	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	16	24	0.21%	14.20%	KPLIGSVLAK	2.7	1,025.67
ATP	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	16	24	0.21%	14.20%	KPLIGSVLAKDPDAAQR	4.71	1,779.01
ATP	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	16	24	0.21%	14.20%	MLAELYGSDPQEELVY	2.6	1,872.86
ATP	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	16	24	0.21%	14.20%	NLESPSSFTIK	2.42	1,222.63
ATP	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	16	24	0.21%	14.20%	NTGDVYALER	2.8	1,137.55
ATP	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	16	24	0.21%	14.20%	PSLYAQVQKPPR	3.13	1,383.77
ATP	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	16	24	0.21%	14.20%	TSDKGQFFGITK	2.72	1,328.68

ATP	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	16	24	0.21%	14.20%	VDKNTGDVYALER	4.01	1,479.74
ATP	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	16	24	0.21%	14.20%	VGSPLGSLFVEDPDEPQNR	4.69	2,056.00
ATP	6018	vascular endothelial cadherin precursor	gi|34305299,gi|48675381,gi|75071940	87,450.60	100.00%	11	16	24	0.21%	14.20%	YSFVQGEYR	2.85	1,148.54
ATP	6018	EH-domain containing 1	gi|110331767,gi|158455084,gi|59858079,gi|62751751,gi|75070053	60,666.10	100.00%	3	3	3	0.03%	13.70%	IGPEPTTDSFIAVMHGPTEGVVPGNALVVDPR	3.56	3,288.66
ATP	6018	EH-domain containing 1	gi|110331767,gi|158455084,gi|59858079,gi|62751751,gi|75070053	60,666.10	100.00%	3	3	3	0.03%	13.70%	LADVDRDGLLDDEEFALANHLIK	2.8	2,582.31
ATP	6018	EH-domain containing 1	gi|110331767,gi|158455084,gi|59858079,gi|62751751,gi|75070053	60,666.10	100.00%	3	3	3	0.03%	13.70%	LFEAEEQDLFKDIQSLPR	4.01	2,178.11
ATP	6018	LOC515309 protein	gi|148878460,gi|149773584	31,548.40	99.80%	2	3	3	0.03%	11.00%	KEEEEEEEEYDEGSNLKR	4.63	2,241.96
ATP	6018	LOC515309 protein	gi|148878460,gi|149773584	31,548.40	99.80%	2	3	3	0.03%	11.00%	SNPEDQILYQTER	3.8	1,592.76
ATP	6018	SCO cytochrome oxidase deficient homolog 1 (yeast)	gi|119223914,gi|122692513,gi|134035032	33,641.50	99.80%	2	3	3	0.03%	12.10%	LIGLTGTKEEIDQVAR	3.81	1,742.97
ATP	6018	SCO cytochrome oxidase deficient homolog 1 (yeast)	gi|119223914,gi|122692513,gi|134035032	33,641.50	99.80%	2	3	3	0.03%	12.10%	SIGKPLLGGPFSLTTHTGEPK	4.12	2,137.17
ATP	6018	LMAN1 protein	gi|148744096,gi|149773586	58,038.50	100.00%	4	4	5	0.04%	10.40%	GAGAPGQQGQTFQQELDTVVNTQHEILR	2.78	3,022.50
ATP	6018	LMAN1 protein	gi|148744096,gi|149773586	58,038.50	100.00%	4	4	5	0.04%	10.40%	YQEEFEHFQQELDK	1.92	1,869.83
ATP	6018	LMAN1 protein	gi|148744096,gi|149773586	58,038.50	100.00%	4	4	5	0.04%	10.40%	YVSSLTEEISK	3.39	1,255.64

ATP	6018	LMAN1 protein	gi|148744096,gi|149773586	58,038.50	100.00%	4	4	5	0.04%	10.40%	YVSSLTEEISKR	2.77	1,411.74
ATP	6018	acyl-CoA synthetase long-chain family member 5	gi|115497154,gi|152941112,gi|94534758	76,013.10	100.00%	3	4	4	0.03%	5.86%	ALVLISNVEK	2.35	1,085.66
ATP	6018	acyl-CoA synthetase long-chain family member 5	gi|115497154,gi|152941112,gi|94534758	76,013.10	100.00%	3	4	4	0.03%	5.86%	GAMLTHANIVSNASGFLK	3.66	1,846.95
ATP	6018	acyl-CoA synthetase long-chain family member 5	gi|115497154,gi|152941112,gi|94534758	76,013.10	100.00%	3	4	4	0.03%	5.86%	TLKPTLFPTVPR	2.29	1,369.82
ATP	6018	PREDICTED: similar to ER lipid raft associated 1 isoform 2	gi|194678978	39,049.70	100.00%	3	3	3	0.03%	18.70%	DLNVMAPGLTIQAVR	3.48	1,613.87
ATP	6018	PREDICTED: similar to ER lipid raft associated 1 isoform 2	gi|194678978	39,049.70	100.00%	3	3	3	0.03%	18.70%	EALEPSGESPIQNK	3.66	1,498.74
ATP	6018	PREDICTED: similar to ER lipid raft associated 1 isoform 2	gi|194678978	39,049.70	100.00%	3	3	3	0.03%	18.70%	GGALLTSPSGPGYHIMLPFITTFR	2.59	2,549.32
ATP	6018	PREDICTED: similar to ER lipid raft associated 1 isoform 2	gi|194678978	39,049.70	100.00%	3	3	3	0.03%	18.70%	SVQTTLQTDEVK	3.43	1,348.70
ATP	6018	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	100.00%	3	3	3	0.03%	10.20%	LQTVQSADQVLVLR	4.01	1,569.90

ATP	6018	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	100.00%	3	3	3	0.03%	10.20%	QVVLVGQEPVLFSGSVR	4.67	1,814.02
ATP	6018	transporter 2, ATP-binding cassette, sub-family B	gi|114051053,gi|19171652,gi|27806345,gi|63169160	79,287.60	100.00%	3	3	3	0.03%	10.20%	VNFQNVSFAYPSRPDQPALQGLTFTLSPGQMTALVGPNGSGK	3.69	4,408.20
ATP	6018	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein G (hnRNP G) (RNA-binding motif protein, X chromosome) (Glycoprotein p43) isoform 5	gi|119919689	42,296.60	100.00%	3	3	3	0.03%	11.00%	AIKVEQATKPSFESGR	2.88	1,747.93
ATP	6018	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein G (hnRNP G) (RNA-binding motif protein, X chromosome) (Glycoprotein p43) isoform 5	gi|119919689	42,296.60	100.00%	3	3	3	0.03%	11.00%	GFAFVTFESPADAK	2.91	1,486.72

ATP	6018	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein G (hnRNP G) (RNA-binding motif protein, X chromosome) (Glycoprotein p43) isoform 5	gi|119919689	42,296.60	100.00%	3	3	3	0.03%	11.00%	LFIGGLNTETNEK	3.59	1,435.74
ATP	6018	Solute carrier family 39 (zinc transporter), member 7	gi|112362085,gi|115749633,gi|146231764,gi|63169171	42,835.10	99.80%	2	2	2	0.02%	8.77%	DGPVRPQNAEEEKAGSDLR	3.23	2,068.01
ATP	6018	Solute carrier family 39 (zinc transporter), member 7	gi|112362085,gi|115749633,gi|146231764,gi|63169171	42,835.10	99.80%	2	2	2	0.02%	8.77%	EKQSSEEEEKEAGALR	2.72	1,819.87
ATP	6018	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	10	13	0.11%	35.50%	AGAGSATLSMAYAGAR	3.93	1,470.70
ATP	6018	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	10	13	0.11%	35.50%	ANAFVAELKDLDPAR	2.78	1,629.86

ATP	6018	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	10	13	0.11%	35.50%	GYLGPEQLPDCLKGCDVVVIPAGVPR	3.75	2,695.40
ATP	6018	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	10	13	0.11%	35.50%	LTLYDIAHTPGVAADLSHIETR	5.5	2,393.25
ATP	6018	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	10	13	0.11%	35.50%	MIAEAIPELK	3.02	1,130.61
ATP	6018	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	10	13	0.11%	35.50%	VAVLGASGGIGQPLSLLLK	7.17	1,793.09
ATP	6018	RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor	gi|118572778,gi|81674781	35,651.00	100.00%	7	10	13	0.11%	35.50%	VNVPVIGGHAGK	3.25	1,147.66
ATP	6018	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	4	4	16	0.14%	21.50%	FGLIPEEFFQFLYPK	2.91	1,874.97

ATP	6018	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	4	4	16	0.14%	21.50%	HYLFDVQR	2.72	1,077.55
ATP	6018	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	4	4	16	0.14%	21.50%	NNIAMALEVTYR	3.76	1,410.70
ATP	6018	Chain A, Subcomplex Of The Stator Of Bovine Mitochondrial Atp Synthase	gi|110591026,gi|110591029,gi|602033	24,651.00	100.00%	4	4	16	0.14%	21.50%	PVPPLPEHGGK	1.7	1,127.62
ATP	6018	Ribosomal protein S8	gi|119224110,gi|58760384,gi|59858489,gi|70778956,gi|74268417,gi|75070020	24,188.40	99.80%	2	2	3	0.03%	13.50%	IIDVVYNASNNELVR	3.52	1,718.91
ATP	6018	Ribosomal protein S8	gi|119224110,gi|58760384,gi|59858489,gi|70778956,gi|74268417,gi|75070020	24,188.40	99.80%	2	2	3	0.03%	13.50%	ISSLLEEQFQQGK	4.14	1,506.78
ATP	6018	PREDICTED: similar to oxysterol 7alpha-hydroxylase	gi|194672764	90,479.20	99.80%	2	3	3	0.03%	4.96%	AMAVLRDEIDHLLQSTGQK	4.07	2,141.10
ATP	6018	PREDICTED: similar to oxysterol 7alpha-hydroxylase	gi|194672764	90,479.20	99.80%	2	3	3	0.03%	4.96%	MLTDSDLIDEIHSTYQFLQGK	3.45	2,470.18
ATP	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	10	15	23	0.20%	33.70%	AVFVDLEPTVIDEVR	5.31	1,701.91
ATP	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	10	15	23	0.20%	33.70%	DVNAAIATIK	3.38	1,015.58
ATP	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	10	15	23	0.20%	33.70%	EIIDLVLDR	2.44	1,085.62

ATP	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	10	15	23	0.20%	33.70%	FDGALNVDLTEFQTNLVPYPR	4.74	2,409.21
ATP	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	10	15	23	0.20%	33.70%	IHFPLATYAPVISAEK	3.15	1,756.96
ATP	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	10	15	23	0.20%	33.70%	LDHKFDLMYAK	2.87	1,396.69
ATP	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	10	15	23	0.20%	33.70%	LISQIVSSITASLR	4.7	1,487.88
ATP	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	10	15	23	0.20%	33.70%	QLFHPEQLITGKEDAANNYAR	3.44	2,415.21
ATP	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	10	15	23	0.20%	33.70%	RNLDIERPTYTNLNR	3.26	1,874.98
ATP	6018	TUBA1B protein	gi|148878019,gi|168804008	50,133.70	100.00%	10	15	23	0.20%	33.70%	TIGGGDDSFNTFFSETGAGK	3.75	2,007.89
ATP	6018	PREDICTED: similar to transmembrane protein 165	gi|76619924	34,667.10	99.80%	2	3	4	0.03%	13.30%	MSPDEGQEELEEVQAELK	3.61	2,076.93
ATP	6018	PREDICTED: similar to transmembrane protein 165	gi|76619924	34,667.10	99.80%	2	3	4	0.03%	13.30%	NKEPPAPAQQLQPQPAAVQGPEPAR	5.4	2,619.36
ATP	6018	PREDICTED: proteasome (prosome, macropain) 26S subunit, ATPase, 3	gi|119907799,gi|74268141,gi|95769198	49,300.20	100.00%	3	3	3	0.03%	12.70%	AMEVDERPTEQYSDIGGLDK	4.4	2,269.03
ATP	6018	PREDICTED: proteasome (prosome, macropain) 26S subunit, ATPase, 3	gi|119907799,gi|74268141,gi|95769198	49,300.20	100.00%	3	3	3	0.03%	12.70%	TMLELLNQLDGFQPNTQVK	2.89	2,205.12

ATP	6018	PREDICTED: proteasome (prosome, macropain) 26S subunit, ATPase, 3	gi|119907799,gi|74268141,gi|95769198	49,300.20	100.00%	3	3	3	0.03%	12.70%	VIAATNRVDILDPALLR	3.75	1,850.09
ATP	6018	Adaptor-related protein complex 2, beta 1 subunit	gi|115304848,gi|115497346,gi|122132354,gi|124028640	104,551.20	99.80%	2	2	2	0.02%	4.80%	IDNADELLESFLEGFHDESTQVQLTLLTAIVK	3.18	3,588.83
ATP	6018	Adaptor-related protein complex 2, beta 1 subunit	gi|115304848,gi|115497346,gi|122132354,gi|124028640	104,551.20	99.80%	2	2	2	0.02%	4.80%	NVEGQDMLYQSLK	3.36	1,540.73
ATP	6018	RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8; AltName: Full=NADH-ubiquinone oxidoreductase 19 kDa subunit; AltName: Full=Complex I-19kD;	gi|1171870,gi|28461275,gi|599681,gi|86827664	20,073.10	99.80%	2	3	3	0.03%	18.60%	ARPEPNPEVEGDLKPAR	5.81	1,874.97

ATP	6018	RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8; AltName: Full=NADH-ubiquinone oxidoreductase 19 kDa subunit; AltName: Full=Complex I-19kD;	gi|1171870,gi|28461275,gi|599681,gi|86827664	20,073.10	99.80%	2	3	3	0.03%	18.60%	VKTDRPLPENPYHSR	2.74	1,808.94
ATP	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	15	20	30	0.26%	16.10%	AAAQDIFSPK	2.82	1,047.55

ATP	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	15	20	30	0.26%	16.10%	ATILYASETGR	3.71	1,181.62
ATP	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	15	20	30	0.26%	16.10%	AVDTRLEELGGER	2.64	1,444.74

ATP	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	15	20	30	0.26%	16.10%	DFINQYYSSIK	3.9	1,377.67
ATP	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	15	20	30	0.26%	16.10%	DFINQYYSSIKR	3.01	1,533.77

ATP	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	15	20	30	0.26%	16.10%	ESSNTDSAGALGTLR	4.72	1,478.71
ATP	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	15	20	30	0.26%	16.10%	LLSTLAEEPSEQQELETLSQDPR	6.11	2,613.29

ATP	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	15	20	30	0.26%	16.10%	LSTQAEGLQLLPGLIHVHR	2.48	2,082.18
ATP	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	15	20	30	0.26%	16.10%	MFQATVLSVENLQSSK	3.65	1,797.91

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<tr><td>ATP</td><td>6018</td><td>RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN</td><td>gi|266647</td><td>133,270.00</td><td>100.00%</td><td>15</td><td>20</td><td>30</td><td>0.26%</td><td>16.10%</td><td>QALTFFLDITSPPSPR</td><td>2.44</td><td>1,789.95</td></tr>
<tr><td>ATP</td><td>6018</td><td>RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN</td><td>gi|266647</td><td>133,270.00</td><td>100.00%</td><td>15</td><td>20</td><td>30</td><td>0.26%</td><td>16.10%</td><td>SAITVFPQR</td><td>2.6</td><td>1,018.57</td></tr>
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ATP	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	15	20	30	0.26%	16.10%	TYVQDILR	2.95	1,007.55
ATP	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	15	20	30	0.26%	16.10%	VEDPPPPTESVAVEQLEK	4.01	1,963.99

ATP	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	15	20	30	0.26%	16.10%	VLTAFSREPDSPK	2	1,446.76
ATP	6018	RecName: Full=Nitric oxide synthase, endothelial; AltName: Full=Endothelial NOS; Short=eNOS; AltName: Full=EC-NOS; AltName: Full=NOS type III; Short=NOSIII; AltName: Full=Constitutive NOS; Short=cN	gi|266647	133,270.00	100.00%	15	20	30	0.26%	16.10%	YHEDIFGLTLR	3.19	1,363.70
ATP	6018	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	gi|209447036,gi|88954020	67,875.80	99.80%	2	2	2	0.02%	4.29%	VIYAMAEDGLLFK	3.61	1,485.77

ATP	6018	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	gi|209447036,gi|88954020	67,875.80	99.80%	2	2	2	0.02%	4.29%	YQPEQPNTVYQMAR	3.18	1,740.80
ATP	6018	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	6	9	13	0.11%	15.20%	IGGIGTVPVGR	3.32	1,025.61
ATP	6018	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	6	9	13	0.11%	15.20%	IGGIGTVPVGRVETGVLKPGMVVTFAPVNVTTEVK	2.78	3,537.97
ATP	6018	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	6	9	13	0.11%	15.20%	LPLQDVYK	2.52	975.5511
ATP	6018	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	6	9	13	0.11%	15.20%	THINIVVIGHVDSGK	2.84	1,588.88
ATP	6018	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	6	9	13	0.11%	15.20%	VETGVLKPGMVVTFAPVNVTTEVK	5.02	2,531.38

ATP	6018	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 1 isoform 1	gi|119938328,gi|148745492,gi|68299807,gi|86827651	50,141.20	100.00%	6	9	13	0.11%	15.20%	YYVTIIDAPGHR	3.56	1,404.73
ATP	6018	cell division cycle 42 (GTP binding protein, 25kDa)	gi|114052486,gi|122063301,gi|86821687	21,240.70	99.90%	2	3	9	0.08%	19.90%	NVFDEAILAALEPPEPK	4.85	1,852.97
ATP	6018	cell division cycle 42 (GTP binding protein, 25kDa)	gi|114052486,gi|122063301,gi|86821687	21,240.70	99.90%	2	3	9	0.08%	19.90%	TPFLLVGTQIDLRDDPSTIEK	4.23	2,358.26
ATP	6018	RecName: Full=Golgi SNAP receptor complex member 1	gi|108935998,gi|83638559,gi|84370083	28,524.90	100.00%	3	3	3	0.03%	12.00%	FPAVNSLIQR	3.42	1,144.65
ATP	6018	RecName: Full=Golgi SNAP receptor complex member 1	gi|108935998,gi|83638559,gi|84370083	28,524.90	100.00%	3	3	3	0.03%	12.00%	LIEETISIAMATK	3.09	1,435.77
ATP	6018	RecName: Full=Golgi SNAP receptor complex member 1	gi|108935998,gi|83638559,gi|84370083	28,524.90	100.00%	3	3	3	0.03%	12.00%	MNTLANRFPAVNSLIQR	3.46	1,961.04
ATP	6018	minor histocompatibility antigen 13	gi|164448616	41,537.10	100.00%	3	3	6	0.05%	15.60%	GEVTEMFSYEESNPKDPAAVTETR	3.13	2,703.21
ATP	6018	minor histocompatibility antigen 13	gi|164448616	41,537.10	100.00%	3	3	6	0.05%	15.60%	LVFPQDLLEK	2.2	1,201.68
ATP	6018	minor histocompatibility antigen 13	gi|164448616	41,537.10	100.00%	3	3	6	0.05%	15.60%	QYQLLFTQGSGENKEEIINYEFDTK	4.26	2,994.44
ATP	6018	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	8	9	12	0.10%	43.20%	AADPPAENSSAPEAEQGGAE	2.82	1,897.80

ATP	6018	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	8	9	12	0.10%	43.20%	EDGNEEDKENQGDETQGQQPPQR	3.54	2,628.10
ATP	6018	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	8	9	12	0.10%	43.20%	EDGNEEDKENQGDETQGQQPPQRR	2.22	2,784.21
ATP	6018	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	8	9	12	0.10%	43.20%	GAEAANVTGPGGVPVQGSK	4.75	1,695.87
ATP	6018	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	8	9	12	0.10%	43.20%	NDTKEDVFVHQTAIK	3	1,744.89
ATP	6018	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	8	9	12	0.10%	43.20%	NYQQNYQNSESGEKNEGSESAPEGQAQQR	6.32	3,257.40
ATP	6018	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	8	9	12	0.10%	43.20%	QPREDGNEEDKENQGDETQGQQPPQR	2.94	3,009.32
ATP	6018	transcription factor EF1(A)	gi|162983,gi|27807361,gi|54040030,gi|86821283	35,905.70	100.00%	8	9	12	0.10%	43.20%	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	4.74	3,239.53
ATP	6018	PREDICTED: similar to vesicle amine transport protein 1 isoform 1	gi|76671278	42,822.00	100.00%	3	3	3	0.03%	12.20%	GVDIVMDPLGGSDTAK	4.63	1,590.77
ATP	6018	PREDICTED: similar to vesicle amine transport protein 1 isoform 1	gi|76671278	42,822.00	100.00%	3	3	3	0.03%	12.20%	LQTRPAAPPAPGTGQLTLR	2.71	1,945.10
ATP	6018	PREDICTED: similar to vesicle amine transport protein 1 isoform 1	gi|76671278	42,822.00	100.00%	3	3	3	0.03%	12.20%	VVTYGMANLLTGPK	3.2	1,479.79

ATP	6018	RecName: Full=Adenosylhomocysteinase; Short=AdoHcyase; AltName: Full=S-adenosyl-L-homocysteine hydrolase	gi|118573856,gi|146231804,gi|75773598,gi|77735583	47,620.90	100.00%	4	4	5	0.04%	11.30%	GISEETTTGVHNLYK	3.66	1,648.82
ATP	6018	RecName: Full=Adenosylhomocysteinase; Short=AdoHcyase; AltName: Full=S-adenosyl-L-homocysteine hydrolase	gi|118573856,gi|146231804,gi|75773598,gi|77735583	47,620.90	100.00%	4	4	5	0.04%	11.30%	KLDEAVAEAHLGK	4.76	1,380.75
ATP	6018	RecName: Full=Adenosylhomocysteinase; Short=AdoHcyase; AltName: Full=S-adenosyl-L-homocysteine hydrolase	gi|118573856,gi|146231804,gi|75773598,gi|77735583	47,620.90	100.00%	4	4	5	0.04%	11.30%	VPAINVNDSVTK	3.25	1,256.68
ATP	6018	RecName: Full=Adenosylhomocysteinase; Short=AdoHcyase; AltName: Full=S-adenosyl-L-homocysteine hydrolase	gi|118573856,gi|146231804,gi|75773598,gi|77735583	47,620.90	100.00%	4	4	5	0.04%	11.30%	YPQLLSGIR	3.12	1,046.60

ATP	6018	PREDICTED: similar to Feline leukemia virus subgroup C receptor-related protein 1 (Feline leukemia virus subgroup C receptor) (hFLVCR)	gi|194674242	59,731.10	99.80%	2	2	2	0.02%	3.60%	DPGEETPGGEGTLVPR	3.83	1,610.77
ATP	6018	PREDICTED: similar to Feline leukemia virus subgroup C receptor-related protein 1 (Feline leukemia virus subgroup C receptor) (hFLVCR)	gi|194674242	59,731.10	99.80%	2	2	2	0.02%	3.60%	LLPKDPGEETPGGEGTLVPR	2.93	2,062.08
ATP	6018	l-caldesmon	gi|24251217,gi|27806279	62,068.20	99.80%	2	2	2	0.02%	5.79%	LEQYTSAIEGTK	2.94	1,339.67
ATP	6018	l-caldesmon	gi|24251217,gi|27806279	62,068.20	99.80%	2	2	2	0.02%	5.79%	TTTTNTQAEGDDEAALLER	4.3	2,035.94
ATP	6018	H3 histone, family 3A	gi|59858289,gi|62177168,gi|95769331	15,310.70	100.00%	3	5	11	0.09%	38.20%	EIAQDFKTDLR	2.85	1,335.69
ATP	6018	H3 histone, family 3A	gi|59858289,gi|62177168,gi|95769331	15,310.70	100.00%	3	5	11	0.09%	38.20%	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	4.63	3,380.68
ATP	6018	H3 histone, family 3A	gi|59858289,gi|62177168,gi|95769331	15,310.70	100.00%	3	5	11	0.09%	38.20%	YRPGTVALR	2.56	1,032.59
ATP	6018	PREDICTED: eukaryotic translation initiation factor 3, subunit A isoform 4	gi|119924055,gi|154757413	98,873.80	99.80%	2	2	2	0.02%	4.59%	EQPEKEPELQQYVPQLQNNTILR	3.09	2,794.44

ATP	6018	PREDICTED: eukaryotic translation initiation factor 3, subunit A isoform 4	gi|119924055,gi|154757413	98,873.80	99.80%	2	2	2	0.02%	4.59%	LTSLVPFVDAFQLER	3.44	1,734.94
ATP	6018	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	100.00%	3	3	3	0.03%	10.40%	FTSLGLLPR	2.52	1,003.59
ATP	6018	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	100.00%	3	3	3	0.03%	10.40%	LTEDGLPLGINLGK	4.21	1,439.81
ATP	6018	dihydroorotate dehydrogenase precursor	gi|110665638,gi|112362407,gi|59857979,gi|62751827,gi|75057853	42,758.80	100.00%	3	3	3	0.03%	10.40%	VPIVGVGGVSSGQDALEK	5.18	1,711.92
ATP	6018	inositol monophosphatase domain containing 1	gi|114052460,gi|122136157,gi|86827736	38,905.90	99.80%	2	2	2	0.02%	8.84%	TREGADDKMTSGDVLSNR	3.03	1,967.91
ATP	6018	inositol monophosphatase domain containing 1	gi|114052460,gi|122136157,gi|86827736	38,905.90	99.80%	2	2	2	0.02%	8.84%	VLALLDVPDKSQEK	2.88	1,554.87
ATP	6018	PREDICTED: eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) isoform 1	gi|119906216,gi|146231746,gi|172047287	32,883.70	99.80%	2	2	2	0.02%	8.03%	GVVQDLQQAVSK	2.65	1,271.70

ATP	6018	PREDICTED: eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) isoform 1	gi|119906216,gi|146231746,gi|172047287	32,883.70	99.80%	2	2	2	0.02%	8.03%	IASLEVENQSLR	3.53	1,358.73
ATP	6018	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	3	3	6	0.05%	6.54%	AENLGEVLR	2.74	1,000.54
ATP	6018	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	3	3	6	0.05%	6.54%	ISEDYYVHLIADNLPVATR	4.36	2,189.12
ATP	6018	TM9SF4 protein	gi|146186797,gi|166063945,gi|172047290	74,351.10	100.00%	3	3	6	0.05%	6.54%	IVNTPFQVLMNSEK	3.43	1,635.84
ATP	6018	PREDICTED: plexin A2	gi|194674254	210,938.30	99.80%	2	2	2	0.02%	1.58%	FVDDLFETLFSTVHR	2.67	1,825.91
ATP	6018	PREDICTED: plexin A2	gi|194674254	210,938.30	99.80%	2	2	2	0.02%	1.58%	QTSSYNIPASASISR	3.49	1,581.79
ATP	6018	PREDICTED: similar to plexin B2 isoform 1	gi|194681262	204,931.90	100.00%	5	5	5	0.04%	4.12%	DTAHNLPEFIVK	3.07	1,383.73
ATP	6018	PREDICTED: similar to plexin B2 isoform 1	gi|194681262	204,931.90	100.00%	5	5	5	0.04%	4.12%	EAFEAYTDHATYK	3.87	1,545.69
ATP	6018	PREDICTED: similar to plexin B2 isoform 1	gi|194681262	204,931.90	100.00%	5	5	5	0.04%	4.12%	LQQIAAALENKVTDL	3.68	1,626.91
ATP	6018	PREDICTED: similar to plexin B2 isoform 1	gi|194681262	204,931.90	100.00%	5	5	5	0.04%	4.12%	NLDTVQGSPLLVGSDLLK	4.66	1,869.03
ATP	6018	PREDICTED: similar to plexin B2 isoform 1	gi|194681262	204,931.90	100.00%	5	5	5	0.04%	4.12%	VGVSQQPEDSQQDLPGER	4.31	1,968.93

ATP	6018	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	100.00%	3	4	7	0.06%	15.90%	AITIFQERDPANIK	3.08	1,615.88
ATP	6018	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	100.00%	3	4	7	0.06%	15.90%	GAAQNIIPASTGAAK	4.61	1,369.74
ATP	6018	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase isoform 2	gi|119893091,gi|1841758,gi|2285903,gi|73587299,gi|77404273,gi|89573947	35,850.00	100.00%	3	4	7	0.06%	15.90%	VIHDHFGIVEGLMTTVHAITATQK	3.78	2,634.37
ATP	6018	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	gi|155371851	60,580.30	100.00%	3	4	5	0.04%	7.58%	GRVPYPGMVNR	2.83	1,261.65
ATP	6018	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	gi|155371851	60,580.30	100.00%	3	4	5	0.04%	7.58%	IADFGLAR	2.03	862.4782
ATP	6018	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	gi|155371851	60,580.30	100.00%	3	4	5	0.04%	7.58%	LVPLYAVVSEEPIYIVTEFMSK	3.52	2,543.34
ATP	6018	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	100.00%	4	6	6	0.05%	18.00%	FFLSAGLIDKVDNFK	4.32	1,713.92
ATP	6018	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	100.00%	4	6	6	0.05%	18.00%	LEDPHVDIIR	2.48	1,206.65
ATP	6018	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	100.00%	4	6	6	0.05%	18.00%	NPSAMAVESFTATAPFVQIGR	3.03	2,210.09

ATP	6018	TMEM43 protein	gi|151556045,gi|156523072	44,774.20	100.00%	4	6	6	0.05%	18.00%	VSFSYAGLSSDDPDLGPAHVVTVIAR	3.66	2,673.35
ATP	6018	intergral membrane protein 1	gi|114051696,gi|122136222,gi|152941168,gi|86823970	80,641.10	100.00%	3	3	6	0.05%	4.68%	FESVIHEFDPYFNYR	3.53	1,962.90
ATP	6018	intergral membrane protein 1	gi|114051696,gi|122136222,gi|152941168,gi|86823970	80,641.10	100.00%	3	3	6	0.05%	4.68%	FYSLLDPSYAK	3.15	1,303.66
ATP	6018	intergral membrane protein 1	gi|114051696,gi|122136222,gi|152941168,gi|86823970	80,641.10	100.00%	3	3	6	0.05%	4.68%	IIFDDFR	2.54	925.4779
ATP	6018	Myeloid-associated differentiation marker	gi|111308557,gi|115497460	35,291.10	100.00%	3	5	11	0.09%	14.60%	ARPGEITGYMATVPGLLK	3.84	1,890.02
ATP	6018	Myeloid-associated differentiation marker	gi|111308557,gi|115497460	35,291.10	100.00%	3	5	11	0.09%	14.60%	LVFVRV	1.97	732.4766
ATP	6018	Myeloid-associated differentiation marker	gi|111308557,gi|115497460	35,291.10	100.00%	3	5	11	0.09%	14.60%	TTVTTTMSSSSGLGSPTIVGSPR	5.43	2,240.11
ATP	6018	ribosomal protein L24	gi|27806129,gi|28189314,gi|28189753,gi|28189757,gi|28189765,gi|3132823,gi|41019240,gi|74267598	17,630.30	99.80%	2	2	2	0.02%	13.50%	AITGASLADIMAK	3.96	1,277.68
ATP	6018	ribosomal protein L24	gi|27806129,gi|28189314,gi|28189753,gi|28189757,gi|28189765,gi|3132823,gi|41019240,gi|74267598	17,630.30	99.80%	2	2	2	0.02%	13.50%	VFQFLNAK	2.22	966.5407

ATP	6018	Myosin regulatory light chain MRCL3	gi|109659359,gi|134024635,gi|139948749,gi|148744185,gi|194678093,gi|205829192,gi|59858321,gi|62751407	19,848.30	100.00%	3	4	4	0.03%	22.10%	ATSNVFAMFDQSQIQEFK	3.32	2,106.98
ATP	6018	Myosin regulatory light chain MRCL3	gi|109659359,gi|134024635,gi|139948749,gi|148744185,gi|194678093,gi|205829192,gi|59858321,gi|62751407	19,848.30	100.00%	3	4	4	0.03%	22.10%	ELLTTMGDRFTDEEVDELYR	3.53	2,448.12
ATP	6018	Myosin regulatory light chain MRCL3	gi|109659359,gi|134024635,gi|139948749,gi|148744185,gi|194678093,gi|205829192,gi|59858321,gi|62751407	19,848.30	100.00%	3	4	4	0.03%	22.10%	FTDEEVDELYR	2.9	1,415.63
ATP	6018	PREDICTED: similar to Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A) (Guanylate cyclase) (NPR-A) (Atrial natriuretic peptide A-type receptor)	gi|194665089	119,021.60	100.00%	3	3	3	0.03%	3.67%	IITYKEPDNPEYLEFLQK	3.41	2,240.15

ATP	6018	PREDICTED: similar to Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A) (Guanylate cyclase) (NPR-A) (Atrial natriuretic peptide A-type receptor)	gi|194665089	119,021.60	100.00%	3	3	3	0.03%	3.67%	MALALLDAVR	2.73	1,088.61
ATP	6018	PREDICTED: similar to Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A) (Guanylate cyclase) (NPR-A) (Atrial natriuretic peptide A-type receptor)	gi|194665089	119,021.60	100.00%	3	3	3	0.03%	3.67%	VGPAVELALAR	3.55	1,095.65
ATP	6018	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	9	17	0.15%	12.00%	DAEAWFNEK	2.96	1,109.49

ATP	6018	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	9	17	0.15%	12.00%	IRLENEIQTYR	4.35	1,434.77
ATP	6018	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	9	17	0.15%	12.00%	LASYLDKVR	2.98	1,064.61
ATP	6018	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	9	17	0.15%	12.00%	LENEIQTYR	3.63	1,165.58
ATP	6018	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	9	17	0.15%	12.00%	QSLEASLAETEGR	4.56	1,390.68
ATP	6018	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	9	17	0.15%	12.00%	RVLDELTLTK	2.82	1,187.70

ATP	6018	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	9	17	0.15%	12.00%	SQYEQLAEKNR	4.64	1,365.68
ATP	6018	PREDICTED: similar to Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) isoform 2	gi|194685481,gi|194685483	54,832.90	100.00%	7	9	17	0.15%	12.00%	VLDELTLTK	3.77	1,031.60
ATP	6018	PREDICTED: similar to Laminin subunit gamma-1 precursor (Laminin B2 chain)	gi|194674274	143,183.80	99.80%	2	2	2	0.02%	2.78%	EAQQALGNAAADATEAR	3.12	1,686.80
ATP	6018	PREDICTED: similar to Laminin subunit gamma-1 precursor (Laminin B2 chain)	gi|194674274	143,183.80	99.80%	2	2	2	0.02%	2.78%	VSVPLIAQGNSYPSETTVK	4.31	1,990.05
ATP	6018	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	4	6	6	0.05%	10.30%	DLDELSRYPEDKITPENLPQILLQLK	3.91	3,080.65
ATP	6018	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	4	6	6	0.05%	10.30%	DSFDDRGPSLNPVLDYDHGSR	4.76	2,362.07
ATP	6018	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	4	6	6	0.05%	10.30%	VIHLSNLPHSGYSDSAVLK	3.87	2,037.08
ATP	6018	MATR3 protein	gi|134024643,gi|156523084	93,810.30	100.00%	4	6	6	0.05%	10.30%	YQLLQLVEPFGVISNHLILNK	3.62	2,438.38

ATP	6018	PREDICTED: similar to dynein, cytoplasmic, heavy polypeptide 1 isoform 3	gi|194677009	531,935.00	100.00%	3	3	3	0.03%	1.38%	ILDDDTIITTLENLKR	2.11	1,873.03
ATP	6018	PREDICTED: similar to dynein, cytoplasmic, heavy polypeptide 1 isoform 3	gi|194677009	531,935.00	100.00%	3	3	3	0.03%	1.38%	KLVPLLLEDGGEAPAALEAALEEK	3.63	2,476.35
ATP	6018	PREDICTED: similar to dynein, cytoplasmic, heavy polypeptide 1 isoform 3	gi|194677009	531,935.00	100.00%	3	3	3	0.03%	1.38%	VLRPQVTAVAQQNQGEVPEPQDMK	2.79	2,678.36
ATP	6018	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	4	6	8	0.07%	23.30%	GKESEKELALLK	3.78	1,344.77
ATP	6018	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	4	6	8	0.07%	23.30%	GVGDDQLGEESEERDDHLLPM	3.26	2,357.02
ATP	6018	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	4	6	8	0.07%	23.30%	HTLADNFNPVSEER	4.71	1,628.77
ATP	6018	Mannose-6-phosphate receptor (cation dependent)	gi|111308551,gi|119936494,gi|127292,gi|28461185	31,183.50	100.00%	4	6	8	0.07%	23.30%	SFESTVGQSPDMYSYVFR	4.2	2,115.93

ATP	6018	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	gi|111308649,gi|116241263	44,825.80	99.90%	2	2	2	0.02%	5.22%	GMSVSRPNAVIGK	2.53	1,331.71
ATP	6018	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	gi|111308649,gi|116241263	44,825.80	99.90%	2	2	2	0.02%	5.22%	VAIIIPFR	2.03	928.5979
ATP	6018	ADP-ribosylation-like factor 6 interacting protein 5	gi|59858163,gi|62460474,gi|74354855,gi|75057806	21,648.60	99.80%	2	3	9	0.08%	13.80%	FARPDFR	1.98	908.4737
ATP	6018	ADP-ribosylation-like factor 6 interacting protein 5	gi|59858163,gi|62460474,gi|74354855,gi|75057806	21,648.60	99.80%	2	3	9	0.08%	13.80%	TPMGIVLDALEQQEETITK	5.38	2,132.08
ATP	6018	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	gi|124829038,gi|125630707,gi|171769867	51,147.90	100.00%	3	3	4	0.03%	9.27%	ADYLQNYEFPHLQNFIK	4.84	2,140.05
ATP	6018	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	gi|124829038,gi|125630707,gi|171769867	51,147.90	100.00%	3	3	4	0.03%	9.27%	LLLVSFDGFR	3.36	1,166.66
ATP	6018	Ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	gi|124829038,gi|125630707,gi|171769867	51,147.90	100.00%	3	3	4	0.03%	9.27%	VLEEIDEHIGELVHR	3.02	1,787.93
ATP	6018	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	3	3	5	0.04%	8.36%	EKPYFPIPEDYTFIQNVPLEDR	4.5	2,710.34

ATP	6018	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	3	3	5	0.04%	8.36%	LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR	6.31	3,142.43
ATP	6018	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	gi|124828988,gi|125991756	90,435.30	100.00%	3	3	5	0.04%	8.36%	NFILDQTNVSAAAQR	3.52	1,647.84
ATP	6018	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	5	5	5	0.04%	10.80%	EESREPAPASPAPAGVEIR	4.31	1,962.99
ATP	6018	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	5	5	5	0.04%	10.80%	IFNLYPR	2.31	922.5145
ATP	6018	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	5	5	5	0.04%	10.80%	MDENQFVAVTSTNAAK	3.45	1,741.81
ATP	6018	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	5	5	5	0.04%	10.80%	NLHQSGFSLSGTQVDEGVR	3.79	2,030.99
ATP	6018	DPYSL3 protein	gi|154426078,gi|155371867	73,970.90	100.00%	5	5	5	0.04%	10.80%	QIGDNLIVPGGVK	2.67	1,309.75
ATP	6018	RecName: Full=Receptor expression-enhancing protein 5	gi|109892956,gi|114053301,gi|88954091	21,400.00	99.80%	2	2	2	0.02%	12.20%	HESQVDNVVNDLKDK	3.06	1,739.86
ATP	6018	RecName: Full=Receptor expression-enhancing protein 5	gi|109892956,gi|114053301,gi|88954091	21,400.00	99.80%	2	2	2	0.02%	12.20%	IIRPFFLK	2.28	1,033.66
ATP	6018	TOMM22 protein	gi|151556851,gi|154152189	15,275.00	100.00%	3	3	4	0.03%	44.30%	GDAEKPEEELEEEDDEELDETLSER	5.55	2,935.23
ATP	6018	TOMM22 protein	gi|151556851,gi|154152189	15,275.00	100.00%	3	3	4	0.03%	44.30%	LQMEQQQQLQQR	3.24	1,573.78
ATP	6018	TOMM22 protein	gi|151556851,gi|154152189	15,275.00	100.00%	3	3	4	0.03%	44.30%	QILLGPNTGLSGGMPGALPSLPGKI	4.45	2,404.33

ATP	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	15	17	27	0.23%	53.50%	AIAELGIYPAVDPLDSTSR	4.68	1,988.03
ATP	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	15	17	27	0.23%	53.50%	DQEGQDVLLFIDNIFR	4.51	1,921.97
ATP	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	15	17	27	0.23%	53.50%	GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	3.63	3,350.64
ATP	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	15	17	27	0.23%	53.50%	IMDPNIVGSEHYDVAR	3.14	1,831.86
ATP	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	15	17	27	0.23%	53.50%	IMNVIGEPIDER	2.69	1,401.70

ATP	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	15	17	27	0.23%	53.50%	IPVGPETLGR	3.14	1,038.59
ATP	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	15	17	27	0.23%	53.50%	IVAVIGAVVDVQFDEGLPPILNALEVQGR	3.04	3,031.68
ATP	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	15	17	27	0.23%	53.50%	LVLEVAQHLGESTVR	3.39	1,650.92
ATP	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	15	17	27	0.23%	53.50%	QFAAIHAEAPEFVEMSVEQEILVTGIK	3.68	3,002.52
ATP	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	15	17	27	0.23%	53.50%	SLQDIIAILGMDELSEEDKLTVSR	2.79	2,691.38

ATP	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	15	17	27	0.23%	53.50%	TVLIMELINNVAK	4.59	1,473.83
ATP	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	15	17	27	0.23%	53.50%	VALTGLTVAEYFR	3.52	1,439.79
ATP	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	15	17	27	0.23%	53.50%	VALVYGQMNEPPGAR	4.39	1,617.81
ATP	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	15	17	27	0.23%	53.50%	VLDSGAPIRIPVGPETLGR	4.01	1,947.10
ATP	6018	RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor	gi|114543,gi|158429023,gi|158429024,gi|158429025,gi|158431069,gi|158431070,gi|158431071,gi|28461221,gi|94574271	51,687.60	100.00%	15	17	27	0.23%	53.50%	VVDLLAPYAK	2.53	1,088.64
ATP	6018	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	4	6	7	0.06%	18.80%	AEQINQAAGEASAVLAK	4.05	1,670.87

ATP	6018	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	4	6	7	0.06%	18.80%	ASYGVEDPEYAVTQLAQTTMR	4.34	2,346.09
ATP	6018	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	4	6	7	0.06%	18.80%	ILEPGLNILIPVLDR	3.54	1,675.02
ATP	6018	RecName: Full=Stomatin-like protein 2; Short=SLP-2	gi|118573893,gi|148745563,gi|81674229,gi|84000113	38,715.70	100.00%	4	6	7	0.06%	18.80%	STDASLDEELDRVK	3.25	1,577.77
ATP	6018	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	6	7	9	0.08%	7.45%	FVDENEGYLVDIHDFSLGSSPR	4.01	2,496.17
ATP	6018	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	6	7	9	0.08%	7.45%	IEFPILDDSSELQVK	3.54	1,732.90
ATP	6018	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	6	7	9	0.08%	7.45%	IPVQLVFK	2.71	943.5976
ATP	6018	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	6	7	9	0.08%	7.45%	SPVTLTAYIVTSLLGYK	4.98	1,826.03
ATP	6018	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	6	7	9	0.08%	7.45%	SYSQSILLDLTDSTLQTTLK	3.68	2,227.17
ATP	6018	PREDICTED: similar to CD109, partial	gi|119921375	142,518.70	100.00%	6	7	9	0.08%	7.45%	VGSPFELVVIGNK	4.19	1,358.77
ATP	6018	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	100.00%	4	5	16	0.14%	21.70%	FLVGFTNK	2.52	925.5142
ATP	6018	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	100.00%	4	5	16	0.14%	21.70%	GEDFPANNIVK	3.17	1,203.60
ATP	6018	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	100.00%	4	5	16	0.14%	21.70%	GTEDFIVESLDASFR	4.54	1,685.80

ATP	6018	SSR1 protein	gi|151553610,gi|156120891,gi|187611488	32,036.80	100.00%	4	5	16	0.14%	21.70%	QATFEYSFIPAEPMGGRPFGLVINLNYK	2.74	3,175.59
ATP	6018	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	7	8	9	0.08%	21.40%	FGTFHSPALEDADFDGKPMVLVAGQYSTGK	3.33	3,201.52
ATP	6018	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	7	8	9	0.08%	21.40%	LEGHGLPTNLPR	3.25	1,303.71
ATP	6018	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	7	8	9	0.08%	21.40%	LFELEEQDLFR	3.59	1,438.72
ATP	6018	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	7	8	9	0.08%	21.40%	LFELEEQDLFRDIQGLPR	4.24	2,218.15
ATP	6018	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	7	8	9	0.08%	21.40%	LLEALDEMLTHDIAK	4.51	1,727.89
ATP	6018	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	7	8	9	0.08%	21.40%	LSDVDRDGMLDDEEFALASHLIEAK	4.38	2,805.33
ATP	6018	EH-domain containing 2	gi|114051716,gi|86822020	61,201.30	100.00%	7	8	9	0.08%	21.40%	SKYDEIFYNLAPADGK	4.38	1,830.89
ATP	6018	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	3	4	4	0.03%	7.32%	ALGVEQDLALPAIAVIGDQSSGK	3.85	2,252.21
ATP	6018	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	3	4	4	0.03%	7.32%	SSVLEALSGVALPR	4.63	1,398.80
ATP	6018	GTP-binding protein MX2	gi|13430404,gi|27806835,gi|75066885	81,436.40	100.00%	3	4	4	0.03%	7.32%	VAVENQPQDIGLQIK	3.54	1,651.90
ATP	6018	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	5	5	9	0.08%	18.10%	KQDAFYKEQLAR	3.81	1,496.79
ATP	6018	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	5	5	9	0.08%	18.10%	RVAEELALEQAKK	4.3	1,484.84
ATP	6018	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	5	5	9	0.08%	18.10%	RVTFEADENENITVVK	2.83	1,863.94

ATP	6018	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	5	5	9	0.08%	18.10%	VAEELALEQAK	4.34	1,200.65
ATP	6018	coiled-coil-helix-coiled-coil-helix domain containing 3	gi|59858339,gi|62510470,gi|74354006,gi|78365273	26,082.40	100.00%	5	5	9	0.08%	18.10%	VAEELALEQAKK	4.29	1,328.74
ATP	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	10	13	36	0.31%	18.90%	AEDYPIDLYYLMDLSYSMKDDLENVK	3.45	3,159.44
ATP	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	10	13	36	0.31%	18.90%	LLVFSTDAGFHFAGDGK	2.07	1,781.89
ATP	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	10	13	36	0.31%	18.90%	LPEGVTINYK	3.14	1,133.62
ATP	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	10	13	36	0.31%	18.90%	LQPEDITQIQPQQLVLQLR	5.85	2,260.27
ATP	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	10	13	36	0.31%	18.90%	LSENNIQTIFAVTEEFQPVYK	5.04	2,470.25
ATP	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	10	13	36	0.31%	18.90%	NVLSLTDKGEVFNELVGK	4.35	1,962.05
ATP	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	10	13	36	0.31%	18.90%	SGEPQTFTLK	2.51	1,107.57
ATP	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	10	13	36	0.31%	18.90%	SKGTAEKLQPEDITQIQPQQLVLQLR	2.69	2,961.64
ATP	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	10	13	36	0.31%	18.90%	SLGTDLMNEMR	3.05	1,282.58
ATP	6018	integrin beta 1	gi|111183155,gi|218563327	88,075.70	100.00%	10	13	36	0.31%	18.90%	TVMPYISTTPAK	3.26	1,324.68
ATP	6018	TPM3 protein	gi|79153472	29,015.30	100.00%	7	8	9	0.08%	31.50%	ALKDEEKMELQEIQLK	3.27	1,961.03
ATP	6018	TPM3 protein	gi|79153472	29,015.30	100.00%	7	8	9	0.08%	31.50%	IQLVEEELDR	3.08	1,243.65
ATP	6018	TPM3 protein	gi|79153472	29,015.30	100.00%	7	8	9	0.08%	31.50%	IQLVEEELDRAQER	3.79	1,727.89
ATP	6018	TPM3 protein	gi|79153472	29,015.30	100.00%	7	8	9	0.08%	31.50%	KIQVLQQQADDAEERAER	3.11	2,127.08
ATP	6018	TPM3 protein	gi|79153472	29,015.30	100.00%	7	8	9	0.08%	31.50%	LEEAEKAADESERGMK	3.77	1,808.83
ATP	6018	TPM3 protein	gi|79153472	29,015.30	100.00%	7	8	9	0.08%	31.50%	RIQLVEEELDRAQER	2.56	1,883.99

ATP	6018	TPM3 protein	gi|79153472	29,015.30	100.00%	7	8	9	0.08%	31.50%	YSQKEDKYEEEIK	3.54	1,688.80
ATP	6018	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	4	5	7	0.06%	19.40%	LSQNNFALGYK	3.77	1,254.65
ATP	6018	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	4	5	7	0.06%	19.40%	LTLDTIFVPNTGK	4.65	1,418.79
ATP	6018	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	4	5	7	0.06%	19.40%	LTLDTIFVPNTGKK	2.39	1,546.88

ATP	6018	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	4	5	7	0.06%	19.40%	LTLSALIDGK	3.89	1,030.61
ATP	6018	RecName: Full=Voltage-dependent anion-selective channel protein 3; Short=VDAC-3; AltName: Full=Outer mitochondrial membrane protein porin 3	gi|13124452,gi|148878077,gi|27807415,gi|8810224	30,853.30	100.00%	4	5	7	0.06%	19.40%	VNNASLIGLGYTQTLRPGVK	4.34	2,101.18
ATP	6018	SLC25A3 protein	gi|151556064	39,986.50	100.00%	4	6	14	0.12%	9.70%	FGFYEVFK	2.02	1,036.51
ATP	6018	SLC25A3 protein	gi|151556064	39,986.50	100.00%	4	6	14	0.12%	9.70%	IQTQPGYANTLR	3.9	1,361.72
ATP	6018	SLC25A3 protein	gi|151556064	39,986.50	100.00%	4	6	14	0.12%	9.70%	LPRPPPPEMPESLK	4.55	1,603.85
ATP	6018	SLC25A3 protein	gi|151556064	39,986.50	100.00%	4	6	14	0.12%	9.70%	LPRPPPPEMPESLKK	4.24	1,731.95
ATP	6018	ALCAM/CD166	gi|13111304,gi|41386784,gi|47605539	64,749.10	100.00%	3	4	4	0.03%	4.63%	KSVQYDDVPEYKDR	2.91	1,741.84
ATP	6018	ALCAM/CD166	gi|13111304,gi|41386784,gi|47605539	64,749.10	100.00%	3	4	4	0.03%	4.63%	SVQYDDVPEYKDR	2.56	1,613.74
ATP	6018	ALCAM/CD166	gi|13111304,gi|41386784,gi|47605539	64,749.10	100.00%	3	4	4	0.03%	4.63%	VFKQPSKPEIVSK	2.71	1,486.86

ATP	6018	Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	gi|109659140,gi|27806841,gi|28372116,gi|2920652,gi|3046232,gi|33111880,gi|68067472	74,789.50	99.90%	2	2	2	0.02%	7.72%	IEDIRLEQENEAEK	2.88	1,715.84
ATP	6018	Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	gi|109659140,gi|27806841,gi|28372116,gi|2920652,gi|3046232,gi|33111880,gi|68067472	74,789.50	99.90%	2	2	2	0.02%	7.72%	QETINLVVVPANVDIATTEALR	2.92	2,366.29
ATP	6018	Myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	gi|109659140,gi|27806841,gi|28372116,gi|2920652,gi|3046232,gi|33111880,gi|68067472	74,789.50	99.90%	2	2	2	0.02%	7.72%	SSVLEALSGVALPR	4.63	1,398.80
ATP	6018	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor 1; AltName: Full=p40; AltName: Full=Protein C10	gi|122066007,gi|28189773,gi|73587277	18,591.70	100.00%	4	4	4	0.03%	35.70%	AIVAIENPADVSISSR	3.72	1,740.95

ATP	6018	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor 1; AltName: Full=p40; AltName: Full=Protein C10	gi|122066007,gi|28189773,gi|73587277	18,591.70	100.00%	4	4	4	0.03%	35.70%	FAAATGATPIAGR	4.82	1,203.65
ATP	6018	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor 1; AltName: Full=p40; AltName: Full=Protein C10	gi|122066007,gi|28189773,gi|73587277	18,591.70	100.00%	4	4	4	0.03%	35.70%	FLAAGTHLGGTNLDFQMEQYIYK	4.73	2,633.27
ATP	6018	RecName: Full=40S ribosomal protein SA; AltName: Full=Laminin receptor 1; AltName: Full=p40; AltName: Full=Protein C10	gi|122066007,gi|28189773,gi|73587277	18,591.70	100.00%	4	4	4	0.03%	35.70%	LLVVTDPR	2.39	912.5514
ATP	6018	alpha isoform of regulatory subunit A, protein phosphatase 2	gi|146231714,gi|79153525,gi|82697383	65,273.60	99.80%	2	2	2	0.02%	5.43%	SEIIPMFSNLASDEQDSVR	3.88	2,154.00

ATP	6018	alpha isoform of regulatory subunit A, protein phosphatase 2	gi|146231714,gi|79153525,gi|82697383	65,273.60	99.80%	2	2	2	0.02%	5.43%	VLAMSGDPNYLHR	2.37	1,488.73
ATP	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	5	7	12	0.10%	31.80%	GIVDQSQQAYQEAFEISK	3.98	2,040.99
ATP	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	5	7	12	0.10%	31.80%	GIVDQSQQAYQEAFEISKK	3.08	2,169.08
ATP	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	5	7	12	0.10%	31.80%	LAEQAERYDDMAACMK	3.56	1,860.79
ATP	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	5	7	12	0.10%	31.80%	SVTEQGAELSNEER	4.59	1,548.71

ATP	6018	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi|27807367,gi|4557908,gi|4557913,gi|4557914,gi|4557915,gi|4557916,gi|4930273,gi|4930274,gi|52000886,gi|73587275	27,727.90	100.00%	5	7	12	0.10%	31.80%	TAFDEAIAELDTLSEESYKDSTLIMQLLR	5.38	3,318.63
ATP	6018	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	4	4	5	0.04%	16.50%	IALTDNALIAR	3.66	1,170.68
ATP	6018	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	4	4	5	0.04%	16.50%	KVPAVPETLK	2.51	1,081.66
ATP	6018	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	4	4	5	0.04%	16.50%	KVPAVPETLKK	3.22	1,209.76
ATP	6018	PREDICTED: similar to ribosomal protein L7	gi|119919984,gi|61553181,gi|62460552,gi|71649267	29,152.80	100.00%	4	4	5	0.04%	16.50%	TTHFVEGGDAGNREDQINR	2.15	2,115.98
ATP	6018	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	5	5	7	0.06%	13.20%	ADLINNLGTIAK	2.59	1,242.71
ATP	6018	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	5	5	7	0.06%	13.20%	ELISNSSDALDK	2.7	1,291.64
ATP	6018	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	5	5	7	0.06%	13.20%	ELISNSSDALDKIR	3.71	1,560.82
ATP	6018	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	5	5	7	0.06%	13.20%	GVVDSEDLPLNISR	4.63	1,513.79
ATP	6018	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	5	5	7	0.06%	13.20%	HLEINPDHSIIETLR	3.16	1,786.94
ATP	6018	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	5	5	7	0.06%	13.20%	NPDDITNEEYGEFYK	3.18	1,833.78

ATP	6018	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	5	5	7	0.06%	13.20%	TLTIVDTGIGMTK	4.41	1,365.73
ATP	6018	90-kDa heat shock protein alpha	gi|34392343,gi|60592792,gi|75072500	84,716.20	100.00%	5	5	7	0.06%	13.20%	YESLTDPSKLDSGK	4.17	1,539.75
ATP	6018	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	3	3	10	0.09%	19.80%	AMGIMNSFVNDIFER	4.38	1,759.81
ATP	6018	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	3	3	10	0.09%	19.80%	ESYSVYVYK	2.35	1,137.55
ATP	6018	PREDICTED: similar to histone cluster 1, H2bd	gi|119915707,gi|119915717,gi|119915727,gi|119936491,gi|82697375	13,888.60	100.00%	3	3	10	0.09%	19.80%	KESYSVYVYK	2.81	1,265.64
ATP	6018	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	6	6	7	0.06%	18.60%	EATESFASDPILYRPVAVALDTKGPEIR	4.24	3,045.59
ATP	6018	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	6	6	7	0.06%	18.60%	GDLGIEIPAEK	3.44	1,141.61
ATP	6018	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	6	6	7	0.06%	18.60%	IYVDDGLISLLVK	3.21	1,447.84
ATP	6018	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	6	6	7	0.06%	18.60%	LDIDSPPITAR	3.07	1,197.65
ATP	6018	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	6	6	7	0.06%	18.60%	LSPITSDPTEAAAVGAVEASFK	3.82	2,161.10
ATP	6018	pyruvate kinase 3	gi|146231736,gi|194670470,gi|73587283	61,410.20	100.00%	6	6	7	0.06%	18.60%	QKGPDFLVTEVENGGSLGSK	3.41	2,062.05
ATP	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	10	13	30	0.26%	33.20%	AMGNLQIDFADPSR	4.49	1,550.73

ATP	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	10	13	30	0.26%	33.20%	AMGNLQIDFADPSRADDAR	3.27	2,078.96
ATP	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	10	13	30	0.26%	33.20%	AVVYSNTIQSIMAIVK	4.94	1,752.96
ATP	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	10	13	30	0.26%	33.20%	EYQLNDSAAYYLNDLER	4.21	2,076.95
ATP	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	10	13	30	0.26%	33.20%	IAQSDYIPTQQDVLR	4.2	1,746.90
ATP	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	10	13	30	0.26%	33.20%	LLLLGAGESGK	3.63	1,057.63
ATP	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	10	13	30	0.26%	33.20%	NVQFVFDAVTDVIIK	2.93	1,707.93

ATP	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	10	13	30	0.26%	33.20%	SREYQLNDSAAYYLNDLER	4.66	2,320.08
ATP	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	10	13	30	0.26%	33.20%	TTGIVETHFTFK	3.35	1,380.72
ATP	6018	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	gi|198282135	40,460.10	100.00%	10	13	30	0.26%	33.20%	YDEAASYIQSK	3.16	1,274.59
ATP	6018	Paraoxonase 2	gi|109939919,gi|61553203,gi|61888862,gi|71648804	39,404.60	100.00%	4	6	8	0.07%	14.70%	LFVYDPK	2.16	881.4768
ATP	6018	Paraoxonase 2	gi|109939919,gi|61553203,gi|61888862,gi|71648804	39,404.60	100.00%	4	6	8	0.07%	14.70%	LLIGTLYHR	2.46	1,085.65
ATP	6018	Paraoxonase 2	gi|109939919,gi|61553203,gi|61888862,gi|71648804	39,404.60	100.00%	4	6	8	0.07%	14.70%	VVAEGFDSANGINISPDKK	4.57	1,961.00
ATP	6018	Paraoxonase 2	gi|109939919,gi|61553203,gi|61888862,gi|71648804	39,404.60	100.00%	4	6	8	0.07%	14.70%	YIYVADILAHEIHVLEK	1.97	2,026.10
ATP	6018	RecName: Full=Adenylyl cyclase-associated protein 1; Short=CAP 1	gi|122056071,gi|152001126,gi|74267948,gi|78042488	51,254.80	100.00%	3	4	4	0.03%	16.10%	ELSGLPSGPSAGSGPPPPPPGPPPPPVPTSSGSDDSASR	4.53	3,586.73

ATP	6018	RecName: Full=Adenylyl cyclase-associated protein 1; Short=CAP 1	gi|122056071,gi|152001126,gi|74267948,gi|78042488	51,254.80	100.00%	3	4	4	0.03%	16.10%	LSDLLAPISEQIQEVVTFR	3.43	2,158.18
ATP	6018	RecName: Full=Adenylyl cyclase-associated protein 1; Short=CAP 1	gi|122056071,gi|152001126,gi|74267948,gi|78042488	51,254.80	100.00%	3	4	4	0.03%	16.10%	SALFAQINQGESITHALK	2.5	1,928.02
ATP	6018	RecName: Full=Complement component 1 Q subcomponent-binding protein, mitochondrial; Flags: Precursor	gi|115311784,gi|74354078,gi|77736001	30,588.80	99.80%	2	4	8	0.07%	18.00%	AEEQEPELTSTPNFVVEVTK	3.81	2,247.10
ATP	6018	RecName: Full=Complement component 1 Q subcomponent-binding protein, mitochondrial; Flags: Precursor	gi|115311784,gi|74354078,gi|77736001	30,588.80	99.80%	2	4	8	0.07%	18.00%	GVDNTFADELVELSTALEHQEYISFLEDLK	5.71	3,425.66
ATP	6018	plastin 3	gi|152941116	70,782.90	100.00%	4	4	4	0.03%	8.41%	AYFHLLNQIAPK	3.63	1,414.78
ATP	6018	plastin 3	gi|152941116	70,782.90	100.00%	4	4	4	0.03%	8.41%	IDINMSGFNETDDLKR	3.16	1,883.88
ATP	6018	plastin 3	gi|152941116	70,782.90	100.00%	4	4	4	0.03%	8.41%	LNLAFVANLFNK	3.76	1,363.77
ATP	6018	plastin 3	gi|152941116	70,782.90	100.00%	4	4	4	0.03%	8.41%	MINLSVPDTIDER	4.21	1,518.75
ATP	6018	vascular cell adhesion molecule-1 7D variant	gi|11907511,gi|11990448,gi|41386707	81,381.40	99.80%	2	2	2	0.02%	3.25%	LPIDEMEFELK	2.55	1,363.68

ATP	6018	vascular cell adhesion molecule-1 7D variant	gi|11907511,gi|11990448,gi|41386707	81,381.40	99.80%	2	2	2	0.02%	3.25%	QSTQTLYVNVAPR	2.89	1,476.78
ATP	6018	ARF1 protein	gi|146327384,gi|28603778,gi|59858233,gi|62751462	20,583.70	100.00%	3	3	4	0.03%	24.30%	ILMVGLDAAGK	3.55	1,103.61
ATP	6018	ARF1 protein	gi|146327384,gi|28603778,gi|59858233,gi|62751462	20,583.70	100.00%	3	3	4	0.03%	24.30%	MLAEDELRDAVLLVFANK	3.63	2,063.08
ATP	6018	ARF1 protein	gi|146327384,gi|28603778,gi|59858233,gi|62751462	20,583.70	100.00%	3	3	4	0.03%	24.30%	QDLPNAMNAAEITDK	2.94	1,646.77
ATP	6018	H2A histone family, member X	gi|109659379,gi|119331192,gi|119889440	13,977.80	99.80%	2	3	4	0.03%	23.10%	LLGGVTIAQGGVLPNIQAVLLPK	4.74	2,271.38
ATP	6018	H2A histone family, member X	gi|109659379,gi|119331192,gi|119889440	13,977.80	99.80%	2	3	4	0.03%	23.10%	NDEELNKLLGGVTIAQGGVLPNIQAVLLPK	5.75	3,113.76
ATP	6018	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	100.00%	3	3	3	0.03%	11.10%	GAGTDEFTLNR	3.1	1,180.56
ATP	6018	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	100.00%	3	3	3	0.03%	11.10%	SEIDLLDIR	3.46	1,073.58
ATP	6018	RecName: Full=Annexin A3; AltName: Full=Annexin-3; AltName: Full=Annexin III	gi|115299847,gi|74356332,gi|78369184	36,125.00	100.00%	3	3	3	0.03%	11.10%	SLGDEISSETSGDFRK	3.68	1,727.81

ATP	6018	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	10	16	0.14%	15.00%	GLNTIPLFVQLLYSPIENIQR	4.81	2,428.36
ATP	6018	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	10	16	0.14%	15.00%	LHYGLPVVVK	3.28	1,124.68
ATP	6018	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	10	16	0.14%	15.00%	LIILASGGPQALVNIMR	4.45	1,782.03
ATP	6018	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	10	16	0.14%	15.00%	LLNDEDQVVVNK	3.97	1,385.73
ATP	6018	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	10	16	0.14%	15.00%	MLGSPVDSVLFYAITTLHNLLLHQEGAK	4.16	3,083.62
ATP	6018	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	10	16	0.14%	15.00%	NEGVATYAAAVLFR	4.12	1,481.77
ATP	6018	Catenin (cadherin-associated protein), beta 1, 88kDa	gi|111304624,gi|115497488,gi|122145603,gi|152941124	85,493.00	100.00%	7	10	16	0.14%	15.00%	TSMGGTQQQFVEGVR	3.42	1,640.77
ATP	6018	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	gi|117306519,gi|118151180,gi|158512477	51,340.60	100.00%	2	2	3	0.03%	7.87%	SHLTDKGMLTAATEDK	3.21	1,733.84
ATP	6018	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	gi|117306519,gi|118151180,gi|158512477	51,340.60	100.00%	2	2	3	0.03%	7.87%	VAREPEAPPEDKESESEAK	3.98	2,097.99

ATP	6018	PREDICTED: similar to Inner nuclear membrane protein Man1 (LEM domain-containing protein 3)	gi|76618511	100,104.80	99.80%	2	2	2	0.02%	3.29%	RPAAPELQSPSGR	2.87	1,365.72
ATP	6018	PREDICTED: similar to Inner nuclear membrane protein Man1 (LEM domain-containing protein 3)	gi|76618511	100,104.80	99.80%	2	2	2	0.02%	3.29%	VLLGFSSDESDVEASPR	1.66	1,807.87
ATP	6018	SET translocation (myeloid leukemia-associated)	gi|152941192,gi|83638675,gi|84370163	32,099.40	99.80%	2	2	2	0.02%	8.66%	IDFYFDENPYFENK	2.63	1,840.81
ATP	6018	SET translocation (myeloid leukemia-associated)	gi|152941192,gi|83638675,gi|84370163	32,099.40	99.80%	2	2	2	0.02%	8.66%	VEVTEFEDIK	2.92	1,208.60
ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	FNQMLNQIPNDYHSSR	3.6	1,979.90
ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	GEVQTVTFDTDEVK	3.69	1,567.75
ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	GGNTLTGMALNFIR	2.71	1,480.76
ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	GLTSSEPVSIMEK	3.27	1,393.69
ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	GPGDLEAPSNLVLSER	3.91	1,653.84

ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	IIYSPTVGDPIDEYTTVPGR	3.13	2,193.11
ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	ITVDPTTDGPTK	2.7	1,244.64
ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	ITYQPSTGEGNEQTTTIGGR	5.12	2,110.01
ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	IVEVFEIGPK	2.89	1,130.65
ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	LFYAPTAGGPEELVPIPGNTNYAILR	4.61	2,773.46
ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	LKPDTPYTITVSSLYPDGEGGR	3.4	2,366.19
ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	LQPQTTYDITVLPVYK	2.24	1,879.02
ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	NAFVNQPTVELHPNGLPPSYTIILLFR	2.32	3,050.65
ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	NIGVEVFSLGIK	3.66	1,275.73
ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	NNVILQPLQPDTPYK	3.75	1,739.93
ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	NVQVYNPTPNSLDVR	3.81	1,715.87

ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	SLPADVIHTVIENLQPETK	2.75	2,104.13
ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	VEDIIEAINTFPYR	4.65	1,679.86
ATP	6018	PREDICTED: collagen, type XII, alpha 1 isoform 1	gi|194669778	351,243.80	100.00%	19	19	21	0.18%	9.72%	VQIALAQYSGDPR	3.78	1,417.74
ATP	6018	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	3	5	6	0.05%	13.10%	ANVDKVFFDLMR	4.05	1,470.74
ATP	6018	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	3	5	6	0.05%	13.10%	VFFDLMR	2.1	943.4707
ATP	6018	V-ral simian leukemia viral oncogene homolog A (ras related)	gi|73586513,gi|77736231,gi|95768203	23,522.20	100.00%	3	5	6	0.05%	13.10%	VKEDENVPFLLVGNK	4.68	1,700.92
ATP	6018	ALDOA protein	gi|151554749,gi|156120479	39,418.80	99.80%	2	2	5	0.04%	7.97%	GILAADESTGSIAK	3.16	1,332.70
ATP	6018	ALDOA protein	gi|151554749,gi|156120479	39,418.80	99.80%	2	2	5	0.04%	7.97%	RLQSIGTENTEENRR	3.37	1,802.91
ATP	6018	Small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)	gi|86821409,gi|87080799	35,394.40	99.80%	2	2	2	0.02%	5.59%	KQQPVAGSADSKPVDVSR	3.81	1,868.98

ATP	6018	Small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)	gi|86821409,gi|87080799	35,394.40	99.80%	2	2	2	0.02%	5.59%	QQPVAGSADSKPVDVSR	2.73	1,740.89
ATP	6018	NADH dehydrogenase (ubiquinone) 39 kDa subunit	gi|230,gi|28603782,gi|464254,gi|74267974	37,737.50	99.80%	2	2	2	0.02%	10.60%	LLQYADALEHLLSTGQGVVLER	3.23	2,425.31
ATP	6018	NADH dehydrogenase (ubiquinone) 39 kDa subunit	gi|230,gi|28603782,gi|464254,gi|74267974	37,737.50	99.80%	2	2	2	0.02%	10.60%	LQYGPLAYILGEK	3.42	1,464.81
ATP	6018	PREDICTED: similar to small GTP binding protein RAB23	gi|194677545	37,951.40	99.80%	2	4	7	0.06%	9.91%	LKQQIAENPESMHSSSNK	3.54	2,043.98
ATP	6018	PREDICTED: similar to small GTP binding protein RAB23	gi|194677545	37,951.40	99.80%	2	4	7	0.06%	9.91%	VVAEVGDIPTALVQNK	3.83	1,652.92
ATP	6018	RecName: Full=Transmembrane emp24 domain-containing protein 1; Flags: Precursor	gi|114152289,gi|83638714,gi|84370158	25,119.90	99.80%	2	3	5	0.04%	11.50%	KADGVHTVEPTEAGDYK	4.54	1,816.87
ATP	6018	RecName: Full=Transmembrane emp24 domain-containing protein 1; Flags: Precursor	gi|114152289,gi|83638714,gi|84370158	25,119.90	99.80%	2	3	5	0.04%	11.50%	SIQVLTLLR	2.74	1,042.66

ATP	6018	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein L isoform 1	gi|76641417	64,057.80	99.80%	2	3	3	0.03%	10.70%	GLIDGVVEADLVEALQEFGPISYVVVMPK	4.35	3,103.63
ATP	6018	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein L isoform 1	gi|76641417	64,057.80	99.80%	2	3	3	0.03%	10.70%	TDNAGDQHGGGGGGGGGAGAAGGGGGENYDDPHK	2.38	2,924.18
ATP	6018	NADH:ubiquinone oxidoreductase ASHI subunit [Homo sapiens]	gi|33150722	21,747.60	99.80%	2	2	2	0.02%	16.10%	QYPYNNLYLER	2.15	1,472.72
ATP	6018	NADH:ubiquinone oxidoreductase ASHI subunit [Homo sapiens]	gi|33150722	21,747.60	99.80%	2	2	2	0.02%	16.10%	VEDYEPYPDDGMGYGDYPK	2.9	2,225.89
ATP	6018	proteasome activator subunit 2	gi|59858279,gi|62460470,gi|73921837,gi|74267960	27,362.30	99.80%	2	3	3	0.03%	14.20%	IIYLNQLLQEDSFNVTDLNSLR	5.08	2,608.36
ATP	6018	proteasome activator subunit 2	gi|59858279,gi|62460470,gi|73921837,gi|74267960	27,362.30	99.80%	2	3	3	0.03%	14.20%	TKVEAFQTTISK	3.05	1,352.74
ATP	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	12	23	0.20%	26.90%	IIGAVDQIQLTQAQLEER	5.7	2,025.10
ATP	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	12	23	0.20%	26.90%	IREGQVEVLK	3.76	1,170.68
ATP	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	12	23	0.20%	26.90%	KLEVNEAELLR	4.1	1,313.74

ATP	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	12	23	0.20%	26.90%	KSFTPDHVVYAR	2.67	1,419.74
ATP	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	12	23	0.20%	26.90%	QAEMEGAVQSIQGELSK	4.72	1,820.87
ATP	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	12	23	0.20%	26.90%	SDQVNGVLVLSLLDK	3.81	1,599.90
ATP	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	12	23	0.20%	26.90%	SDQVNGVLVLSLLDKIIGAVDQIQLTQAQLEER	3.89	3,605.98
ATP	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	12	23	0.20%	26.90%	SFTPDHVVYAR	3.1	1,291.64
ATP	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	12	23	0.20%	26.90%	VMIYQDEVKLPAK	4.04	1,549.83
ATP	6018	polymerase I and transcript release factor isoform 2	gi|162287374	43,446.30	100.00%	10	12	23	0.20%	26.90%	VPPFTFHVK	2.32	1,071.60
ATP	6018	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	5	5	9	0.08%	9.72%	DAFLGSFLYEYSR	3.32	1,567.74
ATP	6018	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	5	5	9	0.08%	9.72%	FKDLGEEHFK	4.15	1,249.62

ATP	6018	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	5	5	9	0.08%	9.72%	HLVDEPQNLIK	2.84	1,305.72
ATP	6018	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	5	5	9	0.08%	9.72%	KVPQVSTPTLVEVSR	4.41	1,639.94
ATP	6018	unnamed protein product	gi|110292444,gi|1351907,gi|148744077,gi|162648,gi|2190337,gi|23307791,gi|30794280,gi|3336842	69,296.20	100.00%	5	5	9	0.08%	9.72%	LVNELTEFAK	3.6	1,163.63
ATP	6018	RNA binding motif (RNP1, RRM) protein 3	gi|73587236,gi|77735675	9,735.50	100.00%	3	3	3	0.03%	55.60%	ALEDHFSSFGPISEVVVVK	3.36	2,060.07
ATP	6018	RNA binding motif (RNP1, RRM) protein 3	gi|73587236,gi|77735675	9,735.50	100.00%	3	3	3	0.03%	55.60%	GFGFITFTNPEHASNAMR	3.74	2,012.93
ATP	6018	RNA binding motif (RNP1, RRM) protein 3	gi|73587236,gi|77735675	9,735.50	100.00%	3	3	3	0.03%	55.60%	LFVGGLNFNTDER	3.44	1,481.74
ATP	6018	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	100.00%	3	6	12	0.10%	16.70%	KYMEENDLLKK	4.34	1,426.72
ATP	6018	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	100.00%	3	6	12	0.10%	16.70%	LQAAVDGPSDKKEE	3.18	1,486.74
ATP	6018	B-cell receptor-associated protein 31	gi|59858303,gi|62460574,gi|74354925	27,884.40	100.00%	3	6	12	0.10%	16.70%	VNLQNNPGAVEHFHMK	4.24	1,850.90
ATP	6018	ITGA3 protein	gi|151556279,gi|156120449	45,035.90	99.80%	2	2	2	0.02%	6.34%	EAGNPGSLFGYSVALHR	2.77	1,774.89
ATP	6018	ITGA3 protein	gi|151556279,gi|156120449	45,035.90	99.80%	2	2	2	0.02%	6.34%	YLLLAGAPR	2.94	973.583

ATP	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	13	15	41	0.35%	54.20%	AKDFSLILDDVAITELSFSR	3.53	2,240.18
ATP	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	13	15	41	0.35%	54.20%	AQVSLLIR	2.35	899.5673
ATP	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	13	15	41	0.35%	54.20%	DLQMVNISLR	3.6	1,204.64
ATP	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	13	15	41	0.35%	54.20%	ESVFTVEGGHR	2.82	1,217.59
ATP	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	13	15	41	0.35%	54.20%	FNASQLITQR	4.13	1,177.63
ATP	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	13	15	41	0.35%	54.20%	IGGVQQDTILAEGLHFR	4.7	1,853.99
ATP	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	13	15	41	0.35%	54.20%	IPWFQYPIIYDIR	3.84	1,723.92
ATP	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	13	15	41	0.35%	54.20%	IVQAEGEAEAAR	3.95	1,243.63
ATP	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	13	15	41	0.35%	54.20%	IYLTADNLVLNLQDESFTR	6.07	2,225.15
ATP	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	13	15	41	0.35%	54.20%	LLLGAGAVAYGIR	4.84	1,273.76
ATP	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	13	15	41	0.35%	54.20%	QKIVQAEGEAEAAR	4.23	1,499.78
ATP	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	13	15	41	0.35%	54.20%	VLPSIVNEVLK	2.77	1,210.74
ATP	6018	RecName: Full=Prohibitin-2	gi|109892820,gi|114051223,gi|87578149	33,340.80	100.00%	13	15	41	0.35%	54.20%	VLSRPNAMELPSMYQR	3.29	1,907.95
ATP	6018	TAP1 protein	gi|151557007	81,933.30	100.00%	6	7	10	0.09%	10.90%	GVVGAALGFR	2.84	946.5469
ATP	6018	TAP1 protein	gi|151557007	81,933.30	100.00%	6	7	10	0.09%	10.90%	IFEYLDR	2.2	955.4884
ATP	6018	TAP1 protein	gi|151557007	81,933.30	100.00%	6	7	10	0.09%	10.90%	QVAAVGQEPLLFGR	4.52	1,484.82
ATP	6018	TAP1 protein	gi|151557007	81,933.30	100.00%	6	7	10	0.09%	10.90%	SSQVAIEVLSAMPTVR	3.31	1,703.90
ATP	6018	TAP1 protein	gi|151557007	81,933.30	100.00%	6	7	10	0.09%	10.90%	STVAALLQNLYQPTEGQVLLDGEPLPK	5.51	2,894.55
ATP	6018	TAP1 protein	gi|151557007	81,933.30	100.00%	6	7	10	0.09%	10.90%	SVLFITQR	2.41	963.5622

ATP	6018	ribosomal protein L3	gi|1092507,gi|154426164,gi|27807287,gi|450499,gi|59858389,gi|7159574,gi|730564,gi|74267942	46,006.40	99.80%	2	2	2	0.02%	9.43%	DDSSKPVHLTAFLGYK	4.31	1,777.91
ATP	6018	ribosomal protein L3	gi|1092507,gi|154426164,gi|27807287,gi|450499,gi|59858389,gi|7159574,gi|730564,gi|74267942	46,006.40	99.80%	2	2	2	0.02%	9.43%	SINPLGGFVHYGEVTNDFVMLK	3.42	2,453.22
ATP	6018	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	99.80%	2	2	4	0.03%	8.06%	FASFIDKVR	1.87	1,082.60
ATP	6018	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	99.80%	2	2	4	0.03%	8.06%	NKYEDEINKR	3.05	1,308.65
ATP	6018	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	99.80%	2	2	4	0.03%	8.06%	NLDLDSIIAEVK	4.83	1,329.73
ATP	6018	PREDICTED: similar to keratin 6A	gi|194687333,gi|61870938,gi|76617862,gi|76617868,gi|76689949	60,808.20	99.80%	2	2	4	0.03%	8.06%	QNLEPLFEQYINNLR	2.36	1,890.97

<table>
<tr><td>ATP</td><td>6018</td><td>RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:</td><td>gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982</td><td>38,523.90</td><td>100.00%</td><td>8</td><td>12</td><td>13</td><td>0.11%</td><td>36.60%</td><td>AYTNFDAERDALNIETAIK</td><td>5.11</td><td>2,155.07</td></tr>
<tr><td>ATP</td><td>6018</td><td>RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:</td><td>gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982</td><td>38,523.90</td><td>100.00%</td><td>8</td><td>12</td><td>13</td><td>0.11%</td><td>36.60%</td><td>GVDEVTIVNILTNR</td><td>4.59</td><td>1,542.85</td></tr>
</table>

ATP	6018	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	8	12	13	0.11%	36.60%	LSLEGDHSTPPSAYGSVK	4.97	1,844.90
ATP	6018	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	8	12	13	0.11%	36.60%	QDIAFAYQR	2.85	1,111.55

ATP	6018	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	8	12	13	0.11%	36.60%	RAEDGSVIDYELIDQDAR	4.45	2,064.98
ATP	6018	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	8	12	13	0.11%	36.60%	SALSGHLETVILGLLK	4.42	1,650.98

ATP	6018	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	8	12	13	0.11%	36.60%	SYSPYDMLESIKK	2.7	1,576.76
ATP	6018	RecName: Full=Annexin A2; AltName: Full=Annexin-2; AltName: Full=Annexin II; AltName: Full=Lipocortin II; AltName: Full=Calpactin I heavy chain; AltName: Full=Chromobindin-8; AltName: Full=p36; AltName:	gi|113948,gi|162779,gi|27807289,gi|59858385,gi|73586982	38,523.90	100.00%	8	12	13	0.11%	36.60%	TDLEKDIVSDTSGDFRK	5.57	1,925.95
ATP	6018	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	7	8	8	0.07%	24.80%	ELIEVLQPLIAEHQAR	3.53	1,859.04

ATP	6018	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	7	8	8	0.07%	24.80%	IGYPKPALLHSTFFPALQGAQTK	3.18	2,485.36
ATP	6018	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	7	8	8	0.07%	24.80%	ISFPAIQAAPSFSNSFPQIFR	3.17	2,325.20
ATP	6018	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	7	8	8	0.07%	24.80%	MADMSNGEQGCGSPLELFHSIAAQGELVR	1.98	3,047.40
ATP	6018	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	7	8	8	0.07%	24.80%	MSASDPNSSIFLTDTAK	3.05	1,800.83

ATP	6018	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	7	8	8	0.07%	24.80%	NAAKDEIDSAVK	3.32	1,260.64
ATP	6018	RecName: Full=Tryptophanyl-tRNA synthetase, cytoplasmic; AltName: Full=Tryptophan--tRNA ligase; Short=TrpRS	gi|110283011,gi|27806353,gi|74354933,gi|825	53,712.80	100.00%	7	8	8	0.07%	24.80%	PALLHSTFFPALQGAQTK	3.88	1,927.04
ATP	6018	PREDICTED: similar to Transmembrane protein 16F	gi|119892265	106,290.10	100.00%	4	4	5	0.04%	8.01%	LLQVDESIIKPEQEFFTAPFEK	3.87	2,608.35
ATP	6018	PREDICTED: similar to Transmembrane protein 16F	gi|119892265	106,290.10	100.00%	4	4	5	0.04%	8.01%	MNDFYIQDRDTFFNPATR	3.62	2,267.02
ATP	6018	PREDICTED: similar to Transmembrane protein 16F	gi|119892265	106,290.10	100.00%	4	4	5	0.04%	8.01%	TPEFEEFNGKPDSLYFNDGQR	3.49	2,490.12
ATP	6018	PREDICTED: similar to Transmembrane protein 16F	gi|119892265	106,290.10	100.00%	4	4	5	0.04%	8.01%	TQTDYENSLTMK	2.56	1,446.64
ATP	6018	PREDICTED: similar to AGTPBP1 protein isoform 1	gi|119900741	133,423.40	99.80%	2	2	2	0.02%	6.08%	DYGLPVTVLTCTKACSHVAACGNVLFEGRTVQLGK	2.75	3,650.85

ATP	6018	PREDICTED: similar to AGTPBP1 protein isoform 1	gi|119900741	133,423.40	99.80%	2	2	2	0.02%	6.08%	IAQDIERLIHQSDIIDRVVYDLDNPNYTIPEEADVLK	2.34	4,323.21
ATP	6018	Vesicle-associated membrane protein 7	gi|109658341,gi|115495041,gi|122144644	24,944.90	99.80%	2	2	2	0.02%	9.55%	AFNFLNEIK	2.81	1,095.58
ATP	6018	Vesicle-associated membrane protein 7	gi|109658341,gi|115495041,gi|122144644	24,944.90	99.80%	2	2	2	0.02%	9.55%	VMETQAQVDELK	3.76	1,406.68
ATP	6018	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	4	6	10	0.09%	16.90%	ALSSSLDDTEVKK	4.64	1,392.72
ATP	6018	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	4	6	10	0.09%	16.90%	FRGPFTDVVTTNLK	3.63	1,594.86
ATP	6018	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	4	6	10	0.09%	16.90%	GPFTDVVTTNLK	4.12	1,291.69
ATP	6018	VAPB protein	gi|126010784,gi|129270105,gi|160210887	27,140.50	100.00%	4	6	10	0.09%	16.90%	VEQVLSLEPQHELK	5.02	1,648.89
ATP	6018	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	8	10	14	0.12%	20.60%	AKFYPEDVSEELIQDITQR	3.75	2,281.13
ATP	6018	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	8	10	14	0.12%	20.60%	APDFVFYAPR	3.78	1,182.59
ATP	6018	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	8	10	14	0.12%	20.60%	FYPEDVSEELIQDITQR	3.47	2,082.00
ATP	6018	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	8	10	14	0.12%	20.60%	GMLREDAVLEYLK	4.19	1,552.80
ATP	6018	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	8	10	14	0.12%	20.60%	KAQQELEEQTRR	2.17	1,515.79
ATP	6018	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	8	10	14	0.12%	20.60%	TAMSTPHVAEPAENEQDEQDENGAEASAELR	6.82	3,342.43
ATP	6018	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	8	10	14	0.12%	20.60%	TQEQLALEMAELTAR	3.24	1,719.86
ATP	6018	moesin	gi|114050715,gi|118583148,gi|87578169	67,959.00	100.00%	8	10	14	0.12%	20.60%	VTTMDAELEFAIQPNTTGK	2.6	2,082.01

ATP	6018	RecName: Full=Protein-glutamine gamma-glutamyltransferase 2; AltName: Full=Tissue transglutaminase; AltName: Full=TGase C; Short=TGC; Short=TG(C); AltName: Full=Transglutaminase-2	gi|1729922,gi|29135313,gi|73586866,gi|818	77,094.70	99.80%	2	2	2	0.02%	4.51%	DHHTADLCRERLVVR	2.1	1,819.93
ATP	6018	RecName: Full=Protein-glutamine gamma-glutamyltransferase 2; AltName: Full=Tissue transglutaminase; AltName: Full=TGase C; Short=TGC; Short=TG(C); AltName: Full=Transglutaminase-2	gi|1729922,gi|29135313,gi|73586866,gi|818	77,094.70	99.80%	2	2	2	0.02%	4.51%	GLLIEPANSYLLAER	3.43	1,729.95
ATP	6018	PDZ and LIM domain 1	gi|148877479	35,802.30	100.00%	3	3	3	0.03%	15.90%	ALDHSQLPSGLVIDKESEVYK	4.45	2,328.21
ATP	6018	PDZ and LIM domain 1	gi|148877479	35,802.30	100.00%	3	3	3	0.03%	15.90%	LVGGKDFEQPLAISR	2.75	1,629.90
ATP	6018	PDZ and LIM domain 1	gi|148877479	35,802.30	100.00%	3	3	3	0.03%	15.90%	SAVPFTASPASSSAPR	4.31	1,532.77

ATP	6018	PREDICTED: similar to Keratin, type I cytoskeletal 24 (Cytokeratin-24) (Keratin-24) (Type I keratin-24)	gi|194676109	55,111.70	99.80%	2	3	5	0.04%	5.33%	KVLDDLTMTR	2.88	1,207.64
ATP	6018	PREDICTED: similar to Keratin, type I cytoskeletal 24 (Cytokeratin-24) (Keratin-24) (Type I keratin-24)	gi|194676109	55,111.70	99.80%	2	3	5	0.04%	5.33%	SDLEMQIESLTEELAYLK	3.84	2,112.04
ATP	6018	H2A histone family, member Y	gi|114052404,gi|87578157	39,516.80	99.80%	2	4	8	0.07%	13.70%	AASADSTTEGTPADGFTVLSTK	4.35	2,127.01
ATP	6018	H2A histone family, member Y	gi|114052404,gi|87578157	39,516.80	99.80%	2	4	8	0.07%	13.70%	IGVGAPVYMAAVLEYLTAEILELAGNAAR	4.53	2,991.59
ATP	6018	PREDICTED: transmembrane protein 33 isoform 2	gi|119893815,gi|119922774	27,968.00	99.80%	2	2	2	0.02%	8.10%	ALLANALTSALR	3.73	1,213.73
ATP	6018	PREDICTED: transmembrane protein 33 isoform 2	gi|119893815,gi|119922774	27,968.00	99.80%	2	2	2	0.02%	8.10%	LPHFQLSR	2.64	997.5578
ATP	6018	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	6	7	13	0.11%	50.70%	DSLLQDGEFTMDLR	4.03	1,655.76

ATP	6018	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	6	7	13	0.11%	50.70%	SSFFVNGLTLGGQK	3.46	1,454.76
ATP	6018	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	6	7	13	0.11%	50.70%	STGGAPTFNITVTMTAK	4.03	1,712.85
ATP	6018	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	6	7	13	0.11%	50.70%	TFVNITPAEVGILVGK	4.75	1,657.95
ATP	6018	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	6	7	13	0.11%	50.70%	TFVNITPAEVGILVGKDR	2.78	1,929.08
ATP	6018	Chain A, Crystallization And Structure Determination Of Bovine Profilin At 2.0 Angstroms Resolution	gi|157833536,gi|157878211,gi|576369,gi|59858521,gi|62288870,gi|62751593,gi|73586531	15,039.50	100.00%	6	7	13	0.11%	50.70%	TLVLLMGK	2.19	890.5382

ATP	6018	Cell adhesion molecule 1	gi|83638798,gi|84370145	45,751.20	99.80%	2	3	3	0.03%	12.70%	GADDAADADTAIINAEGGQNNSEEKKEYFI	6.31	3,156.42
ATP	6018	Cell adhesion molecule 1	gi|83638798,gi|84370145	45,751.20	99.80%	2	3	3	0.03%	12.70%	YLEVQYKPQVHIQMTYPLQGLTR	4.43	2,821.47
ATP	6018	Brain abundant, membrane attached signal protein 1	gi|115304757,gi|1930063,gi|27807507,gi|6686271	22,992.60	100.00%	3	3	4	0.03%	20.30%	AQAPAAPADEVKPAETPAANSDQTVAVK	2.84	2,747.38
ATP	6018	Brain abundant, membrane attached signal protein 1	gi|115304757,gi|1930063,gi|27807507,gi|6686271	22,992.60	100.00%	3	3	4	0.03%	20.30%	AQAPAAPADEVKPAETPAANSDQTVAVKE	3.14	2,876.43
ATP	6018	Brain abundant, membrane attached signal protein 1	gi|115304757,gi|1930063,gi|27807507,gi|6686271	22,992.60	100.00%	3	3	4	0.03%	20.30%	ASEAEAAEPAAPTKDDK	2.21	1,700.80
ATP	6018	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	5	7	8	0.07%	31.10%	ALNLPSSGEGLAFFTFPNIASATK	5.16	2,453.27
ATP	6018	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	5	7	8	0.07%	31.10%	EATKEVHTQAENAEFMK	3.1	1,978.92
ATP	6018	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	5	7	8	0.07%	31.10%	LVMASLYHIYVALEEEIER	4.28	2,294.17
ATP	6018	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	5	7	8	0.07%	31.10%	NKENPVYTPLYFPEELHR	5.86	2,246.12
ATP	6018	Heme oxygenase (decycling) 1	gi|158455152,gi|59858301,gi|62460520,gi|73919958	32,922.40	100.00%	5	7	8	0.07%	31.10%	YLGDLSGGQVLK	2.88	1,249.68
ATP	6018	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	8	8	9	0.08%	8.89%	DTDMDGVGDQCDNCPLEHNPDQLDSDSDR	4.73	3,222.22

ATP	6018	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	8	8	9	0.08%	8.89%	FQDLVDAVR	3.02	1,062.56
ATP	6018	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	8	8	9	0.08%	8.89%	FVFGTTPEDILR	3.13	1,394.73
ATP	6018	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	8	8	9	0.08%	8.89%	GGVNDNFQGVLQNVR	3.75	1,616.81
ATP	6018	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	8	8	9	0.08%	8.89%	IEDANLIPPVPDKK	2.93	1,548.86
ATP	6018	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	8	8	9	0.08%	8.89%	KVTEENKELANELR	4.31	1,672.89
ATP	6018	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	8	8	9	0.08%	8.89%	TIVTTLQDSIR	2.28	1,246.70
ATP	6018	RecName: Full=Thrombospondin-1; Flags: Precursor	gi|12644428,gi|2244707,gi|41386685	129,515.10	100.00%	8	8	9	0.08%	8.89%	VTEENKELANELR	2.85	1,544.79
ATP	6018	RecName: Full=CD151 antigen; AltName: CD_antigen=CD151	gi|122140784,gi|152941162,gi|73587135,gi|78369214	27,969.10	99.80%	2	2	4	0.03%	20.60%	RNLLRLYFGLLLIIFLLEIIAGALAYIYYQQLNAELK	3.47	4,355.53

ATP	6018	RecName: Full=CD151 antigen; AltName: CD_antigen=CD151	gi|122140784,gi|152941162,gi|73587135,gi|78369214	27,969.10	99.80%	2	2	4	0.03%	20.60%	YHQPGHEGVTSAVDK	3.88	1,624.77
ATP	6018	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	100.00%	3	4	4	0.03%	15.80%	FSQMLHPIFEEASNVIKEEYPNANQVVFAR	6.25	3,523.73
ATP	6018	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	100.00%	3	4	4	0.03%	15.80%	HMYVFGDFRDVLIPGK	2	1,909.96
ATP	6018	RecName: Full=Thioredoxin domain-containing protein 4; Flags: Precursor	gi|108861917,gi|74354589,gi|78042524	46,819.40	100.00%	3	4	4	0.03%	15.80%	SDPIQELHDLAEITPDR	4.49	2,050.01
ATP	6018	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32,gi|59857977	33,881.70	100.00%	3	4	5	0.04%	14.80%	AVVVNAAQLASYSQSK	4.39	1,635.87

ATP	6018	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32,gi|59857977	33,881.70	100.00%	3	4	5	0.04%	14.80%	FLFGGLAGMGATVFVQPLDLVK	5.52	2,296.24
ATP	6018	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11	gi|126664,gi|146231676,gi|148744036,gi|148878065,gi|163432,gi|163434,gi|27807211,gi|32,gi|59857977	33,881.70	100.00%	3	4	5	0.04%	14.80%	NVFNALFR	2.11	980.5311
ATP	6018	prolyl 4-hydroxylase, alpha I subunit	gi|115495019,gi|122144801,gi|151556370,gi|92097479	60,994.20	99.80%	2	2	2	0.02%	3.93%	LQDTYNLDTDTISK	3.99	1,626.79
ATP	6018	prolyl 4-hydroxylase, alpha I subunit	gi|115495019,gi|122144801,gi|151556370,gi|92097479	60,994.20	99.80%	2	2	2	0.02%	3.93%	LQDTYNLDTDTISKGDLPGVK	3.45	2,293.16
ATP	6018	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	3	3	4	0.03%	14.20%	GGALLTSTSGPGFHLMLPFITSYK	3.59	2,511.30
ATP	6018	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	3	3	4	0.03%	14.20%	SVQTTLQTDEVK	3.43	1,348.70
ATP	6018	ER lipid raft associated 2	gi|114051093,gi|122134590,gi|92097476	37,713.20	100.00%	3	3	4	0.03%	14.20%	VAQVAEITFGQK	2.87	1,290.71
ATP	6018	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	10	13	0.11%	17.90%	ATLNAFLHR	2.85	1,042.58
ATP	6018	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	10	13	0.11%	17.90%	ITVLEALR	2.66	914.567

ATP	6018	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	10	13	0.11%	17.90%	LKEYEAAVEQLKGDQIR	4.54	1,990.06
ATP	6018	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	10	13	0.11%	17.90%	MYFDKYVLKPATEGK	3.19	1,805.91
ATP	6018	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	10	13	0.11%	17.90%	NVLMYGPPGTGK	3.18	1,249.62
ATP	6018	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	10	13	0.11%	17.90%	QQQLLNEENLR	2.7	1,384.72
ATP	6018	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	10	13	0.11%	17.90%	RLLSKPQDALEGVVLSPSLEAR	5.04	2,378.34
ATP	6018	ATAD3A protein	gi|157278889,gi|157428048,gi|162416153	66,090.40	100.00%	8	10	13	0.11%	17.90%	TAGTLFGEGFR	3.31	1,155.58
ATP	6018	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	6	7	9	0.08%	9.95%	EEASDYLELDTIK	4.27	1,525.73
ATP	6018	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	6	7	9	0.08%	9.95%	ELISNASDALDKIR	3.84	1,544.83
ATP	6018	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	6	7	9	0.08%	9.95%	FQSSHHPSDMTSLDQYVER	4.77	2,280.00
ATP	6018	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	6	7	9	0.08%	9.95%	GLFDEYGSK	2.2	1,015.47
ATP	6018	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	6	7	9	0.08%	9.95%	NLLHVTDTGVGMTR	4.62	1,529.77
ATP	6018	glucose-regulated protein GRP94 precursor	gi|16041057,gi|27807263,gi|33301108,gi|75775556	92,411.40	100.00%	6	7	9	0.08%	9.95%	SILFVPTSAPR	3.66	1,187.68

ATP	6018	PREDICTED: similar to FXYD domain-containing ion transport regulator 5 isoform 1	gi|76641186	18,921.80	99.80%	2	2	2	0.02%	10.40%	EDDPFFYDEDTLR	3.19	1,661.70
ATP	6018	PREDICTED: similar to FXYD domain-containing ion transport regulator 5 isoform 1	gi|76641186	18,921.80	99.80%	2	2	2	0.02%	10.40%	QPGSKEDDPFFYDEDTLR	3.51	2,158.96
ATP	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	11	12	15	0.13%	12.20%	ALSAIADLLTNEHER	4.7	1,652.86
ATP	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	11	12	15	0.13%	12.20%	APSRQDVYGPQPQVR	4.39	1,697.87
ATP	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	11	12	15	0.13%	12.20%	FHPEPYGLEDDQR	3.16	1,602.72
ATP	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	11	12	15	0.13%	12.20%	FVGDADLER	2.83	1,021.50
ATP	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	11	12	15	0.13%	12.20%	GKKPTEDPTNDTVDFPK	3.9	1,888.93
ATP	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	11	12	15	0.13%	12.20%	HYEDGYPGSGDNYGSLSR	3.87	1,973.83
ATP	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	11	12	15	0.13%	12.20%	KPTEDPTNDTVDFPK	3.19	1,703.81
ATP	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	11	12	15	0.13%	12.20%	KPTEDPTNDTVDFPKR	4.66	1,859.91
ATP	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	11	12	15	0.13%	12.20%	QDVYGPQPQVR	2.72	1,286.65

ATP	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	11	12	15	0.13%	12.20%	SLDNNYSTLNER	3.72	1,425.66
ATP	6018	PREDICTED: similar to catenin, delta 1	gi|194673532	106,846.20	100.00%	11	12	15	0.13%	12.20%	VSPQDASPLLANGTLTR	5.54	1,739.93
ATP	6018	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	5	6	12	0.10%	15.30%	DPLVIELGQK	3.5	1,111.64
ATP	6018	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	5	6	12	0.10%	15.30%	IFDTSLTRDPLVIELGQK	4.75	2,045.13
ATP	6018	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	5	6	12	0.10%	15.30%	RVIIPSHLAYGK	3.94	1,353.80
ATP	6018	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	5	6	12	0.10%	15.30%	VIIPSHLAYGK	2.82	1,197.70
ATP	6018	FK506 binding protein 11, 19 kDa	gi|114053349,gi|122138212,gi|82571590	22,457.80	100.00%	5	6	12	0.10%	15.30%	VIIPSHLAYGKR	1.76	1,353.80
ATP	6018	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	4	4	6	0.05%	16.40%	EEQKDFVSLYQDFENFYTR	4.04	2,458.12
ATP	6018	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	4	4	6	0.05%	16.40%	LVANFLGVEAAMAYGMGFATNSMNIPALVSK	3.11	3,203.59
ATP	6018	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	4	4	6	0.05%	16.40%	NIGVVVVGFPATPIIESR	5.54	1,868.06
ATP	6018	SPTLC2 protein	gi|148745525,gi|149642795	62,871.50	100.00%	4	4	6	0.05%	16.40%	SSAAAAAAAAGQIHHVTENGGLYK	3.97	2,295.15
ATP	6018	endoglin	gi|115497110,gi|92097469	69,885.10	99.90%	2	3	5	0.04%	3.25%	FSFLLR	1.7	782.4559
ATP	6018	endoglin	gi|115497110,gi|92097469	69,885.10	99.90%	2	3	5	0.04%	3.25%	LQAPGIPLQLAYDSK	3.99	1,613.89
ATP	6018	non-POU domain containing, octamer-binding	gi|114053303,gi|86821913	54,103.50	99.80%	2	2	2	0.02%	7.45%	GIVEFSGKPAAR	2.88	1,231.68

ATP	6018	non-POU domain containing, octamer-binding	gi|114053303,gi|86821913	54,103.50	99.80%	2	2	2	0.02%	7.45%	NLPQYVSNELLEEAFSVFGQVER	4.39	2,668.33
ATP	6018	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	4	5	6	0.05%	7.04%	DKLNPQSTYSEA	2.97	1,352.63
ATP	6018	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	4	5	6	0.05%	7.04%	IAPSSFVSSGPFLFIK	3.55	1,696.93
ATP	6018	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	4	5	6	0.05%	7.04%	SFEGNNNYDTPELR	3.62	1,655.73
ATP	6018	PREDICTED: similar to neuropilin-1 isoform 1	gi|76632212,gi|76632226	102,993.80	100.00%	4	5	6	0.05%	7.04%	TGPIQDHTGDGNFIYSQADENQK	4.52	2,535.14
ATP	6018	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	6	6	6	0.05%	13.90%	GGTGADPVQTVTGGLR	3.94	1,485.77
ATP	6018	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	6	6	6	0.05%	13.90%	LFEAEAQDLFR	3.28	1,338.67
ATP	6018	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	6	6	6	0.05%	13.90%	LIEAVDNMLTNK	3.33	1,376.71
ATP	6018	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	6	6	6	0.05%	13.90%	LPEIYIQLQR	3.19	1,272.73
ATP	6018	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	6	6	6	0.05%	13.90%	SISIIDSPGILSGEK	4.32	1,515.83
ATP	6018	PREDICTED: similar to pincher isoform 1	gi|76627466	61,009.90	100.00%	6	6	6	0.05%	13.90%	YLLEQDFPGMR	2.91	1,384.66
ATP	6018	RRAS2 protein	gi|148743916,gi|149944707	23,381.60	99.80%	2	2	2	0.02%	13.70%	LDILDTAGQEEFGAMR	4.99	1,781.84
ATP	6018	RRAS2 protein	gi|148743916,gi|149944707	23,381.60	99.80%	2	2	2	0.02%	13.70%	MNVDQAFHELVR	2.96	1,474.71
ATP	6018	STX6 protein	gi|126010683,gi|126723527	29,055.10	99.80%	2	2	2	0.02%	9.41%	AVNTAQGLFQR	3.27	1,204.64

ATP	6018	STX6 protein	gi|126010683,gi|126723527	29,055.10	99.80%	2	2	2	0.02%	9.41%	KFNLDATELSIRK	3.32	1,534.86
ATP	6018	ERGIC and golgi 2	gi|113912114,gi|115497448	42,596.10	100.00%	2	2	2	0.02%	9.28%	IDHLSFGELVPGIINPLDGTEK	2.98	2,364.25
ATP	6018	ERGIC and golgi 2	gi|113912114,gi|115497448	42,596.10	100.00%	2	2	2	0.02%	9.28%	ISADTHQFAVTER	3.01	1,474.73
ATP	6018	heme oxygenase (decycling) 2	gi|164448721	37,538.70	99.80%	2	2	2	0.02%	10.20%	AFEFNMQVFNELDQAGSLLAK	2.88	2,388.15
ATP	6018	heme oxygenase (decycling) 2	gi|164448721	37,538.70	99.80%	2	2	2	0.02%	10.20%	YMGDLSGGQVLKK	3.24	1,411.73
ATP	6018	ATPase, Na+/K+ transporting, beta 3 polypeptide	gi|74354619,gi|78369424,gi|90111969	31,504.70	99.80%	2	3	3	0.03%	8.60%	DQIPSPGLMVFPK	2.49	1,444.75
ATP	6018	ATPase, Na+/K+ transporting, beta 3 polypeptide	gi|74354619,gi|78369424,gi|90111969	31,504.70	99.80%	2	3	3	0.03%	8.60%	IIGLKPQGEPR	3	1,207.72
ATP	6018	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	gi|59858119,gi|60650208,gi|60650268,gi|61889066,gi|75070049,gi|88954151	42,933.90	100.00%	3	3	3	0.03%	11.30%	FTRPIIAGMEFSR	4.43	1,540.79
ATP	6018	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	gi|59858119,gi|60650208,gi|60650268,gi|61889066,gi|75070049,gi|88954151	42,933.90	100.00%	3	3	3	0.03%	11.30%	SDNSSHPQKDDGDNPETIMSSGNVNSSS	4.96	2,922.19
ATP	6018	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	gi|59858119,gi|60650208,gi|60650268,gi|61889066,gi|75070049,gi|88954151	42,933.90	100.00%	3	3	3	0.03%	11.30%	SKSDNSSHPQKDDGDNPETIMSSGNVNSSS	3.18	3,137.32

ATP	6018	Chromosome 20 open reading frame 108 ortholog	gi|119224079,gi|122692571	20,430.00	99.80%	2	2	2	0.02%	12.50%	ISITLVSVPLIVR	3.46	1,409.91
ATP	6018	Chromosome 20 open reading frame 108 ortholog	gi|119224079,gi|122692571	20,430.00	99.80%	2	2	2	0.02%	12.50%	VGIFKPPAAKP	2.58	1,124.68
ATP	6018	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	3	4	6	0.05%	8.01%	SISHYHETLGEALQGVELEFSGLDIK	4.32	2,872.44
ATP	6018	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	3	4	6	0.05%	8.01%	VNAVPRPIPEK	2.19	1,219.72
ATP	6018	PREDICTED: similar to mKIAA4036 protein isoform 2	gi|119917518	67,513.30	100.00%	3	4	6	0.05%	8.01%	YLDPSFFQHR	2.43	1,309.63
ATP	6018	PREDICTED: similar to Transmembrane emp24 domain-containing protein 2 precursor (Membrane protein p24A)	gi|194674620	22,715.40	99.80%	2	2	10	0.09%	12.40%	IVMFTIDIGEAPK	3.87	1,449.77
ATP	6018	PREDICTED: similar to Transmembrane emp24 domain-containing protein 2 precursor (Membrane protein p24A)	gi|194674620	22,715.40	99.80%	2	2	10	0.09%	12.40%	YTFAAHMDGTYK	3.72	1,420.62

ATP	6018	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	5	6	9	0.08%	6.12%	EATSTFTNITYR	3.78	1,403.68
ATP	6018	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	5	6	9	0.08%	6.12%	GTGDSSQITQVSPQR	4.37	1,560.76
ATP	6018	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	5	6	9	0.08%	6.12%	HVLTLTDQVTR	2.91	1,282.71
ATP	6018	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	5	6	9	0.08%	6.12%	ILEARPLSDKGTGDSSQITQVSPQR	6.05	2,683.40
ATP	6018	PREDICTED: integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) isoform 1	gi|76670657	86,518.30	100.00%	5	6	9	0.08%	6.12%	PLSDKGTGDSSQITQVSPQR	5.61	2,101.05
ATP	6018	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	6	6	10	0.09%	13.30%	ELISNASDALDKIR	3.84	1,544.83
ATP	6018	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	6	6	10	0.09%	13.30%	EQVANSAFVER	2.1	1,249.62
ATP	6018	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	6	6	10	0.09%	13.30%	GVVDSEDLPLNISR	4.63	1,513.79
ATP	6018	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	6	6	10	0.09%	13.30%	HSQFIGYPITLYLEK	3.13	1,808.96

ATP	6018	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	6	6	10	0.09%	13.30%	NPDDITQEEYGEFYK	3.72	1,847.80
ATP	6018	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	6	6	10	0.09%	13.30%	TLTLVDTGIGMTK	4.41	1,365.73
ATP	6018	heat shock 90kDa protein 1, beta	gi|118601868,gi|34392345,gi|75072499,gi|95767684	83,238.20	100.00%	6	6	10	0.09%	13.30%	YESLTDPSKLDSGK	4.17	1,539.75
ATP	6018	RecName: Full=Adiponectin; AltName: Full=Adipocyte, C1q and collagen domain-containing protein; AltName: Full=30 kDa adipocyte complement-related protein; AltName: Full=Adipocyte complement-related 30	gi|114158576,gi|146186777,gi|73697558	26,115.60	100.00%	3	3	3	0.03%	15.00%	ALLFTHDQFQDK	3.09	1,462.73
ATP	6018	RecName: Full=Adiponectin; AltName: Full=Adipocyte, C1q and collagen domain-containing protein; AltName: Full=30 kDa adipocyte complement-related protein; AltName: Full=Adipocyte complement-related 30	gi|114158576,gi|146186777,gi|73697558	26,115.60	100.00%	3	3	3	0.03%	15.00%	IFYNQQNHYDGTTGK	3.62	1,785.82

ATP	6018	RecName: Full=Adiponectin; AltName: Full=Adipocyte, C1q and collagen domain-containing protein; AltName: Full=30 kDa adipocyte complement-related protein; AltName: Full=Adipocyte complement-related 30	gi|114158576,gi|146186777,gi|73697558	26,115.60	100.00%	3	3	3	0.03%	15.00%	SAFSVGLER	2.17	965.505
ATP	6018	Solute carrier family 1 (neutral amino acid transporter), member 5	gi|115305216,gi|15145909,gi|21541958,gi|27807087	56,431.20	99.80%	2	2	4	0.03%	4.45%	EVLDSFLDLVR	3.02	1,305.71
ATP	6018	Solute carrier family 1 (neutral amino acid transporter), member 5	gi|115305216,gi|15145909,gi|21541958,gi|27807087	56,431.20	99.80%	2	2	4	0.03%	4.45%	NIFPSNLVSAAFR	3.06	1,435.77
ATP	6018	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	6	0.05%	14.10%	ALDLFSDNAPPPELLEIINEDVAK	4.37	2,623.35
ATP	6018	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	6	0.05%	14.10%	GSFSEQGINEFLR	4.06	1,483.72

ATP	6018	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	6	0.05%	14.10%	GSTAPVGGGAFPTISTR	4.14	1,575.81
ATP	6018	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	6	0.05%	14.10%	LAAVDATVNQVLASR	4.79	1,527.85
ATP	6018	PREDICTED: protein disulfide isomerase family A, member 6 isoform 7	gi|119903961,gi|151553573	64,497.70	100.00%	5	5	6	0.05%	14.10%	TGEAIVDAALSALR	3.3	1,386.76
ATP	6018	Deoxyribonuclease I-like 1	gi|151553571	35,175.30	100.00%	3	4	4	0.03%	9.49%	IVLHGEHLQSLLR	2.65	1,514.88
ATP	6018	Deoxyribonuclease I-like 1	gi|151553571	35,175.30	100.00%	3	4	4	0.03%	9.49%	SKVLPSLVLVPLHTTPK	3.41	1,829.13
ATP	6018	Deoxyribonuclease I-like 1	gi|151553571	35,175.30	100.00%	3	4	4	0.03%	9.49%	VLPSLVLVPLHTTPK	3.34	1,614.00

TABLE S1: Detailed peptide report showing treatment group, subject, protein name, protein accession numbers, protein molecular weight, protein identification probability, number (#) of unique peptides, # of unique spectra, # of total spectra, % total spectra, % sequence coverage, peptide sequence, best Sequest cross (X) correlation score, and calculated 1+H peptide mass (AMU).